FMPH 222 - Final Project

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Libraries Used

```r
library(ggplot2)
library(car)
library(tableone)
library(dplyr)
library(logistf)
library(generalhoslem)
library(ggfortify)
library(ggpubr)
```

To:Do

```r
# Maybe parse the Histology variables differently.

# 0.1 pvalue cut off

# Ignore Treatment
# Ignore other IRAEs

# --- Presentation ---
# Make sure to mention this is an explanatory analysis
```

Data Cleaning

```r
# dt <- read.csv("tumor_data.csv")
dt <- read.csv("tumor_data.csv")

# --- Column form changes ---
colnames(dt)[5] <- "Ethnicity"
colnames(dt)[2] <- "Adverse.Events"

# Change to Numeric
dt$Age <- as.numeric(dt$Age) # Row 1 is an NA value
dt$Age[1] <- 90

dt$PFS..months. <- as.numeric(dt$PFS..months.)

# Change to Factor
dt$GENDER <- as.factor(dt$GENDER)
dt$Ethnicity <- as.factor(dt$Ethnicity)
```

```r
dt$Blood.type. <- as.factor(dt$Blood.type.)
dt$Histology <- as.factor(dt$Histology)
dt$Adverse.Events <- as.factor(dt$Adverse.Events)

# Change Histology to 3 variables only

dt$Histology2 <-
  ifelse(dt$Histology == "Lung" | dt$Histology == "Breast",
         dt$Histology,"Other")

dt$Histology2 <- as.factor(dt$Histology2)

levels(dt$Histology2) <- c("Breast", "Lung", "Other")

# Change Histology to how the paper did it
list_of_Histologies = as.vector(unique(dt$Histology))
list_of_Histologies = list_of_Histologies[!list_of_Histologies %in% c("Skin", "Lung", "Breast")]

dt$Histology3 = dt$Histology

for (i in list_of_Histologies){
  dt$Histology3 = gsub(i, "Other", dt$Histology3)
}

levels(dt$Histology3) <- c("Lung", "Breast", "Skin",  "Other")
dt$Histology3 <- as.factor(dt$Histology3)

# Change O blood vs type A/B/AB blood
dt <- dt %>%
  mutate(
    # Create Categories
    Blood.type.cat = dplyr::case_when(
      Blood.type. %in%  c("A-", "A+", "AB+", "B-", "B+") ~ "A/B/AB",
      Blood.type. %in% c("O-", "O+") ~ "O"
  )
)

dt$Blood.type.cat <- as.factor(dt$Blood.type.cat)

# Change Ethnicity Column

dt <- dt %>%
  mutate(
    # Create Categories
    Ethnicity.2 = dplyr::case_when(
      Ethnicity %in%  c("Asian", "Black", "Hispanic") ~ "Other",
      Ethnicity %in% c("White") ~ "White"
  )
)

dt$Ethnicity.2 <- as.factor(dt$Ethnicity.2)

# Change Age Column
```

```
# Categorize Age
dt <- dt %>%
  mutate(
    # Create Categories
    Age.cat = dplyr::case_when(
      Age >= 28 & Age <= 65 ~ "28-65",
      Age > 65 ~ "65-90"
    )
    )

dt$Age.cat <- factor(dt$Age.cat, levels = c("28-65", "65-90"))
```

Summary Statistics

```
# Variables of Interest
myVars <- c("Age.cat", "Ethnicity.2", "GENDER",
            "Histology3", "Adverse.Events")

# Table Creation
table_3 <- CreateTableOne(vars = myVars, strata = "Blood.type.cat",
                          data = dt)
print(table_3, formatOptions = list(big.mark = ","))
```

```
##                        Stratified by Blood.type.cat
##                          A/B/AB        O           p       test
##   n                      73           47
##   Age.cat = 65-90 (%)    22 (30.1)    14 (29.8)    1.000
##   Ethnicity.2 = White (%) 54 (74.0)   31 (66.0)    0.461
##   GENDER = Male (%)       43 (58.9)   25 (53.2)    0.669
##   Histology3 (%)                                   0.488
##       Breast              2 ( 2.7)     4 ( 8.5)
##       Lung               16 (21.9)     8 (17.0)
##       Other              43 (58.9)    26 (55.3)
##       Skin               12 (16.4)     9 (19.1)
##   Adverse.Events = 1 (%) 24 (32.9)    24 (51.1)    0.073
```

Plots

```
# Blood Type Histogram
ggplot(dt,aes(x=Blood.type.cat)) +
  geom_bar(fill="steelblue",color="black") +
  labs(x="Patient Blood Type", title="Blood Type Counts")
```

Blood Type Counts
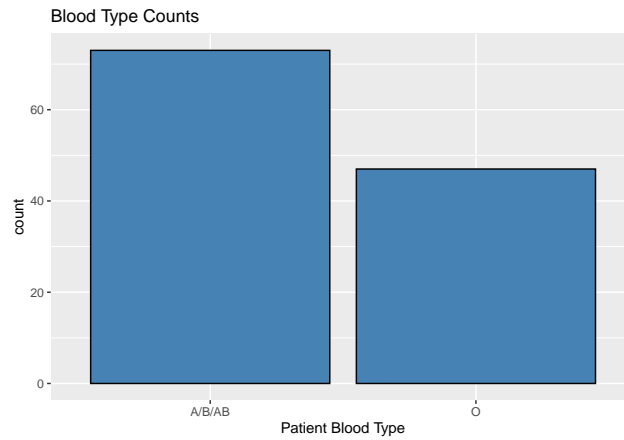

```
# Adverse.Events
ggplot(dt,aes(x=Adverse.Events)) +
  geom_bar(fill="steelblue",color="black") +
  labs(x="IRAE Indicator", title="Immune Related Adverse Event Counts")
```
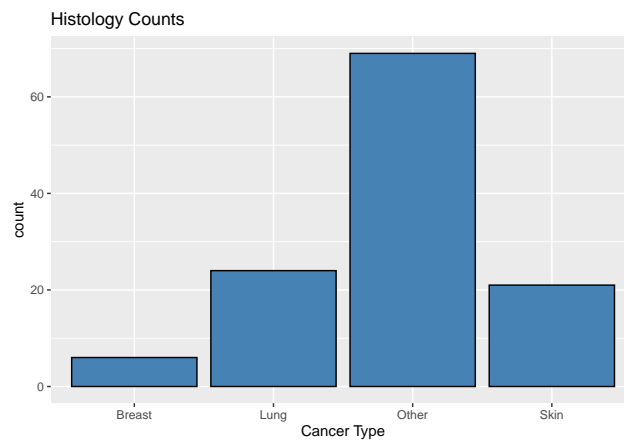
Immune Related Adverse Event Counts
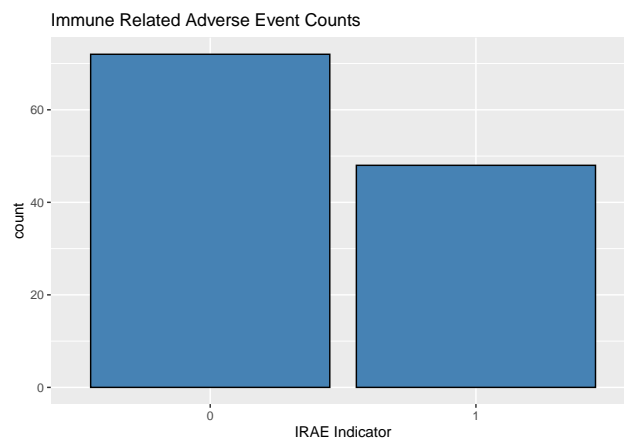

```
# Histology
ggplot(dt,aes(x=Histology3)) +
  geom_bar(fill="steelblue",color="black") +
  labs(x="Cancer Type", title="Histology Counts")
```

Histology Counts

```
## could be causing major problems
```

Pre-Analysis

```
# --- Old Analysis ---

m1 <- glm(Adverse.Events ~ Blood.type. + Ethnicity + Age, family = binomial,
          data = dt )
summary(m1)
```

```
##
## Call:
## glm(formula = Adverse.Events ~ Blood.type. + Ethnicity + Age,
##     family = binomial, data = dt)
##
## Deviance Residuals:
##     Min      1Q  Median      3Q     Max
## -1.4384  -0.9987  -0.6886   1.1211   1.8876
##
## Coefficients:
##                   Estimate Std. Error z value Pr(>|z|)
## (Intercept)       -1.06995    1.50323  -0.712   0.4766
## Blood.type.A+     -1.73253    0.70752  -2.449   0.0143 *
## Blood.type.AB+    -1.08570    1.06224  -1.022   0.3067
## Blood.type.B-     -0.98075    1.37152  -0.715   0.4746
## Blood.type.B+     -1.15779    0.81033  -1.429   0.1531
## Blood.type.O-     -0.51953    1.00693  -0.516   0.6059
## Blood.type.O+     -0.45983    0.66380  -0.693   0.4885
## EthnicityBlack     0.99812    1.38130   0.723   0.4699
## EthnicityHispanic  0.85546    1.29283   0.662   0.5082
## EthnicityWhite     0.70278    1.21069   0.580   0.5616
## Age                0.01396    0.01599   0.873   0.3826
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 161.52  on 119  degrees of freedom
## Residual deviance: 149.79  on 109  degrees of freedom
## AIC: 171.79
##
## Number of Fisher Scoring iterations: 4
```

```
m2 <- glm(Adverse.Events ~ Blood.type. + Ethnicity + Age + Histology2,
          family = binomial , data = dt )
summary(m2)
```

```
##
## Call:
## glm(formula = Adverse.Events ~ Blood.type. + Ethnicity + Age +
##     Histology2, family = binomial, data = dt)
##
## Deviance Residuals:
##     Min      1Q  Median      3Q     Max
```

```
## -1.470  -1.042  -0.673   1.147   1.903
##
## Coefficients:
##                  Estimate Std. Error z value Pr(>|z|)
## (Intercept)      -1.06839    1.67584  -0.638   0.5238
## Blood.type.A+    -1.78748    0.71480  -2.501   0.0124 *
## Blood.type.AB+   -1.06506    1.07035  -0.995   0.3197
## Blood.type.B-    -1.10510    1.38983  -0.795   0.4265
## Blood.type.B+    -1.15051    0.81024  -1.420   0.1556
## Blood.type.O-    -0.46451    1.02375  -0.454   0.6500
## Blood.type.O+    -0.44741    0.66685  -0.671   0.5023
## EthnicityBlack    0.91241    1.38534   0.659   0.5101
## EthnicityHispanic 0.82944    1.30138   0.637   0.5239
## EthnicityWhite    0.65377    1.21552   0.538   0.5907
## Age               0.01012    0.01687   0.600   0.5484
## Histology2Lung    0.60413    1.07334   0.563   0.5735
## Histology2Other   0.20626    0.97841   0.211   0.8330
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 161.52  on 119  degrees of freedom
## Residual deviance: 149.13  on 107  degrees of freedom
## AIC: 175.13
##
## Number of Fisher Scoring iterations: 4
```

```
anova(m1,m2)
```

Resid. Df	Resid. Dev	Df	Deviance
109	149.7938	NA	NA
107	149.1257	2	0.6681261

```
# Blood type A+ is significant (THE ONLY ONE too)
```

Initial Analysis

```
# Main variable of interest:
# Y = Adverse.Events
# X_n = Blood.type.cat, Histology3
# Confounders: Ethnicity, Age, Gender

# DO NOT INCLUDE variables:
# - Treatment..Clean.
# - PFS..months.

m1 <- glm(Adverse.Events ~ Blood.type.cat + Ethnicity.2 + Age + Histology3 +
    GENDER, family = binomial, data = dt)

summary(m1)
```

```
##
```

```
## Call:
## glm(formula = Adverse.Events ~ Blood.type.cat + Ethnicity.2 +
##     Age + Histology3 + GENDER, family = binomial, data = dt)
##
## Deviance Residuals:
##     Min      1Q   Median      3Q      Max
## -1.4638  -1.0185  -0.7623   1.2504   1.7684
##
## Coefficients:
##                  Estimate Std. Error z value Pr(>|z|)
## (Intercept)      -1.92667    1.22995  -1.566    0.117
## Blood.type.cat0   0.77276    0.39942   1.935    0.053 .
## Ethnicity.2White  0.07563    0.43094   0.175    0.861
## Age               0.01331    0.01644   0.809    0.418
## Histology3Lung    0.83844    1.03340   0.811    0.417
## Histology3Other   0.73765    0.97150   0.759    0.448
## Histology3Skin    0.93112    1.06295   0.876    0.381
## GENDERMale       -0.69448    0.42269  -1.643    0.100
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 161.52  on 119  degrees of freedom
## Residual deviance: 153.43  on 112  degrees of freedom
## AIC: 169.43
##
## Number of Fisher Scoring iterations: 4
```

```
(H_L_m1 = generalhoslem::logitgof(dt$Adverse.Events,m1$fitted.values))
```

```
##
##  Hosmer and Lemeshow test (binary model)
##
## data:  dt$Adverse.Events, m1$fitted.values
## X-squared = 3.4314, df = 8, p-value = 0.9044
```

Linear Model Check

```
# reduced - treat histology as linear term
dt$Histology.lin[dt$Histology3=="Breast"] <- 1
dt$Histology.lin[dt$Histology3=="Lung"] <- 2
dt$Histology.lin[dt$Histology3=="Skin"] <- 3
dt$Histology.lin[dt$Histology3=="Other"] <- 4


m1.lin <- glm(Adverse.Events ~ Blood.type.cat + Ethnicity.2 + Age + Histology.lin+
    GENDER, family = binomial, data = dt)

anova(m1.lin,m1,test="LRT")
```

Resid. Df	Resid. Dev	Df	Deviance	Pr(>Chi)
114	154.2508	NA	NA	NA
112	153.4337	2	0.8171169	0.6646076

```
# p-value 0.39 -> linear model is better

summary(m1.lin)


##
## Call:
## glm(formula = Adverse.Events ~ Blood.type.cat + Ethnicity.2 +
##     Age + Histology.lin + GENDER, family = binomial, data = dt)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.4037  -1.0051  -0.7766   1.2333   1.7676
##
## Coefficients:
##                  Estimate Std. Error z value Pr(>|z|)
## (Intercept)      -1.44693    1.14806  -1.260   0.2076
## Blood.type.cat0   0.73290    0.39158   1.872   0.0613 .
## Ethnicity.2White  0.07014    0.42880   0.164   0.8701
## Age               0.01513    0.01536   0.985   0.3245
## Histology.lin     0.04320    0.20635   0.209   0.8342
## GENDERMale       -0.60907    0.39804  -1.530   0.1260
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 161.52  on 119  degrees of freedom
## Residual deviance: 154.25  on 114  degrees of freedom
## AIC: 166.25
##
## Number of Fisher Scoring iterations: 4
# blood type is no longer significant
# stick with m1
```

Backwards Selection

```
# backward() function
m1.back <- logistf(Adverse.Events ~ Ethnicity.2 + Age + GENDER,
                family = binomial(link="logit"), data = dt)
mod.m1.back <- backward(m1.back,slstay=0.1)


## Step  0 : starting model
## Step  1 : removed  Ethnicity.2 GENDER  (P= 1 )

summary(mod.m1.back)


## logistf(formula = Adverse.Events ~ Age + GENDER, data = dt, family = binomial(link = "logit"))
##
## Model fitted by Penalized ML
## Coefficients:
##                   coef    se(coef)  lower 0.95 upper 0.95    Chisq         p
## (Intercept) -0.99012522 0.89515793 -2.79745993 0.74491528 1.241711 0.2651416
## Age          0.01572507 0.01462231 -0.01262653 0.04521729 1.172459 0.2788965
## GENDERMale  -0.59350925 0.37490212 -1.33671698 0.13842755 2.524117 0.1121175
```

```
##             method
## (Intercept)    2
## Age            2
## GENDERMale     2
##
## Method: 1-Wald, 2-Profile penalized log-likelihood, 3-None
##
## Likelihood ratio test=3.603624 on 2 df, p=0.1649996, n=120
## Wald test = 7.705891 on 2 df, p = 0.02121715
```

```
# add main variables
m2 <- glm(Adverse.Events ~ Age + GENDER + Blood.type.cat + Histology3,
          family = binomial(link="logit"), data=dt)
summary(m2)
```

```
##
## Call:
## glm(formula = Adverse.Events ~ Age + GENDER + Blood.type.cat +
##     Histology3, family = binomial(link = "logit"), data = dt)
##
## Deviance Residuals:
##     Min      1Q  Median      3Q     Max
## -1.4531  -1.0100  -0.7663   1.2552   1.7801
##
## Coefficients:
##                 Estimate Std. Error z value Pr(>|z|)
## (Intercept)     -1.88454    1.20494  -1.564   0.1178
## Age              0.01363    0.01637   0.833   0.4051
## GENDERMale      -0.68984    0.42169  -1.636   0.1019
## Blood.type.catO  0.76607    0.39740   1.928   0.0539 .
## Histology3Lung   0.83350    1.03226   0.807   0.4194
## Histology3Other  0.72893    0.96915   0.752   0.4520
## Histology3Skin   0.92430    1.06147   0.871   0.3839
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 161.52  on 119  degrees of freedom
## Residual deviance: 153.46  on 113  degrees of freedom
## AIC: 167.46
##
## Number of Fisher Scoring iterations: 4
```

Comparing The Two Models

```
anova(m1, m2, test = "LRT")
```

Resid. Df	Resid. Dev	Df	Deviance	Pr(>Chi)
112	153.4337	NA	NA	NA
113	153.4646	-1	-0.0308687	0.8605337

```
influencePlot(m2)
```
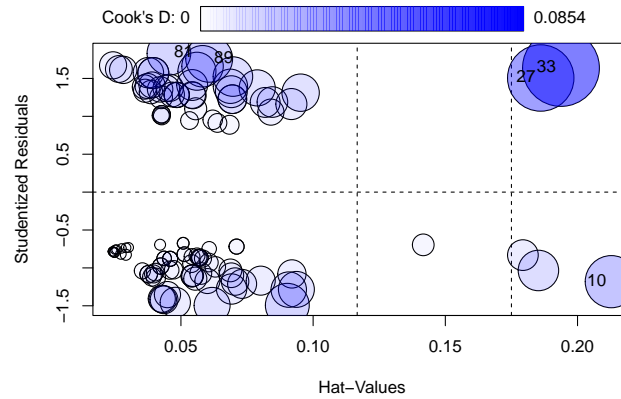

	StudRes	Hat	CookD
10	-1.181731	0.2127751	0.0394053
27	1.505868	0.1860824	0.0638358
33	1.637955	0.1937406	0.0853923
81	1.831165	0.0454517	0.0276204
89	1.758988	0.0606842	0.0317539

```
influencePlot(m1)
```
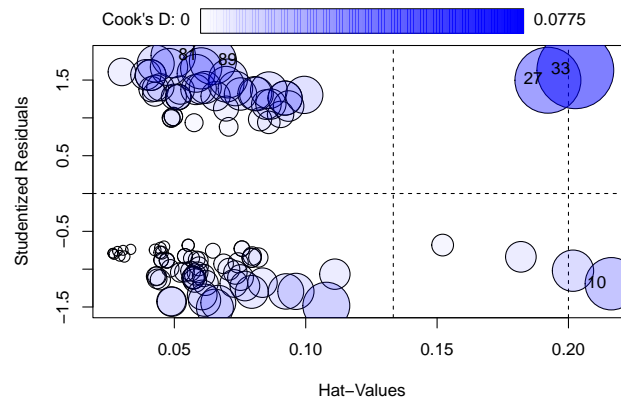

	StudRes	Hat	CookD
10	-1.192633	0.2163074	0.0360476
27	1.497613	0.1921835	0.0571287
33	1.629499	0.2026208	0.0775135
81	1.823276	0.0495818	0.0259101
89	1.751030	0.0646816	0.0291471

```
autoplot(m2)
```
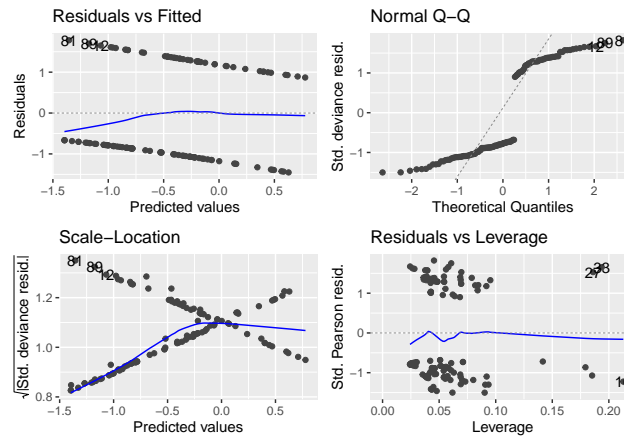
Hosmer Lemeshow Test

```
(H_L = generalhoslem::logitgof(dt$Adverse.Events,m2$fitted.values))
```

```
##
##  Hosmer and Lemeshow test (binary model)
##
## data:  dt$Adverse.Events, m2$fitted.values
## X-squared = 2.4051, df = 8, p-value = 0.966
```

- p-value is high
- model is good fit (model is a good fit as the insignificant p value indicates that there are no issues with the model)

Aggregating Data

```
new_dt = dt[,c("Adverse.Events" ,"Ethnicity.2" , "GENDER" ,
                    "Blood.type.cat" , "Histology3" , "Age.cat")]

new_dt$Histology3 <- relevel(new_dt$Histology3, ref = "Other")

new_dt[] = lapply(new_dt, as.character)
new_dt$Adverse.Events = as.numeric(as.character(new_dt$Adverse.Events))

agg_data = aggregate(Adverse.Events ~ Ethnicity.2 + GENDER +
                    Blood.type.cat + Histology3 + Age.cat,
                  data = new_dt,
                  FUN = sum)
agg_data = cbind(agg_data,
              aggregate(Adverse.Events ~ Ethnicity.2 + GENDER +
                      Blood.type.cat + Histology3 + Age.cat,
                    data = new_dt,
                    FUN = length))

names(agg_data)[12] = "Adverse.Events_tot"
agg_data = agg_data[, !duplicated(colnames(agg_data))]
head(agg_data)
```

Ethnicity.2	GENDER	Blood.type.cat	Histology3	Age.cat	Adverse.Events	Adverse.Events_tot
Other	Female	A/B/AB	Breast	28-65	0	1
White	Female	A/B/AB	Breast	28-65	0	1
Other	Female	O	Breast	28-65	0	1
White	Female	O	Breast	28-65	2	2
Other	Female	A/B/AB	Lung	28-65	2	2
White	Female	A/B/AB	Lung	28-65	1	6

```
agg_data$Histology3 <- as.factor(x = agg_data$Histology3)
agg_data$Histology3 <- relevel(agg_data$Histology3, ref = "Other")
```

Aggregated Model

```
agg_model = glm(Adverse.Events/Adverse.Events_tot ~ Ethnicity.2 + Age.cat + GENDER +
                Blood.type.cat + Histology3,
             family = binomial(link = "logit"),
             data = agg_data,
             weight = Adverse.Events_tot)

summary(agg_model)
```

```
##
## Call:
## glm(formula = Adverse.Events/Adverse.Events_tot ~ Ethnicity.2 +
##     Age.cat + GENDER + Blood.type.cat + Histology3, family = binomial(link = "logit"),
##     data = agg_data, weights = Adverse.Events_tot)
##
## Deviance Residuals:
##     Min      1Q  Median      3Q     Max
## -2.0183  -1.0142  -0.1285   0.9840   1.9787
##
## Coefficients:
##                   Estimate Std. Error z value Pr(>|z|)
## (Intercept)       -0.46825    0.48300  -0.969   0.3323
## Ethnicity.2White   0.02881    0.44383   0.065   0.9482
## Age.cat65-90       0.33600    0.45330   0.741   0.4586
## GENDERMale        -0.72152    0.42759  -1.687   0.0915 .
## Blood.type.catO    0.79629    0.39800   2.001   0.0454 *
## Histology3Breast  -0.86442    0.95866  -0.902   0.3672
## Histology3Lung     0.12401    0.50756   0.244   0.8070
## Histology3Skin     0.18235    0.55530   0.328   0.7426
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 60.889  on 39  degrees of freedom
## Residual deviance: 52.912  on 32  degrees of freedom
## AIC: 100.14
##
## Number of Fisher Scoring iterations: 4
```

Backwards Selection

```r
# using backward() function
agg_back_b = logistf(Adverse.Events/Adverse.Events_tot ~ Ethnicity.2 + Age.cat + GENDER,
                     family = binomial(link="logit"),
                     data = agg_data,
                     weights = Adverse.Events_tot)
agg_reduced_b = backward(agg_back_b, slstay = 0.1)
```

```
## Step  0 : starting model
## Step  1 : removed  Age.cat  (P= 0.362972 )
## Step  2 : removed  GENDER  (P= 0.2026073 )
```

```r
summary(agg_reduced_b)
```

```
## logistf(formula = Adverse.Events/Adverse.Events_tot ~ Ethnicity.2,
##     data = agg_data, pl = FALSE, weights = Adverse.Events_tot,
##     family = binomial(link = "logit"))
##
## Model fitted by Penalized ML
## Coefficients:
##                      coef  se(coef) lower 0.95 upper 0.95     Chisq
## (Intercept)     -1.3350011 0.4103913  -2.139353 -0.5306488 10.581978
## Ethnicity.2White -0.8752107 0.5467819  -1.946883  0.1964621  2.562106
##                          p method
## (Intercept)     0.001141954      1
## Ethnicity.2White 0.109452715      1
##
## Method: 1-Wald, 2-Profile penalized log-likelihood, 3-None
##
## Likelihood ratio test=2.490393 on 1 df, p=0.1145432, n=120
## Wald test = 48.00105 on 1 df, p = 4.259926e-12
```

```r
# adding in variables of main interest
agg_final = glm(Adverse.Events/Adverse.Events_tot ~ Ethnicity.2 + Blood.type.cat + Histology3,
                family = binomial(link="logit"),
                data = agg_data,
                weight = Adverse.Events_tot)
summary(agg_final)
```

```
##
## Call:
## glm(formula = Adverse.Events/Adverse.Events_tot ~ Ethnicity.2 +
##     Blood.type.cat + Histology3, family = binomial(link = "logit"),
##     data = agg_data, weights = Adverse.Events_tot)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -2.0905  -0.9843  -0.2473   1.0689   2.1992
##
## Coefficients:
##                  Estimate Std. Error z value Pr(>|z|)
## (Intercept)      -0.80572    0.42781  -1.883   0.0597 .
## Ethnicity.2White  0.06164    0.42102   0.146   0.8836
## Blood.type.cat0   0.81326    0.39234   2.073   0.0382 *
## Histology3Breast -0.49849    0.92325  -0.540   0.5892
```

```
## Histology3Lung     0.31844     0.48845    0.652    0.5144
## Histology3Skin    -0.09038     0.52315   -0.173    0.8628
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 60.889  on 39  degrees of freedom
## Residual deviance: 56.018  on 34  degrees of freedom
## AIC: 99.245
##
## Number of Fisher Scoring iterations: 4
```

Comparing Aggregated Models

```
anova(agg_model, agg_final, test = "LRT")
```

Resid. Df	Resid. Dev	Df	Deviance	Pr(>Chi)
32	52.91191	NA	NA	NA
34	56.01756	-2	-3.105646	0.2116497

Checking For Model Significance And Influential Points

```
pchisq(summary(agg_final)$deviance,
       df = summary(agg_final)$df[2],
       lower.tail = F)
```

```
## [1] 0.01010138
```

```
influencePlot(agg_final)
```
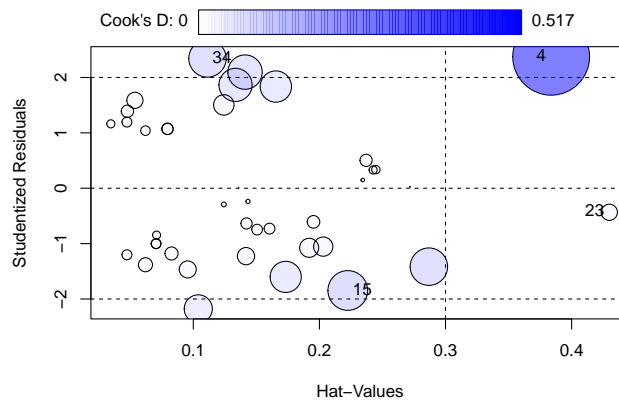

	StudRes	Hat	CookD
4	2.3740184	0.3837633	0.5174754
15	-1.8462425	0.2225077	0.1386077
23	-0.4342275	0.4298657	0.0232038
34	2.3432763	0.1112538	0.1227610

```
Std.res = rstandard(agg_final)
Std.res[Std.res == max(Std.res)]
```

```
##        4
## 2.457829
```

```
autoplot(agg_final)
```
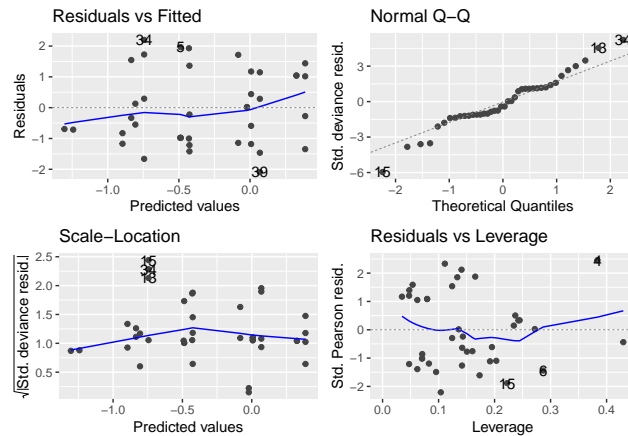


```
CD = cooks.distance((agg_final))
CD[CD==max(CD)]
```

```
##         4
## 0.5174754
```

Determining Outliers

```
outlierTest(agg_final)
```

```
## No Studentized residuals with Bonferroni p < 0.05
## Largest |rstudent|:
##   rstudent unadjusted p-value Bonferroni p
## 4 2.374018          0.017596      0.70383
```

```
(outliers <- match(4, row.names(agg_data)))
```

```
## [1] 4
```

```
agg_data[outliers,]
```

	Ethnicity.2	GENDERBlood.type.cat	Histology3	Age.cat	Adverse.Events	Adverse.Events_tot
4	White	Female O	Breast	28-65	2	2

Removing Outliers And Recreating Model

```
agg_data = agg_data[-4,]

agg_final_adjusted = glm(Adverse.Events/Adverse.Events_tot ~ Ethnicity.2 + Blood.type.cat +
                         Histology3,
                     family = binomial(link="logit"),
                     data = agg_data,
```

```
                                    weight = Adverse.Events_tot)
summary(agg_final_adjusted)
```

```
##
## Call:
## glm(formula = Adverse.Events/Adverse.Events_tot ~ Ethnicity.2 +
##      Blood.type.cat + Histology3, family = binomial(link = "logit"),
##      data = agg_data, weights = Adverse.Events_tot)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -2.02865  -1.02405  -0.00025   1.03971   2.20286
##
## Coefficients:
##                   Estimate Std. Error z value Pr(>|z|)
## (Intercept)       -0.69151    0.43147  -1.603   0.1090
## Ethnicity.2White  -0.05596    0.42896  -0.130   0.8962
## Blood.type.cat0    0.73293    0.39925   1.836   0.0664 .
## Histology3Breast -17.23422 1934.16698  -0.009   0.9929
## Histology3Lung     0.31950    0.48688   0.656   0.5117
## Histology3Skin    -0.08322    0.52151  -0.160   0.8732
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 57.173  on 38  degrees of freedom
## Residual deviance: 49.245  on 33  degrees of freedom
## AIC: 92.472
##
## Number of Fisher Scoring iterations: 16
```

```
pchisq(summary(agg_final_adjusted)$deviance,
       df = summary(agg_final_adjusted)$df[2],
       lower.tail = F)
```

```
## [1] 0.03427618
```

Final Model Diagnostics

```
# PLOT AFTER AGGREGATING DATA
scatter.smooth(jitter(agg_final_adjusted$fitted.values, amount=0),
               agg_data$Adverse.Events,
               lpars = list(col = "red", lwd = 2))
```
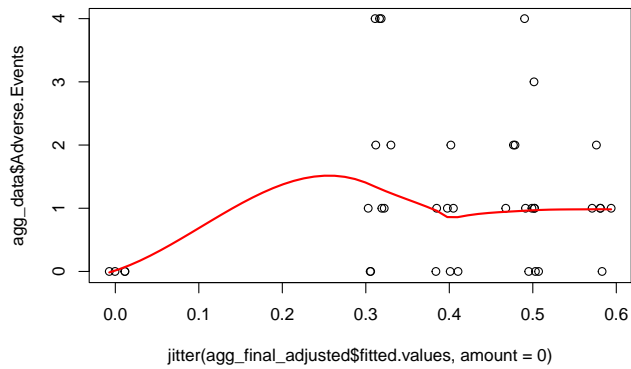
```
# Adverse.Events_tot
ggplot(agg_data,aes(x=jitter(agg_final_adjusted$fitted.values,amount=0),
                    y=agg_data$Adverse.Events_tot)) +
  geom_point(aes(color=Blood.type.cat))+
  labs(y="Immune Related Adverse Events Indicator",
       x="agg_final_adjusted Fitted Values")+
  guides(color = guide_legend(title = "Blood Type"))
```
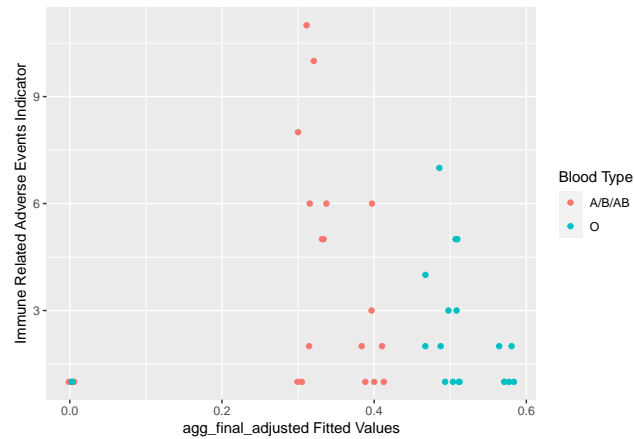


```
# Adverse.Events
ggplot(agg_data,aes(x=jitter(agg_final_adjusted$fitted.values,amount=0),
                    y=agg_data$Adverse.Events)) +
  geom_point(aes(color=Blood.type.cat))+
  labs(y="Immune Related Adverse Events Indicator",
       x="agg_final_adjusted Fitted Values")+
  guides(color = guide_legend(title = "Blood Type"))
```

17
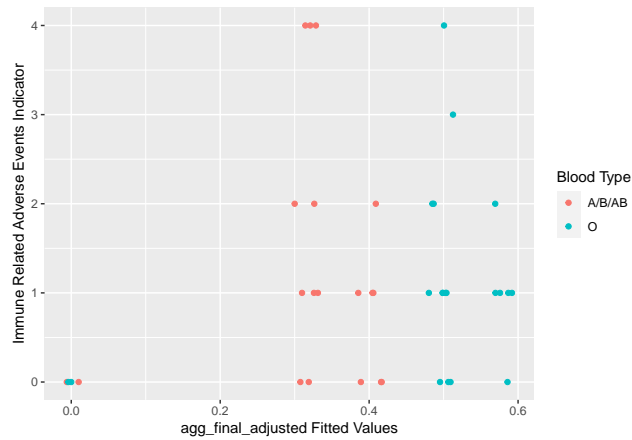
```
autoplot(agg_final_adjusted)
```
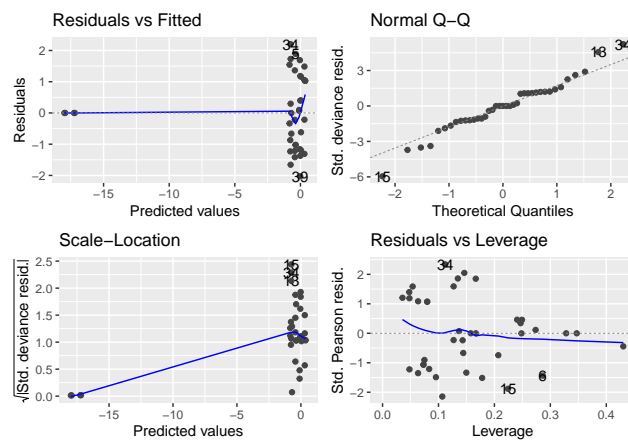

Interpretation

```r
# comparing proportions

# Blood Type
bt_p <- ggplot(dt, aes(fill=Adverse.Events, x=Blood.type.cat)) +
    geom_bar(position="fill")+scale_y_continuous(labels = scales::percent)+labs(x="Blood Type",y="Percer

# Histology
hist_p <- ggplot(dt, aes(fill=Adverse.Events, x=Histology3)) +
    geom_bar(position="fill")+scale_y_continuous(labels = scales::percent)+labs(x="Histology",y="Percen

ggarrange(bt_p,hist_p,ncol=2,nrow=1,labels=c("A","B"))
```
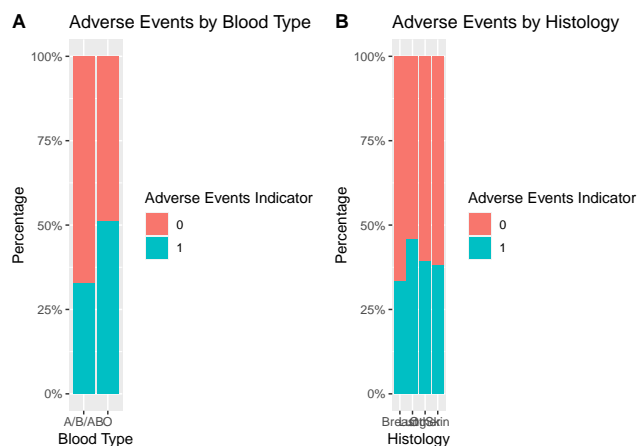
Table Of Coefficients, P-Values, Standard Errors, And Confidence Intervals

```
final_table = cbind(exp(agg_final_adjusted$coefficients),
                    summary(agg_final_adjusted)$coefficients[,4],
                    confint(agg_final_adjusted, level = 0.9),
                    sqrt(diag(vcov(agg_final_adjusted))))
colnames(final_table) = c("Estimate", "Pr(>|z|)", "5%", "95%", "Std. Error")
print(final_table)
```

```
##                      Estimate   Pr(>|z|)          5%          95%   Std. Error
## (Intercept)      5.008199e-01 0.10900103 -1.42108944 6.658973e-03    0.4314650
## Ethnicity.2White 9.455747e-01 0.89620225 -0.75834494 6.586172e-01    0.4289609
## Blood.type.catO  2.081179e+00 0.06638868  0.07935668 1.396369e+00    0.3992474
## Histology3Breast 3.275452e-08 0.99289061          NA 1.529957e+02 1934.1669754
## Histology3Lung   1.376436e+00 0.51168543 -0.48775231 1.122850e+00    0.4868786
## Histology3Skin   9.201482e-01 0.87321496 -0.96358075 7.646407e-01    0.5215098
```

Interactions

```
int_model = glm(Adverse.Events ~ Ethnicity.2 * Age.cat * GENDER *
                  Blood.type.cat * Histology3,
              family = binomial(link = "logit"),
              data = dt)
summary(int_model)
```

```
##
## Call:
## glm(formula = Adverse.Events ~ Ethnicity.2 * Age.cat * GENDER *
##     Blood.type.cat * Histology3, family = binomial(link = "logit"),
##     data = dt)
##
## Deviance Residuals:
##     Min       1Q    Median       3Q      Max
## -1.79412  -0.75853  -0.00013  0.66805  2.14597
##
## Coefficients: (24 not defined because of singularities)
##                                                                   Estimate
## (Intercept)                                                      -1.857e+01
## Ethnicity.2White                                                 -4.943e-08
```

```
## Age.cat65-90                                                        -1.617e+02
## GENDERMale                                                           1.996e-07
## Blood.type.cat0                                                      -6.316e-11
## Histology3Lung                                                        3.713e+01
## Histology3Other                                                       1.718e+01
## Histology3Skin                                                       -1.864e-07
## Ethnicity.2White:Age.cat65-90                                         1.069e+02
## Ethnicity.2White:GENDERMale                                          -1.966e+01
## Age.cat65-90:GENDERMale                                               7.244e+01
## Ethnicity.2White:Blood.type.cat0                                      3.713e+01
## Age.cat65-90:Blood.type.cat0                                          8.838e+01
## GENDERMale:Blood.type.cat0                                            3.713e+01
## Ethnicity.2White:Histology3Lung                                      -2.018e+01
## Ethnicity.2White:Histology3Other                                      2.079e+00
## Ethnicity.2White:Histology3Skin                                       3.713e+01
## Age.cat65-90:Histology3Lung                                           9.248e+01
## Age.cat65-90:Histology3Other                                          5.541e+01
## Age.cat65-90:Histology3Skin                                           7.259e+01
## GENDERMale:Histology3Lung                                            -3.713e+01
## GENDERMale:Histology3Other                                            6.931e-01
## GENDERMale:Histology3Skin                                                     NA
## Blood.type.cat0:Histology3Lung                                       -1.072e-07
## Blood.type.cat0:Histology3Other                                       6.931e-01
## Blood.type.cat0:Histology3Skin                                        1.514e-07
## Ethnicity.2White:Age.cat65-90:GENDERMale                             -7.149e+01
## Ethnicity.2White:Age.cat65-90:Blood.type.cat0                        -7.080e+01
## Ethnicity.2White:GENDERMale:Blood.type.cat0                           8.109e-01
## Age.cat65-90:GENDERMale:Blood.type.cat0                              -3.640e+01
## Ethnicity.2White:Age.cat65-90:Histology3Lung                         -5.472e+01
## Ethnicity.2White:Age.cat65-90:Histology3Other                                NA
## Ethnicity.2White:Age.cat65-90:Histology3Skin                                 NA
## Ethnicity.2White:GENDERMale:Histology3Lung                            7.697e+01
## Ethnicity.2White:GENDERMale:Histology3Other                           1.608e+01
## Ethnicity.2White:GENDERMale:Histology3Skin                                   NA
## Age.cat65-90:GENDERMale:Histology3Lung                               -3.247e+00
## Age.cat65-90:GENDERMale:Histology3Other                                      NA
## Age.cat65-90:GENDERMale:Histology3Skin                                       NA
## Ethnicity.2White:Blood.type.cat0:Histology3Lung                      -1.696e+01
## Ethnicity.2White:Blood.type.cat0:Histology3Other                     -3.823e+01
## Ethnicity.2White:Blood.type.cat0:Histology3Skin                      -7.398e+01
## Age.cat65-90:Blood.type.cat0:Histology3Lung                          -1.919e+01
## Age.cat65-90:Blood.type.cat0:Histology3Other                                 NA
## Age.cat65-90:Blood.type.cat0:Histology3Skin                                  NA
## GENDERMale:Blood.type.cat0:Histology3Lung                            -9.525e+01
## GENDERMale:Blood.type.cat0:Histology3Other                           -3.673e+01
## GENDERMale:Blood.type.cat0:Histology3Skin                                    NA
## Ethnicity.2White:Age.cat65-90:GENDERMale:Blood.type.cat0                     NA
## Ethnicity.2White:Age.cat65-90:GENDERMale:Histology3Lung                      NA
## Ethnicity.2White:Age.cat65-90:GENDERMale:Histology3Other                     NA
## Ethnicity.2White:Age.cat65-90:GENDERMale:Histology3Skin                      NA
## Ethnicity.2White:Age.cat65-90:Blood.type.cat0:Histology3Lung                 NA
## Ethnicity.2White:Age.cat65-90:Blood.type.cat0:Histology3Other                NA
## Ethnicity.2White:Age.cat65-90:Blood.type.cat0:Histology3Skin                 NA
## Ethnicity.2White:GENDERMale:Blood.type.cat0:Histology3Lung                   NA
```

```
## Ethnicity.2White:GENDERMale:Blood.type.cat0:Histology3Other                              NA
## Ethnicity.2White:GENDERMale:Blood.type.cat0:Histology3Skin                               NA
## Age.cat65-90:GENDERMale:Blood.type.cat0:Histology3Lung                              9.440e+01
## Age.cat65-90:GENDERMale:Blood.type.cat0:Histology3Other                                  NA
## Age.cat65-90:GENDERMale:Blood.type.cat0:Histology3Skin                                   NA
## Ethnicity.2White:Age.cat65-90:GENDERMale:Blood.type.cat0:Histology3Lung                  NA
## Ethnicity.2White:Age.cat65-90:GENDERMale:Blood.type.cat0:Histology3Other                 NA
## Ethnicity.2White:Age.cat65-90:GENDERMale:Blood.type.cat0:Histology3Skin                  NA
##                                                                                    Std. Error
## (Intercept)                                                                         6.523e+03
## Ethnicity.2White                                                                    9.224e+03
## Age.cat65-90                                                                        3.048e+04
## GENDERMale                                                                          7.989e+03
## Blood.type.cat0                                                                     9.224e+03
## Histology3Lung                                                                      7.989e+03
## Histology3Other                                                                     6.523e+03
## Histology3Skin                                                                      9.224e+03
## Ethnicity.2White:Age.cat65-90                                                       2.554e+04
## Ethnicity.2White:GENDERMale                                                         1.031e+04
## Age.cat65-90:GENDERMale                                                             1.191e+04
## Ethnicity.2White:Blood.type.cat0                                                    1.220e+04
## Age.cat65-90:Blood.type.cat0                                                        2.291e+04
## GENDERMale:Blood.type.cat0                                                          1.130e+04
## Ethnicity.2White:Histology3Lung                                                     1.031e+04
## Ethnicity.2White:Histology3Other                                                    9.224e+03
## Ethnicity.2White:Histology3Skin                                                     1.305e+04
## Age.cat65-90:Histology3Lung                                                         2.063e+04
## Age.cat65-90:Histology3Other                                                        1.031e+04
## Age.cat65-90:Histology3Skin                                                         1.098e+04
## GENDERMale:Histology3Lung                                                           1.130e+04
## GENDERMale:Histology3Other                                                          7.989e+03
## GENDERMale:Histology3Skin                                                                 NA
## Blood.type.cat0:Histology3Lung                                                      1.220e+04
## Blood.type.cat0:Histology3Other                                                     9.224e+03
## Blood.type.cat0:Histology3Skin                                                      1.305e+04
## Ethnicity.2White:Age.cat65-90:GENDERMale                                            1.191e+04
## Ethnicity.2White:Age.cat65-90:Blood.type.cat0                                       1.993e+04
## Ethnicity.2White:GENDERMale:Blood.type.cat0                                         2.833e+00
## Age.cat65-90:GENDERMale:Blood.type.cat0                                             7.532e+03
## Ethnicity.2White:Age.cat65-90:Histology3Lung                                        1.459e+04
## Ethnicity.2White:Age.cat65-90:Histology3Other                                             NA
## Ethnicity.2White:Age.cat65-90:Histology3Skin                                              NA
## Ethnicity.2White:GENDERMale:Histology3Lung                                          1.459e+04
## Ethnicity.2White:GENDERMale:Histology3Other                                         1.031e+04
## Ethnicity.2White:GENDERMale:Histology3Skin                                                NA
## Age.cat65-90:GENDERMale:Histology3Lung                                              7.989e+03
## Age.cat65-90:GENDERMale:Histology3Other                                                   NA
## Age.cat65-90:GENDERMale:Histology3Skin                                                    NA
## Ethnicity.2White:Blood.type.cat0:Histology3Lung                                     1.598e+04
## Ethnicity.2White:Blood.type.cat0:Histology3Other                                    1.220e+04
## Ethnicity.2White:Blood.type.cat0:Histology3Skin                                     1.384e+04
## Age.cat65-90:Blood.type.cat0:Histology3Lung                                         1.031e+04
## Age.cat65-90:Blood.type.cat0:Histology3Other                                              NA
## Age.cat65-90:Blood.type.cat0:Histology3Skin                                               NA
```

```
## GENDERMale:Blood.type.cat0:Histology3Lung                                        1.598e+04
## GENDERMale:Blood.type.cat0:Histology30ther                                       1.130e+04
## GENDERMale:Blood.type.cat0:Histology3Skin                                               NA
## Ethnicity.2White:Age.cat65-90:GENDERMale:Blood.type.cat0                               NA
## Ethnicity.2White:Age.cat65-90:GENDERMale:Histology3Lung                               NA
## Ethnicity.2White:Age.cat65-90:GENDERMale:Histology30ther                              NA
## Ethnicity.2White:Age.cat65-90:GENDERMale:Histology3Skin                               NA
## Ethnicity.2White:Age.cat65-90:Blood.type.cat0:Histology3Lung                          NA
## Ethnicity.2White:Age.cat65-90:Blood.type.cat0:Histology30ther                         NA
## Ethnicity.2White:Age.cat65-90:Blood.type.cat0:Histology3Skin                          NA
## Ethnicity.2White:GENDERMale:Blood.type.cat0:Histology3Lung                            NA
## Ethnicity.2White:GENDERMale:Blood.type.cat0:Histology30ther                           NA
## Ethnicity.2White:GENDERMale:Blood.type.cat0:Histology3Skin                            NA
## Age.cat65-90:GENDERMale:Blood.type.cat0:Histology3Lung                          1.506e+04
## Age.cat65-90:GENDERMale:Blood.type.cat0:Histology30ther                               NA
## Age.cat65-90:GENDERMale:Blood.type.cat0:Histology3Skin                                NA
## Ethnicity.2White:Age.cat65-90:GENDERMale:Blood.type.cat0:Histology3Lung               NA
## Ethnicity.2White:Age.cat65-90:GENDERMale:Blood.type.cat0:Histology30ther              NA
## Ethnicity.2White:Age.cat65-90:GENDERMale:Blood.type.cat0:Histology3Skin               NA
##                                                                                  z value
## (Intercept)                                                                       -0.003
## Ethnicity.2White                                                                   0.000
## Age.cat65-90                                                                      -0.005
## GENDERMale                                                                         0.000
## Blood.type.cat0                                                                    0.000
## Histology3Lung                                                                     0.005
## Histology30ther                                                                    0.003
## Histology3Skin                                                                     0.000
## Ethnicity.2White:Age.cat65-90                                                      0.004
## Ethnicity.2White:GENDERMale                                                       -0.002
## Age.cat65-90:GENDERMale                                                            0.006
## Ethnicity.2White:Blood.type.cat0                                                   0.003
## Age.cat65-90:Blood.type.cat0                                                       0.004
## GENDERMale:Blood.type.cat0                                                         0.003
## Ethnicity.2White:Histology3Lung                                                   -0.002
## Ethnicity.2White:Histology30ther                                                   0.000
## Ethnicity.2White:Histology3Skin                                                    0.003
## Age.cat65-90:Histology3Lung                                                        0.004
## Age.cat65-90:Histology30ther                                                       0.005
## Age.cat65-90:Histology3Skin                                                        0.007
## GENDERMale:Histology3Lung                                                         -0.003
## GENDERMale:Histology30ther                                                         0.000
## GENDERMale:Histology3Skin                                                              NA
## Blood.type.cat0:Histology3Lung                                                     0.000
## Blood.type.cat0:Histology30ther                                                    0.000
## Blood.type.cat0:Histology3Skin                                                     0.000
## Ethnicity.2White:Age.cat65-90:GENDERMale                                          -0.006
## Ethnicity.2White:Age.cat65-90:Blood.type.cat0                                     -0.004
## Ethnicity.2White:GENDERMale:Blood.type.cat0                                        0.286
## Age.cat65-90:GENDERMale:Blood.type.cat0                                           -0.005
## Ethnicity.2White:Age.cat65-90:Histology3Lung                                      -0.004
## Ethnicity.2White:Age.cat65-90:Histology30ther                                          NA
## Ethnicity.2White:Age.cat65-90:Histology3Skin                                           NA
## Ethnicity.2White:GENDERMale:Histology3Lung                                         0.005
```

```
## Ethnicity.2White:GENDERMale:Histology3Other                                       0.002
## Ethnicity.2White:GENDERMale:Histology3Skin                                          NA
## Age.cat65-90:GENDERMale:Histology3Lung                                            0.000
## Age.cat65-90:GENDERMale:Histology3Other                                             NA
## Age.cat65-90:GENDERMale:Histology3Skin                                              NA
## Ethnicity.2White:Blood.type.cat0:Histology3Lung                                  -0.001
## Ethnicity.2White:Blood.type.cat0:Histology3Other                                 -0.003
## Ethnicity.2White:Blood.type.cat0:Histology3Skin                                  -0.005
## Age.cat65-90:Blood.type.cat0:Histology3Lung                                      -0.002
## Age.cat65-90:Blood.type.cat0:Histology3Other                                        NA
## Age.cat65-90:Blood.type.cat0:Histology3Skin                                         NA
## GENDERMale:Blood.type.cat0:Histology3Lung                                        -0.006
## GENDERMale:Blood.type.cat0:Histology3Other                                       -0.003
## GENDERMale:Blood.type.cat0:Histology3Skin                                           NA
## Ethnicity.2White:Age.cat65-90:GENDERMale:Blood.type.cat0                            NA
## Ethnicity.2White:Age.cat65-90:GENDERMale:Histology3Lung                            NA
## Ethnicity.2White:Age.cat65-90:GENDERMale:Histology3Other                           NA
## Ethnicity.2White:Age.cat65-90:GENDERMale:Histology3Skin                            NA
## Ethnicity.2White:Age.cat65-90:Blood.type.cat0:Histology3Lung                       NA
## Ethnicity.2White:Age.cat65-90:Blood.type.cat0:Histology3Other                      NA
## Ethnicity.2White:Age.cat65-90:Blood.type.cat0:Histology3Skin                       NA
## Ethnicity.2White:GENDERMale:Blood.type.cat0:Histology3Lung                         NA
## Ethnicity.2White:GENDERMale:Blood.type.cat0:Histology3Other                        NA
## Ethnicity.2White:GENDERMale:Blood.type.cat0:Histology3Skin                         NA
## Age.cat65-90:GENDERMale:Blood.type.cat0:Histology3Lung                           0.006
## Age.cat65-90:GENDERMale:Blood.type.cat0:Histology3Other                            NA
## Age.cat65-90:GENDERMale:Blood.type.cat0:Histology3Skin                             NA
## Ethnicity.2White:Age.cat65-90:GENDERMale:Blood.type.cat0:Histology3Lung            NA
## Ethnicity.2White:Age.cat65-90:GENDERMale:Blood.type.cat0:Histology3Other           NA
## Ethnicity.2White:Age.cat65-90:GENDERMale:Blood.type.cat0:Histology3Skin            NA
##                                                                                Pr(>|z|)
## (Intercept)                                                                       0.998
## Ethnicity.2White                                                                  1.000
## Age.cat65-90                                                                      0.996
## GENDERMale                                                                        1.000
## Blood.type.cat0                                                                   1.000
## Histology3Lung                                                                    0.996
## Histology3Other                                                                   0.998
## Histology3Skin                                                                    1.000
## Ethnicity.2White:Age.cat65-90                                                     0.997
## Ethnicity.2White:GENDERMale                                                       0.998
## Age.cat65-90:GENDERMale                                                           0.995
## Ethnicity.2White:Blood.type.cat0                                                  0.998
## Age.cat65-90:Blood.type.cat0                                                      0.997
## GENDERMale:Blood.type.cat0                                                        0.997
## Ethnicity.2White:Histology3Lung                                                   0.998
## Ethnicity.2White:Histology3Other                                                  1.000
## Ethnicity.2White:Histology3Skin                                                   0.998
## Age.cat65-90:Histology3Lung                                                       0.996
## Age.cat65-90:Histology3Other                                                      0.996
## Age.cat65-90:Histology3Skin                                                       0.995
## GENDERMale:Histology3Lung                                                         0.997
## GENDERMale:Histology3Other                                                        1.000
## GENDERMale:Histology3Skin                                                            NA
```

```
## Blood.type.cat0:Histology3Lung                                                        1.000
## Blood.type.cat0:Histology3Other                                                        1.000
## Blood.type.cat0:Histology3Skin                                                         1.000
## Ethnicity.2White:Age.cat65-90:GENDERMale                                               0.995
## Ethnicity.2White:Age.cat65-90:Blood.type.cat0                                          0.997
## Ethnicity.2White:GENDERMale:Blood.type.cat0                                            0.775
## Age.cat65-90:GENDERMale:Blood.type.cat0                                                0.996
## Ethnicity.2White:Age.cat65-90:Histology3Lung                                           0.997
## Ethnicity.2White:Age.cat65-90:Histology3Other                                             NA
## Ethnicity.2White:Age.cat65-90:Histology3Skin                                              NA
## Ethnicity.2White:GENDERMale:Histology3Lung                                             0.996
## Ethnicity.2White:GENDERMale:Histology3Other                                            0.999
## Ethnicity.2White:GENDERMale:Histology3Skin                                                NA
## Age.cat65-90:GENDERMale:Histology3Lung                                                 1.000
## Age.cat65-90:GENDERMale:Histology3Other                                                   NA
## Age.cat65-90:GENDERMale:Histology3Skin                                                    NA
## Ethnicity.2White:Blood.type.cat0:Histology3Lung                                        0.999
## Ethnicity.2White:Blood.type.cat0:Histology3Other                                       0.998
## Ethnicity.2White:Blood.type.cat0:Histology3Skin                                        0.996
## Age.cat65-90:Blood.type.cat0:Histology3Lung                                            0.999
## Age.cat65-90:Blood.type.cat0:Histology3Other                                              NA
## Age.cat65-90:Blood.type.cat0:Histology3Skin                                               NA
## GENDERMale:Blood.type.cat0:Histology3Lung                                              0.995
## GENDERMale:Blood.type.cat0:Histology3Other                                             0.997
## GENDERMale:Blood.type.cat0:Histology3Skin                                                 NA
## Ethnicity.2White:Age.cat65-90:GENDERMale:Blood.type.cat0                                  NA
## Ethnicity.2White:Age.cat65-90:GENDERMale:Histology3Lung                                   NA
## Ethnicity.2White:Age.cat65-90:GENDERMale:Histology3Other                                  NA
## Ethnicity.2White:Age.cat65-90:GENDERMale:Histology3Skin                                   NA
## Ethnicity.2White:Age.cat65-90:Blood.type.cat0:Histology3Lung                              NA
## Ethnicity.2White:Age.cat65-90:Blood.type.cat0:Histology3Other                             NA
## Ethnicity.2White:Age.cat65-90:Blood.type.cat0:Histology3Skin                              NA
## Ethnicity.2White:GENDERMale:Blood.type.cat0:Histology3Lung                                NA
## Ethnicity.2White:GENDERMale:Blood.type.cat0:Histology3Other                               NA
## Ethnicity.2White:GENDERMale:Blood.type.cat0:Histology3Skin                                NA
## Age.cat65-90:GENDERMale:Blood.type.cat0:Histology3Lung                                 0.995
## Age.cat65-90:GENDERMale:Blood.type.cat0:Histology3Other                                   NA
## Age.cat65-90:GENDERMale:Blood.type.cat0:Histology3Skin                                    NA
## Ethnicity.2White:Age.cat65-90:GENDERMale:Blood.type.cat0:Histology3Lung                   NA
## Ethnicity.2White:Age.cat65-90:GENDERMale:Blood.type.cat0:Histology3Other                  NA
## Ethnicity.2White:Age.cat65-90:GENDERMale:Blood.type.cat0:Histology3Skin                   NA
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 161.52  on 119  degrees of freedom
## Residual deviance: 100.63  on  80  degrees of freedom
## AIC: 180.63
##
## Number of Fisher Scoring iterations: 17
```

Identifying Non-Significant Interaction Values

```
Anova(int_model)
```

	LR Chisq	Df	Pr(>Chisq)
Ethnicity.2	0.0192662	1	0.8896061
Age.cat	0.1652290	1	0.6843872
GENDER	2.7627573	1	0.0964818
Blood.type.cat	3.7700610	1	0.0521777
Histology3	1.9680128	3	0.5790722
Ethnicity.2:Age.cat	0.0138203	1	0.9064164
Ethnicity.2:GENDER	4.0771763	1	0.0434662
Age.cat:GENDER	0.8584553	1	0.3541713
Ethnicity.2:Blood.type.cat	1.2093809	1	0.2714548
Age.cat:Blood.type.cat	0.1280819	1	0.7204292
GENDER:Blood.type.cat	0.4153868	1	0.5192479
Ethnicity.2:Histology3	7.1748644	3	0.0665282
Age.cat:Histology3	4.3847334	3	0.2228051
GENDER:Histology3	3.4010340	2	0.1825891
Blood.type.cat:Histology3	7.8814467	3	0.0485265
Ethnicity.2:Age.cat:GENDER	3.5726027	1	0.0587402
Ethnicity.2:Age.cat:Blood.type.cat	NA	0	NA
Ethnicity.2:GENDER:Blood.type.cat	0.0818530	1	0.7748019
Age.cat:GENDER:Blood.type.cat	2.2716863	1	0.1317565
Ethnicity.2:Age.cat:Histology3	-0.0000003	1	1.0000000
Ethnicity.2:GENDER:Histology3	10.1188280	2	0.0063493
Age.cat:GENDER:Histology3	6.4601477	1	0.0110320
Ethnicity.2:Blood.type.cat:Histology3	2.0456171	3	0.5629929
Age.cat:Blood.type.cat:Histology3	7.7283353	1	0.0054361
GENDER:Blood.type.cat:Histology3	5.7841129	2	0.0554620
Ethnicity.2:Age.cat:GENDER:Blood.type.cat	NA	0	NA
Ethnicity.2:Age.cat:GENDER:Histology3	NA	0	NA
Ethnicity.2:Age.cat:Blood.type.cat:Histology3	NA	0	NA
Ethnicity.2:GENDER:Blood.type.cat:Histology3	NA	0	NA
Age.cat:GENDER:Blood.type.cat:Histology3	-0.0000001	1	1.0000000
Ethnicity.2:Age.cat:GENDER:Blood.type.cat:Histology3	NA	0	NA

Final Interaction Model

```
int_final = glm(Adverse.Events ~ Ethnicity.2 * Age.cat * GENDER *
                Blood.type.cat * Histology3 -
                Ethnicity.2:Age.cat:GENDER:Blood.type.cat:Histology3 -
                Age.cat:GENDER:Blood.type.cat:Histology3 -
                Ethnicity.2:GENDER:Blood.type.cat:Histology3 -
                Ethnicity.2:Age.cat:Blood.type.cat:Histology3 -
                Ethnicity.2:Age.cat:GENDER:Histology3 -
                Ethnicity.2:Age.cat:GENDER:Blood.type.cat,
             family = binomial(link = "logit"),
             data = dt)
summary(int_final)

##
## Call:
## glm(formula = Adverse.Events ~ Ethnicity.2 * Age.cat * GENDER *
##     Blood.type.cat * Histology3 - Ethnicity.2:Age.cat:GENDER:Blood.type.cat:Histology3 -
##     Age.cat:GENDER:Blood.type.cat:Histology3 - Ethnicity.2:GENDER:Blood.type.cat:Histology3 -
##     Ethnicity.2:Age.cat:Blood.type.cat:Histology3 - Ethnicity.2:Age.cat:GENDER:Histology3 -
```

```
##      Ethnicity.2:Age.cat:GENDER:Blood.type.cat, family = binomial(link = "logit"),
##      data = dt)
##
## Deviance Residuals:
##     Min        1Q    Median        3Q       Max
## -1.79412  -0.75853  -0.00008   0.66805   2.14597
##
## Coefficients: (9 not defined because of singularities)
##                                                        Estimate Std. Error z value
## (Intercept)                                           -1.957e+01  1.075e+04  -0.002
## Ethnicity.2White                                       7.030e-07  1.521e+04   0.000
## Age.cat65-90                                          -1.635e+02  3.737e+04  -0.004
## GENDERMale                                            -1.292e-07  1.317e+04   0.000
## Blood.type.cat0                                        7.607e-07  1.521e+04   0.000
## Histology3Lung                                         3.913e+01  1.317e+04   0.003
## Histology3Other                                        1.818e+01  1.075e+04   0.002
## Histology3Skin                                         7.531e-07  1.521e+04   0.000
## Ethnicity.2White:Age.cat65-90                          1.078e+02  3.385e+04   0.003
## Ethnicity.2White:GENDERMale                           -2.066e+01  1.700e+04  -0.001
## Age.cat65-90:GENDERMale                                7.331e+01  1.611e+04   0.005
## Ethnicity.2White:Blood.type.cat0                       3.913e+01  2.012e+04   0.002
## Age.cat65-90:Blood.type.cat0                           8.824e+01  2.827e+04   0.003
## GENDERMale:Blood.type.cat0                             3.913e+01  1.863e+04   0.002
## Ethnicity.2White:Histology3Lung                       -2.118e+01  1.700e+04  -0.001
## Ethnicity.2White:Histology3Other                       2.079e+00  1.521e+04   0.000
## Ethnicity.2White:Histology3Skin                        3.913e+01  2.151e+04   0.002
## Age.cat65-90:Histology3Lung                            2.638e+00  2.435e+04   0.000
## Age.cat65-90:Histology3Other                           5.640e+01  1.374e+04   0.004
## Age.cat65-90:Histology3Skin                            7.346e+01  1.420e+04   0.005
## GENDERMale:Histology3Lung                             -3.913e+01  1.863e+04  -0.002
## GENDERMale:Histology3Other                             6.931e-01  1.317e+04   0.000
## GENDERMale:Histology3Skin                                     NA         NA      NA
## Blood.type.cat0:Histology3Lung                        -1.279e-06  2.012e+04   0.000
## Blood.type.cat0:Histology3Other                        6.931e-01  1.521e+04   0.000
## Blood.type.cat0:Histology3Skin                        -8.788e-07  2.151e+04   0.000
## Ethnicity.2White:Age.cat65-90:GENDERMale              -7.237e+01  1.611e+04  -0.004
## Ethnicity.2White:Age.cat65-90:Blood.type.cat0         -7.167e+01  2.744e+04  -0.003
## Ethnicity.2White:GENDERMale:Blood.type.cat0            8.109e-01  2.833e+00   0.286
## Age.cat65-90:GENDERMale:Blood.type.cat0               -3.528e+01  5.302e+03  -0.007
## Ethnicity.2White:Age.cat65-90:Histology3Lung          -5.369e+01  1.944e+04  -0.003
## Ethnicity.2White:Age.cat65-90:Histology3Other                 NA         NA      NA
## Ethnicity.2White:Age.cat65-90:Histology3Skin                  NA         NA      NA
## Ethnicity.2White:GENDERMale:Histology3Lung             7.896e+01  2.186e+04   0.004
## Ethnicity.2White:GENDERMale:Histology3Other            1.708e+01  1.700e+04   0.001
## Ethnicity.2White:GENDERMale:Histology3Skin                    NA         NA      NA
## Age.cat65-90:GENDERMale:Histology3Lung                 8.756e+01  8.527e+03   0.010
## Age.cat65-90:GENDERMale:Histology3Other                       NA         NA      NA
## Age.cat65-90:GENDERMale:Histology3Skin                        NA         NA      NA
## Ethnicity.2White:Blood.type.cat0:Histology3Lung       -1.997e+01  2.437e+04  -0.001
## Ethnicity.2White:Blood.type.cat0:Histology3Other      -4.023e+01  2.012e+04  -0.002
## Ethnicity.2White:Blood.type.cat0:Histology3Skin       -7.798e+01  2.281e+04  -0.003
## Age.cat65-90:Blood.type.cat0:Histology3Lung            7.263e+01  7.568e+03   0.010
## Age.cat65-90:Blood.type.cat0:Histology3Other                  NA         NA      NA
## Age.cat65-90:Blood.type.cat0:Histology3Skin                   NA         NA      NA
```

```
## GENDERMale:Blood.type.cat0:Histology3Lung        -9.421e+01  1.983e+04  -0.005
## GENDERMale:Blood.type.cat0:Histology3Other        -3.873e+01  1.863e+04  -0.002
## GENDERMale:Blood.type.cat0:Histology3Skin                 NA         NA     NA
##                                                    Pr(>|z|)
## (Intercept)                                           0.999
## Ethnicity.2White                                      1.000
## Age.cat65-90                                          0.997
## GENDERMale                                            1.000
## Blood.type.cat0                                       1.000
## Histology3Lung                                        0.998
## Histology3Other                                       0.999
## Histology3Skin                                        1.000
## Ethnicity.2White:Age.cat65-90                         0.997
## Ethnicity.2White:GENDERMale                           0.999
## Age.cat65-90:GENDERMale                               0.996
## Ethnicity.2White:Blood.type.cat0                      0.998
## Age.cat65-90:Blood.type.cat0                          0.998
## GENDERMale:Blood.type.cat0                            0.998
## Ethnicity.2White:Histology3Lung                       0.999
## Ethnicity.2White:Histology3Other                      1.000
## Ethnicity.2White:Histology3Skin                       0.999
## Age.cat65-90:Histology3Lung                           1.000
## Age.cat65-90:Histology3Other                          0.997
## Age.cat65-90:Histology3Skin                           0.996
## GENDERMale:Histology3Lung                             0.998
## GENDERMale:Histology3Other                            1.000
## GENDERMale:Histology3Skin                                NA
## Blood.type.cat0:Histology3Lung                        1.000
## Blood.type.cat0:Histology3Other                       1.000
## Blood.type.cat0:Histology3Skin                        1.000
## Ethnicity.2White:Age.cat65-90:GENDERMale              0.996
## Ethnicity.2White:Age.cat65-90:Blood.type.cat0         0.998
## Ethnicity.2White:GENDERMale:Blood.type.cat0           0.775
## Age.cat65-90:GENDERMale:Blood.type.cat0               0.995
## Ethnicity.2White:Age.cat65-90:Histology3Lung          0.998
## Ethnicity.2White:Age.cat65-90:Histology3Other            NA
## Ethnicity.2White:Age.cat65-90:Histology3Skin             NA
## Ethnicity.2White:GENDERMale:Histology3Lung            0.997
## Ethnicity.2White:GENDERMale:Histology3Other           0.999
## Ethnicity.2White:GENDERMale:Histology3Skin               NA
## Age.cat65-90:GENDERMale:Histology3Lung                0.992
## Age.cat65-90:GENDERMale:Histology3Other                  NA
## Age.cat65-90:GENDERMale:Histology3Skin                   NA
## Ethnicity.2White:Blood.type.cat0:Histology3Lung       0.999
## Ethnicity.2White:Blood.type.cat0:Histology3Other      0.998
## Ethnicity.2White:Blood.type.cat0:Histology3Skin       0.997
## Age.cat65-90:Blood.type.cat0:Histology3Lung           0.992
## Age.cat65-90:Blood.type.cat0:Histology3Other             NA
## Age.cat65-90:Blood.type.cat0:Histology3Skin              NA
## GENDERMale:Blood.type.cat0:Histology3Lung             0.996
## GENDERMale:Blood.type.cat0:Histology3Other            0.998
## GENDERMale:Blood.type.cat0:Histology3Skin                NA
##
## (Dispersion parameter for binomial family taken to be 1)
```

```
## 
##     Null deviance: 161.52  on 119  degrees of freedom
## Residual deviance: 100.63  on  81  degrees of freedom
## AIC: 178.63
## 
## Number of Fisher Scoring iterations: 18
```