

Final Report

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Load Packages

```
library(tidyverse)
library(tidymodels)
library(readxl)
library(dbplyr)
library(ggplot2)
```

Load Data

```
load(file = "~/sta198/Jackie-Fan-Club/data/ICPSR_34363/DS0001/34363-0001-Data.rda")
#rename file
data <- da34363.0001
```

Data Citation: Battle, Juan, Pastrana, Antonio Jay, and Daniels, Jessie. Social Justice Sexuality Project: 2010 National Survey, including Puerto Rico. Ann Arbor, MI: Inter-university Consortium for Political and Social Research [distributor], 2013-08-09. <https://doi.org/10.3886/ICPSR34363.v1>

Data Analysis

To evaluate statistically significant impacts on health outcomes due to sexuality, gender, race, and intersectional identities, we ran a few statistical tests.

```
##
## Call:
## glm(formula = healthInsureAcc ~ race + gender_trans + sexuality_queer,
##      family = "binomial", data = data_relevel)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.9549   0.5782   0.6400   0.7339   0.9823
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)    1.45824    0.14642   9.959  < 2e-16 ***
## raceAsian       0.29236    0.18593   1.572  0.11586
## raceBlack       0.06985    0.10489   0.666  0.50548
## raceHispanic   -0.47353    0.11962  -3.959 7.54e-05 ***
## raceMultiracial -0.23755    0.10799  -2.200  0.02782 *
```

```

## raceNative      -0.59574    0.33724  -1.767  0.07731 .
## raceOther       -0.34082    0.25905  -1.316  0.18828
## gender_trans1   -0.33816    0.11871  -2.849  0.00439 **
## sexuality_queer1 -0.04648    0.12939  -0.359  0.71941
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##    Null deviance: 4916.6  on 4682  degrees of freedom
## Residual deviance: 4868.7  on 4674  degrees of freedom
##    (270 observations deleted due to missingness)
## AIC: 4886.7
##
## Number of Fisher Scoring iterations: 4
##
## Call:
## glm(formula = healthProvideAcc ~ race + gender_trans + sexuality_queer,
##      family = "binomial", data = data_relevel)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.9047   0.6097   0.7018   0.7359   0.9721
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)   1.275621   0.142233   8.969 < 2e-16 ***
## raceAsian     -0.115076   0.161243  -0.714  0.475425
## raceBlack      0.320888   0.103583   3.098  0.001949 **
## raceHispanic  -0.323065   0.117352  -2.753  0.005906 **
## raceMultiracial -0.099533   0.105247  -0.946  0.344294
## raceNative     0.368565   0.400993   0.919  0.358027
## raceOther      0.064777   0.274042   0.236  0.813140
## gender_trans1  -0.440056   0.117257  -3.753  0.000175 ***
## sexuality_queer1 -0.008221   0.126545  -0.065  0.948199
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##    Null deviance: 4958.5  on 4670  degrees of freedom
## Residual deviance: 4904.5  on 4662  degrees of freedom
##    (282 observations deleted due to missingness)
## AIC: 4922.5
##
## Number of Fisher Scoring iterations: 4
##
## Call:
## glm(formula = healthInsureAcc ~ race * gender_trans + gender_trans *
##      sexuality_queer + sexuality_queer * race, family = "binomial",
##      data = data_relevel)
##
## Deviance Residuals:

```

```

##      Min      1Q   Median      3Q      Max
## -1.9988  0.5775  0.6460   0.7459   1.1871
##
## Coefficients:
##
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)      0.80426    0.26626   3.021  0.00252 **
## raceAsian        1.04763    0.51592   2.031  0.04230 *
## raceBlack        0.90561    0.36293   2.495  0.01259 *
## raceHispanic     0.44759    0.41109   1.089  0.27625
## raceMultiracial  0.54466    0.36802   1.480  0.13888
## raceNative     -0.31644    1.67292  -0.189  0.84997
## raceOther       -0.50990    0.73280  -0.696  0.48654
## gender_trans1   -0.33030    0.44236  -0.747  0.45526
## sexuality_queer1  0.69278    0.27897   2.483  0.01302 *
## raceAsian:gender_trans1  0.01243    0.60269   0.021  0.98355
## raceBlack:gender_trans1  0.26002    0.35185   0.739  0.45990
## raceHispanic:gender_trans1  0.05596    0.44613   0.125  0.90018
## raceMultiracial:gender_trans1  0.40846    0.34952   1.169  0.24256
## raceNative:gender_trans1 -0.15752    0.82461  -0.191  0.84851
## raceOther:gender_trans1  0.01304    0.61666   0.021  0.98313
## gender_trans1:sexuality_queer1 -0.22731    0.40448  -0.562  0.57414
## raceAsian:sexuality_queer1 -0.83778    0.54873  -1.527  0.12682
## raceBlack:sexuality_queer1 -0.94187    0.37634  -2.503  0.01232 *
## raceHispanic:sexuality_queer1 -1.01951    0.42852  -2.379  0.01735 *
## raceMultiracial:sexuality_queer1 -0.90439    0.38226  -2.366  0.01799 *
## raceNative:sexuality_queer1 -0.24233    1.62682  -0.149  0.88158
## raceOther:sexuality_queer1  0.25343    0.77473   0.327  0.74358
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 4916.6  on 4682  degrees of freedom
## Residual deviance: 4855.8  on 4661  degrees of freedom
## (270 observations deleted due to missingness)
## AIC: 4899.8
##
## Number of Fisher Scoring iterations: 4
##
## Call:
## glm(formula = healthProvideAcc ~ race * gender_trans + gender_trans *
##       sexuality_queer + sexuality_queer * race, family = "binomial",
##       data = data_relevel)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.9876   0.6034   0.6661   0.7341   1.1118
##
## Coefficients:
##
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)      0.82666    0.26830   3.081  0.00206 **
## raceAsian        0.56621    0.46303   1.223  0.22139
## raceBlack        0.78447    0.36138   2.171  0.02995 *

```

```

## raceHispanic          0.24256    0.40080    0.605    0.54504
## raceMultiracial       0.34510    0.36168    0.954    0.34000
## raceNative            12.15323   229.63045    0.053    0.95779
## raceOther             0.03062    0.77701    0.039    0.96857
## gender_trans1        -0.17389    0.44418   -0.391    0.69544
## sexuality_queer1      0.49386    0.27989    1.764    0.07765
## raceAsian:gender_trans1 -0.41998    0.52078   -0.806    0.42000
## raceBlack:gender_trans1 0.38869    0.35516    1.094    0.27378
## raceHispanic:gender_trans1 0.38897    0.46113    0.843    0.39895
## raceMultiracial:gender_trans1 0.07483    0.33657    0.222    0.82405
## raceNative:gender_trans1 -0.23994    0.88561   -0.271    0.78644
## raceOther:gender_trans1 -0.51226    0.63813   -0.803    0.42212
## gender_trans1:sexuality_queer1 -0.42527    0.40179   -1.058    0.28986
## raceAsian:sexuality_queer1 -0.71129    0.49050   -1.450    0.14703
## raceBlack:sexuality_queer1 -0.54599    0.37493   -1.456    0.14532
## raceHispanic:sexuality_queer1 -0.64560    0.41821   -1.544    0.12265
## raceMultiracial:sexuality_queer1 -0.49195    0.37553   -1.310    0.19018
## raceNative:sexuality_queer1 -11.78735   229.62994   -0.051    0.95906
## raceOther:sexuality_queer1 0.24841    0.82073    0.303    0.76214
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 4958.5 on 4670 degrees of freedom
## Residual deviance: 4893.5 on 4649 degrees of freedom
## (282 observations deleted due to missingness)
## AIC: 4937.5
##
## Number of Fisher Scoring iterations: 11

##   Resid. Df   Resid. Dev      Df    Deviance    Pr(>Chi)
## Min.    :4661   Min.    :4856   Min.    :13   Min.    :12.93   Min.    :0.4535
## 1st Qu.:4664   1st Qu.:4859   1st Qu.:13   1st Qu.:12.93   1st Qu.:0.4535
## Median :4668   Median :4862   Median :13   Median :12.93   Median :0.4535
## Mean    :4668   Mean    :4862   Mean    :13   Mean    :12.93   Mean    :0.4535
## 3rd Qu.:4671   3rd Qu.:4865   3rd Qu.:13   3rd Qu.:12.93   3rd Qu.:0.4535
## Max.    :4674   Max.    :4869   Max.    :13   Max.    :12.93   Max.    :0.4535
##                                     NA's    :1   NA's    :1   NA's    :1

##   Resid. Df   Resid. Dev      Df    Deviance    Pr(>Chi)
## Min.    :4649   Min.    :4894   Min.    :13   Min.    :11.03   Min.    :0.6082
## 1st Qu.:4652   1st Qu.:4896   1st Qu.:13   1st Qu.:11.03   1st Qu.:0.6082
## Median :4656   Median :4899   Median :13   Median :11.03   Median :0.6082
## Mean    :4656   Mean    :4899   Mean    :13   Mean    :11.03   Mean    :0.6082
## 3rd Qu.:4659   3rd Qu.:4902   3rd Qu.:13   3rd Qu.:11.03   3rd Qu.:0.6082
## Max.    :4662   Max.    :4905   Max.    :13   Max.    :11.03   Max.    :0.6082
##                                     NA's    :1   NA's    :1   NA's    :1

```

We ran a multiple regression for each health insurance access and health provider access conditional on gender, race, and sexuality. We saw that our referent group of white, cis, heterosexual individuals are 1.47 as likely to have health insurance than non-white, trans, non-heterosexual counterparts and 1.32 times as likely for access to a regular healthcare provider.

Sexuality is a complicated variable to work with, given that the question posed in the survey offers 12 options that are not all mutually exclusive, yet the answer given must be only one of the above. Also, to retain all

options given would overcomplicate and weaken the model. Therefore, we decided to distinguish between heterosexual and all other sexuality answers in our subsequent models.

In healthcare access, we found that the most negatively affected race group was Hispanic and the most negatively affected gender group was transgender individuals.

We conducted another multiple regression with interaction terms, in order to evaluate intersection of gender and race groups.

```
summary(aov(Q18C~Q25,data=data_filtered2))

##              Df Sum Sq Mean Sq F value    Pr(>F)
## Q25              1    112  111.57    13.73 0.000213 ***
## Residuals    4552  36974     8.12
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 399 observations deleted due to missingness

sexpair <- pairwise.t.test(data_filtered2$Q18C,data_filtered2$Q25, p.adj = "holm")
sigpairs <- broom::tidy(sexpair) %>%
  filter(p.value<0.05) %>%
  arrange(group1,group2)
nrow(sigpairs)

## [1] 2

print(sigpairs)

## # A tibble: 2 x 3
##   group1 group2 p.value
##   <chr>  <chr>   <dbl>
## 1 4      2      0.0217
## 2 5      2      0.0186

4: 2-spirit 5: queer
```