

# Regression Analysis

Group 4

3/7/2021

## Hypothesis 1

Our group decided to test out 2 hypothesis for this project. This is the document for our first hypothesis.

## Read input files from github

Get the link which has the merged data from github, then read the csv file and save it as a dataframe in R for analysis.

```
link='https://raw.githubusercontent.com/Public-Policy-  
COVID/students_merge/main/Merged_data.csv'  
myFile=url(link)  
fromPy=read.csv(file = myFile)
```

## Summary results of merged data

In order to understand our merged dataset, we need to know some of the basic statistical summary for it.

```
summary(fromPy)  
  
## Number_of_beds    Number_of_hospitals    Location    Urban_Rural_Code  
## Min.      :    0.0    Min.      : 0          Length:133    Length:133  
## 1st Qu.:   25.0    1st Qu.: 1          Class :character    Class :character  
## Median :   131.0    Median : 2          Mode  :character    Mode  :character  
## Mean   :   885.4    Mean   : 5  
## 3rd Qu.:   553.0    3rd Qu.: 4  
## Max.    :26672.0    Max.    :112  
## Deaths_COVID    Deaths_total    never    rarely  
## Min.      :    0    Min.      :    0    Min.      :0.00100    Min.      :0.00000  
## 1st Qu.:    0    1st Qu.:    0    1st Qu.:0.01600    1st Qu.:0.01400  
## Median :   22    Median :   637    Median :0.02600    Median :0.02800  
## Mean   :   206    Mean   :  2896    Mean   :0.03513    Mean   :0.03806  
## 3rd Qu.:  128    3rd Qu.:  2537    3rd Qu.:0.04500    3rd Qu.:0.05600  
## Max.    :8034    Max.    :75463    Max.    :0.14000    Max.    :0.20600  
## sometimes    frequently    always    mask_score  
## Min.      :0.00400    Min.      :0.0580    Min.      :0.3050    Min.      :2.470  
## 1st Qu.:0.04800    1st Qu.:0.1410    1st Qu.:0.6160    1st Qu.:3.301  
## Median :0.06900    Median :0.1680    Median :0.6810    Median :3.464  
## Mean   :0.07167    Mean   :0.1736    Mean   :0.6814    Mean   :3.428
```

```
## 3rd Qu.:0.09100 3rd Qu.:0.2040 3rd Qu.:0.7540 3rd Qu.:3.591
## Max. :0.21300 Max. :0.3320 Max. :0.8890 Max. :3.822
## total_population white_total_pct black_total_pct asian_total_pct
## Min. : 1129 Min. :49.28 Min. : 0.000 Min. : 0.590
## 1st Qu.: 24658 1st Qu.:82.16 1st Qu.: 0.770 1st Qu.: 1.430
## Median : 79481 Median :88.64 Median : 1.260 Median : 2.010
## Mean : 385537 Mean :85.50 Mean : 2.318 Mean : 2.985
## 3rd Qu.: 283111 3rd Qu.:91.84 3rd Qu.: 2.620 3rd Qu.: 3.070
## Max. :10039107 Max. :96.13 Max. :14.770 Max. :25.690
## asian_total_pct nhopi_total_pct multiracial_total_pct
## Min. : 0.500 Min. :0.0000 Min. :1.200
## 1st Qu.: 1.210 1st Qu.:0.2100 1st Qu.:3.160
## Median : 1.870 Median :0.2800 Median :3.720
## Mean : 4.961 Mean :0.3838 Mean :3.856
## 3rd Qu.: 5.840 3rd Qu.:0.4500 3rd Qu.:4.440
## Max. :39.020 Max. :1.7100 Max. :7.800
```

## Test hypothesis

We use regression when we have a continuous outcome or dependent variable, and a set of independent variables which can be of different types.

Run a regression to test the hypothesis that as number of hospitals, number of hospital beds and total\_population increases, covid deaths increase and as mask score increases covid deaths decrease.

We use the glm function in R to run a linear regression.

```
hypo1 = formula(Deaths_COVID~
Number_of_hospitals+Number_of_beds+mask_score+total_population)
gauss1=glm(hypo1,
           data = fromPy,
           family = 'gaussian')
```

See the results of our linear regression.

```
summary(gauss1)

##
## Call:
## glm(formula = hypo1, family = "gaussian", data = fromPy)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -670.42   -18.47    24.92    62.44   648.61
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  4.873e+02  2.254e+02  2.161 0.032530 *
## Number_of_hospitals 2.234e+01  9.516e+00  2.348 0.020429 *
## Number_of_beds      7.056e-02  3.975e-02  1.775 0.078268 .
```

```
## mask_score          -1.679e+02  6.596e+01  -2.545 0.012106 *
## total_population    3.114e-04  9.110e-05   3.418 0.000845 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 26565.43)
##
##      Null deviance: 76635132  on 132  degrees of freedom
## Residual deviance: 3400375   on 128  degrees of freedom
## AIC: 1739.3
##
## Number of Fisher Scoring iterations: 2
```

Get R squared of the model. R-squared is the percentage of the dependent variable variation that a linear model explains. R-squared helps us decide how effective this model is and compare it with other hypothesis as well.

```
library(rsq)
rsq(gauss1,adj=T)
## [1] 0.9542424
```

## Summary plots

In order to visualize the results of our hypothesis and the dependent variables, we use different summary plots.

Plotting the regression coefficients.

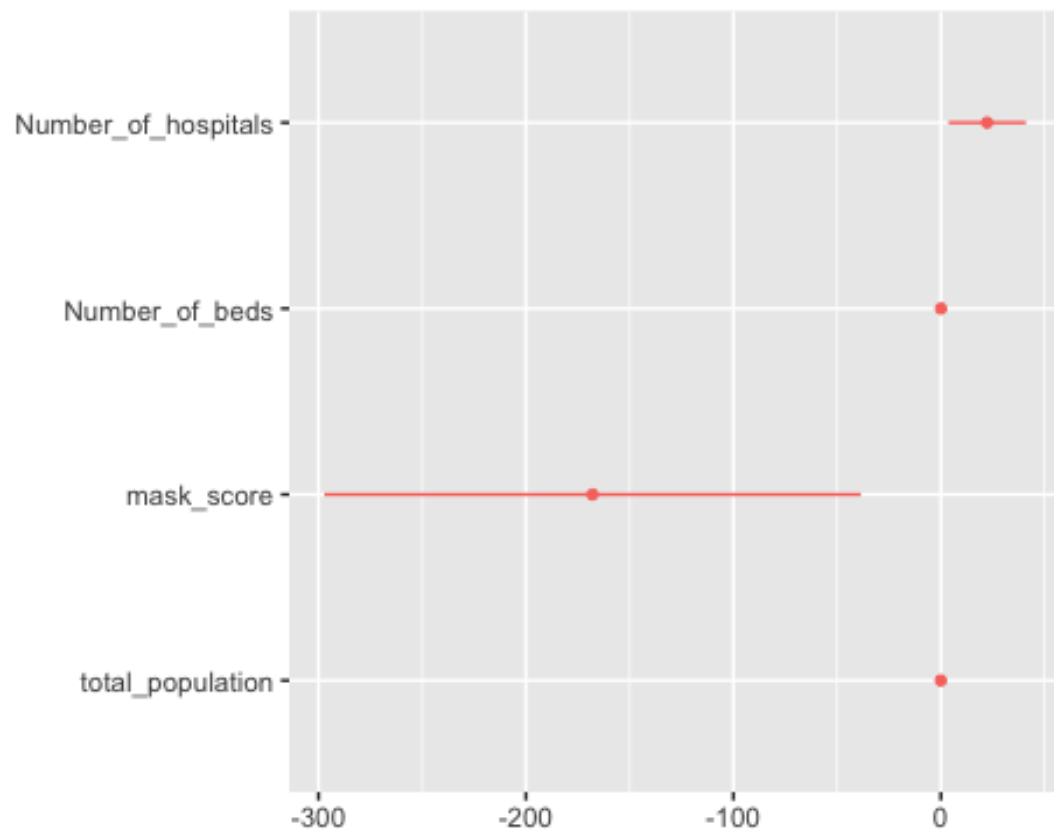
```
# Summary plots
library(dotwhisker)

## Loading required package: ggplot2

## Warning in checkMatrixPackageVersion(): Package version inconsistency
detected.
## TMB was built with Matrix version 1.3.2
## Current Matrix version is 1.2.18
## Please re-install 'TMB' from source using install.packages('TMB', type =
'source') or ask CRAN for a binary version of 'TMB' matching CRAN's 'Matrix'
package

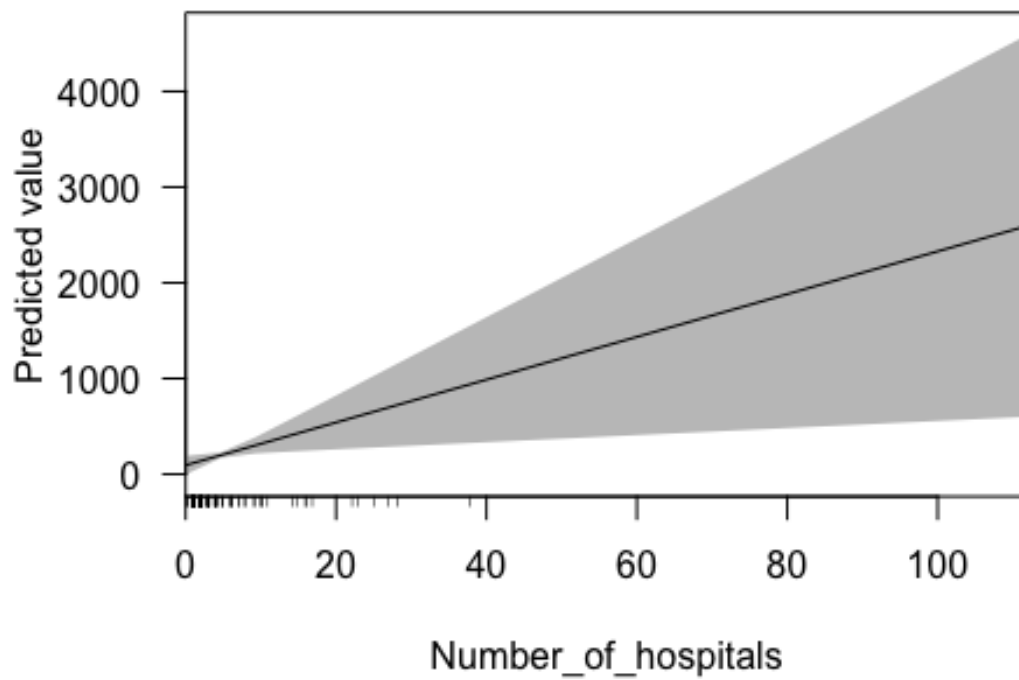
## Registered S3 method overwritten by 'broom.mixed':
##   method      from
##   tidy.gamlss broom

dwplot(gauss1,by_2sd = F)
```



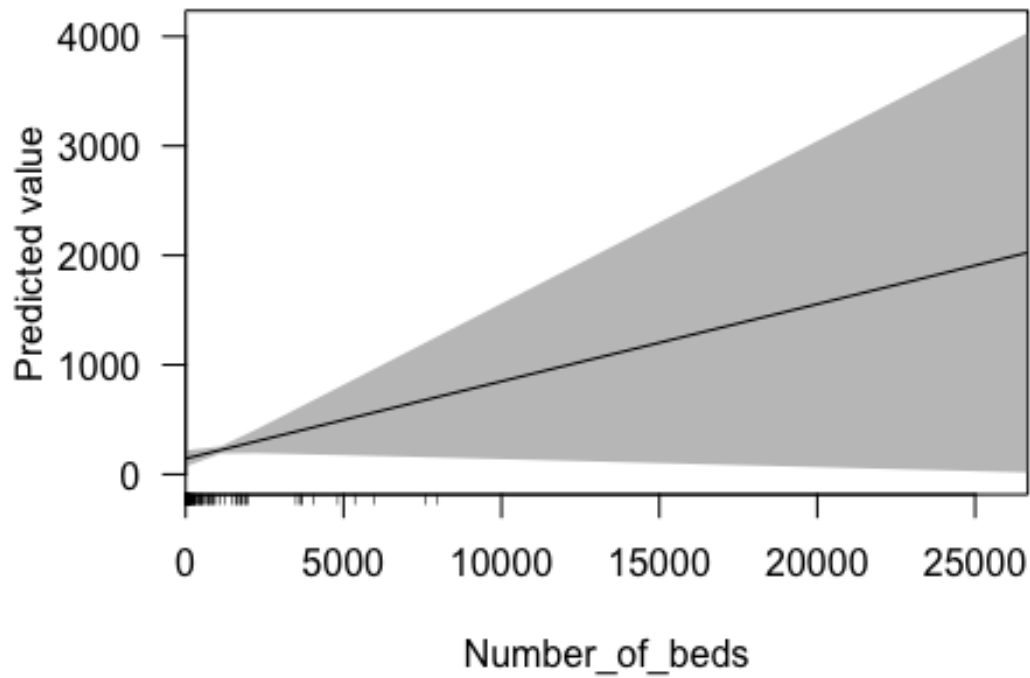
Margin plot for number of hospitals variable.

```
library(margins)
cplot(gauss1, 'Number_of_hospitals')
```



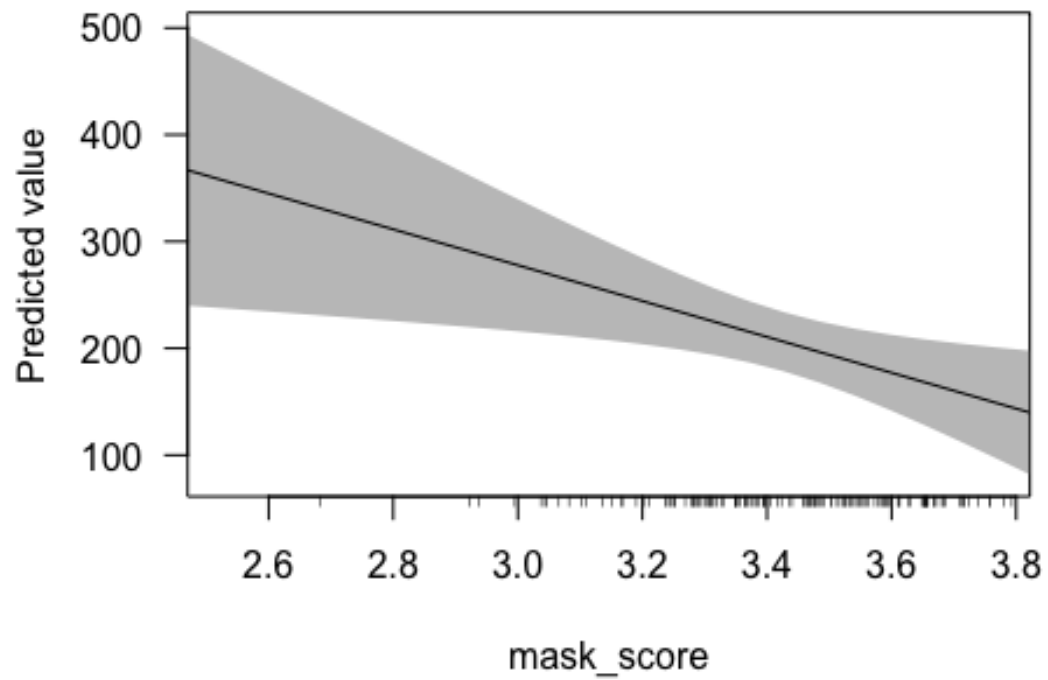
Margin plot for number of beds variable.

```
cplot(gauss1, 'Number_of_beds')
```



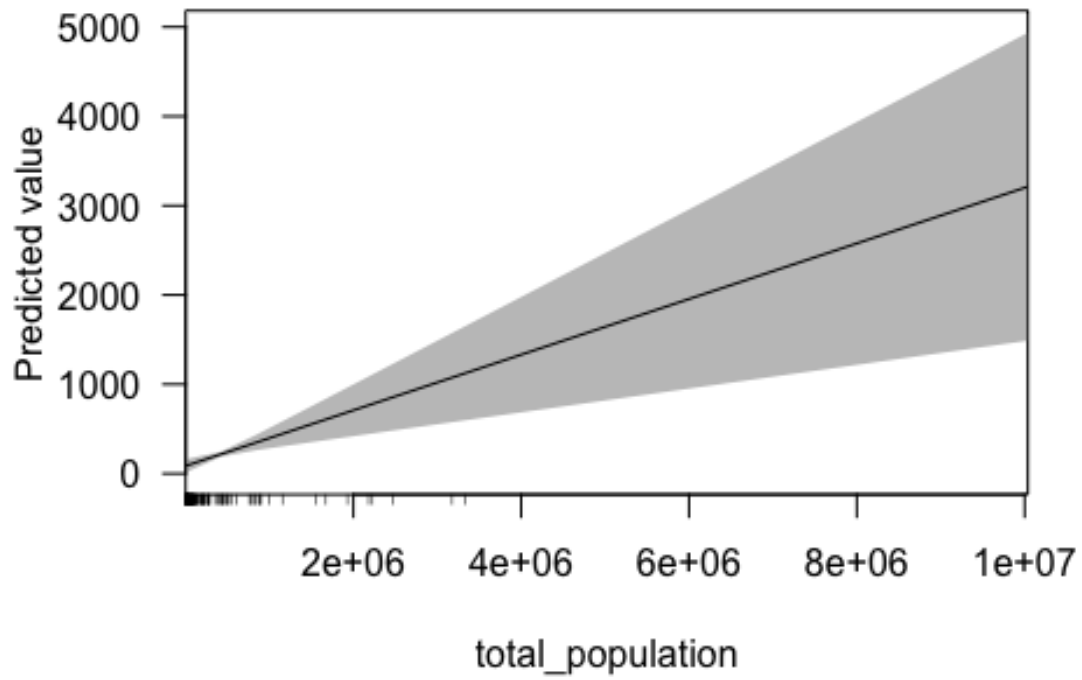
Margin plot for mask score variable.

```
cplot(gauss1, 'mask_score')
```



Margin plot for total population variable.

```
cplot(gauss1, 'total_population')
```



Plot interaction between variables.

```
persp(gauss1)
```



