Project Proposal

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Load Packages

```
library(tidyverse)
library(infer)
library(readxl)
library(skimr)
library(dplyr)
```

Load Data

```
covid1=read_excel("/home/guest/R/the-statistical-power-puffs/data/COVIDiSTRESS_May30_First.xlsx", sheet=
covid2=read_excel("/home/guest/R/the-statistical-power-puffs/data/COVIDiSTRESS_May30_Second.xlsx", shee
covid3=read_excel("/home/guest/R/the-statistical-power-puffs/data/COVIDiSTRESS_May 30_Third.xlsx", shee
covid4=read_excel("/home/guest/R/the-statistical-power-puffs/data/COVIDiSTRESS_May 30_Fourth.xlsx", she
covid5=read_excel("/home/guest/R/the-statistical-power-puffs/data/COVIDiSTRESS_May 30_Fifth.xlsx", shee
```

#Join Data

```
covidstressdata <-covid1 %>%
  full_join(covid2) %>%
  full_join(covid3) %>%
  full_join(covid4) %>%
  full_join(covid5)
```

Our dataset had to be split in order to upload to github. Here the data is joined.

Introduction and Data, including Research Questions

(The introduction should introduce your general research question and your data (where it came from, how it was collected, what are the cases, what are the variables, etc.). Your research questions should be clearly specified. The motivation for your research question should be clear, with citations to relevant literature as appropriate.)

Glimpse

This is the condensed glimpse because there are 154 variables. We have selected the first 19, but the full list can be found in the readme file.

```r
cleancovid <- subset (covidstressdata, select = -c(AD_gain, AD_loss)) #removed because of laTex incompa
glimpsecovid <- subset (covidstressdata, select = -c(Dem_maritalstatus:Scale_UCLA_TRI_avg))  #condensed
glimpse(glimpsecovid)
```

```
## Rows: 125,306
## Columns: 13
## $ ID                    <dbl> 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 1~
## $ answered_all          <chr> "No", "No", "No", "No", "No", "Yes", "Yes", "Yes~
## $ Duration..in.seconds. <dbl> 180, 3100, 127, 1710, 2239, 1221, 1283, 1442, 19~
## $ RecordedDate          <dttm> 2020-05-30 23:47:17, 2020-05-29 23:30:15, 2020-~
## $ UserLanguage          <chr> "SAR", "UR", "SAR", "BG", "SAR", "IT", "SAR", "S~
## $ Dem_age               <dbl> 29, 20, 47, 79, 61, 68, 29, 38, 35, 23, 42, 31, ~
## $ Dem_gender            <chr> "Female", "Male", "Female", "Male", "Female", "M~
## $ Dem_edu               <chr> "College degree, bachelor, master", "College deg~
## $ Dem_edu_mom           <chr> "Some College or equivalent", "None", "Some Coll~
## $ Dem_employment        <chr> "Not employed", "Student", "Self-employed", "Not~
## $ Country               <chr> "Argentina", "Pakistan", "Argentina", "Bulgaria"~
## $ Dem_Expat             <chr> "yes", "yes", "no", "no", "no", "no", "no", "no"~
## $ Dem_state             <chr> "Tucum·n", "<U+0622><U+0632><U+0627><U+062F> <U+~
```

Data Analysis Plan

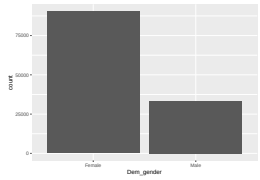
Our research question is "How do age, gender, and the level of isolation affect mental health during COVID-19 globally?" In order to answer this, our predictor variables (x) are age, gender, and level of isolation, while the outcome variables (y) are the results of several measures of psychological well-being during COVID-19. We will pick the three most relevant measures in the study: PSS10, SPS-15, and SLON-3 scales. The PSS scale measures perceived stress in an individual. SPS measures an individual's social connectedness to others. Finally, the SLON-3 scale measures loneliness in individuals. Together, we take these three scales to represent a quantitative measure of psychological well-being. The comparison groups that will be used will be two groupings of ages, the two genders, and the levels of isolation. We will then consider if the relationship between our factors and the various psychological well-being scales is statistically significant in each of our three cases.

Because this dataset is extremely large with over 125,000 observations, we will first examine the dataset by understanding the demographics of the data (the visualizations are below). Then we will calculate the mean levels of the PSS-10, SPS-15, and SLON-3 scales in different age groups, gender, and levels of isolation. We will also create sets of histograms and barplots that visualize the distribution of these scales in different age groups, gender, and levels of isolation. Finally, we will create a series of visualizations just to see the overall geographic distributions with the spatial mapping method. The statistical methods that will be useful in answering our research question would be a two-tailed, two-sample t-test. The two-tailed two-sample t-test will be used because the populations are independent from each other and we are measuring an overall difference. For the age analysis, the age groups will be collapsed into children and adults. For the gender analysis, only female and male individuals will be used while those that answered NA will be discarded. Finally, for the level of isolation, we will collapse the four values of isolation into two groups of isolated or not isolated. We will compare the mean values of our three scales of psychological well-being for a series of nine paired t-tests overall.

Our null hypothesis is that no factor has a statistically significant correlation on any scale of psychological well-being in a global population. Our alternate hypothesis for each of our tests is that age, gender, or level of isolation will have a correlation with our various scales of psychological well-being, PSS-10, SPS-15, and SLON-3. In order for our hypothesized answer to be correct, the mean levels of the well-being scales must be statistically different (p-value <0.05) when comparing mean values of the PSS-10, SPS-15, or SLON-3 scales across each of our two different scenarios of three explanatory variables (age, gender, or isolation).

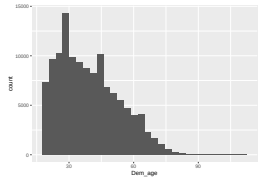
Preliminary visualizations are below.

```r
cleancovid %>%
  filter(Dem_gender %in% c("Male", "Female")) %>%
  ggplot(aes(x = Dem_gender)) + geom_bar()
```




```r
cleancovid %>%
  ggplot(aes(x = Dem_age)) + geom_histogram()
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```




```r
cleancovid %>%
  filter(Dem_isolation %in% c("Isolated", "Life carries on with minor changes", "Life carries on as usua
  ggplot(aes(x = Dem_isolation)) + geom_bar()
```