

stony brook research cleaning

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```
library(tidyverse)
```

```
## -- Attaching packages ----- tidyverse

## v ggplot2 3.3.0      v purrr 0.3.3
## v tibble 3.0.4       v dplyr 1.0.2
## v tidyr 1.0.2        v stringr 1.4.0
## v readr 1.3.1        v forcats 0.4.0

## -- Conflicts ----- tidyverse_conflict

## x dplyr::filter() masks stats::filter()
## x dplyr::lag()     masks stats::lag()

covid_data <- read_csv("~/Clare M Folder/Stony Brook Research 2/COVID-19_December 2, 2020_11.38.csv")

## Warning: Duplicated column names deduplicated: 'PAS_1' =>
## 'PAS_1_1' [126], 'PAS_2' => 'PAS_2_1' [127], 'PAS_3' => 'PAS_3_1' [128],
## 'PAS_4' => 'PAS_4_1' [129], 'PAS_5' => 'PAS_5_1' [130], 'PAS_6' =>
## 'PAS_6_1' [131], 'PAS_7' => 'PAS_7_1' [132], 'PAS_8' => 'PAS_8_1' [133],
## 'PAS_9' => 'PAS_9_1' [134], 'PAS_10' => 'PAS_10_1' [135], 'PAS_11'
## => 'PAS_11_1' [136], 'PAS_12' => 'PAS_12_1' [137], 'PAS_13'
## => 'PAS_13_1' [138], 'PAS_14' => 'PAS_14_1' [139], 'PAS_15' =>
## 'PAS_15_1' [140], 'Health_Behavior' => 'Health_Behavior_1' [240],
## 'Health_Behavior' => 'Health_Behavior_2' [241], 'Health_Behavior' =>
## 'Health_Behavior_3' [242], 'Health_Behavior' => 'Health_Behavior_4' [243],
## 'Health_Behavior' => 'Health_Behavior_5' [244], 'Health_Behavior' =>
## 'Health_Behavior_6' [245], 'Health_Behavior' => 'Health_Behavior_7' [246],
## 'Health_Behavior' => 'Health_Behavior_8' [247], 'Health_Behavior' =>
## 'Health_Behavior_9' [248], 'Health_Behavior' => 'Health_Behavior_10' [249],
## 'COVID-19_1_1' => 'COVID-19_1_1_1' [262], 'COVID-19_2_1' =>
## 'COVID-19_2_1_1' [274], 'COVID-19_2_2' => 'COVID-19_2_2_1' [275],
## 'COVID-19_2_3' => 'COVID-19_2_3_1' [276], 'COVID-19_2_4' =>
## 'COVID-19_2_4_1' [277], 'COVID-19_2_5' => 'COVID-19_2_5_1' [278],
## 'COVID-19_2_6' => 'COVID-19_2_6_1' [279], 'COVID-19_2_1' =>
## 'COVID-19_2_1_2' [280], 'COVID-19_2_2' => 'COVID-19_2_2_2' [281],
## 'COVID-19_2_3' => 'COVID-19_2_3_2' [282], 'COVID-19_2_4' =>
## 'COVID-19_2_4_2' [283], 'COVID-19_2_1' => 'COVID-19_2_1_3' [284],
## 'COVID-19_2_2' => 'COVID-19_2_2_3' [285], 'COVID-19_2_3' =>
## 'COVID-19_2_3_3' [286], 'COVID-19_2_4' => 'COVID-19_2_4_3' [287],
## 'COVID-19_2_5' => 'COVID-19_2_5_2' [288], 'COVID-19_2_6' =>
## 'COVID-19_2_6_2' [289], 'COVID-19_2_1' => 'COVID-19_2_1_4' [290],
## 'COVID-19_2_2' => 'COVID-19_2_2_4' [291], 'COVID-19_2_3' =>
## 'COVID-19_2_3_4' [292]

## Parsed with column specification:
## cols(
##   .default = col_character()
## )

## See spec(...) for full column specifications.
```

hi this is a test