Regression Table

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Data Management

```r
setwd("/Users/charlescostanzo/College/Su 2023/Chopra/Poster Code/")

library(tidyverse)
library(readxl)
library(ez)
library(MASS) # for negative binomial glm
library(AER) # for dispersion test
library(gtsummary) # for regression table
library(gt)


elispot <- read_csv("Data/elispot.csv")
elispot$sex <- factor(elispot$sex)
elispot$vaccinated <- factor(elispot$vaccinated)
elispot$id <- factor(elispot$id)

glm.data <- elispot %>%
  group_by(id) %>%
  mutate(avg_spots = round(mean(spots)),1) %>% # take mean of technical replicates and round to nearest integer
  dplyr::select(id, sex, avg_spots, vaccinated) %>%
  distinct()
```

Negative Binomial GLMs

```r
glm.data <- glm.data %>%
  mutate(vaccinated = case_when(vaccinated == "1" ~ "Vaccine",
                                vaccinated == "0" ~ "Control")) %>%
  rename(Treatment = vaccinated,
         Sex = sex,
         `Mean SFUs` = avg_spots)
# fit full model
nb.mod.full <- glm.nb(`Mean SFUs` ~ Treatment * Sex,
                      link = "log",
                      data = glm.data)
# summary(nb.mod.full)

# fit main effects model
nb.mod.main <- glm.nb(`Mean SFUs` ~ Treatment + Sex,
                      link = "log",
                      data = glm.data)
# summary(nb.mod.main)

# fit reduced model
nb.mod.red <- glm.nb(`Mean SFUs` ~ Treatment,
                     link = "log",
                     data = glm.data)
# summary(nb.mod.red)
```

Create Regression Table

```r
put_vector_in_parentheses <- function(values){
    put_value_in_parentheses <- function(value){
        if(is.na(value)){
            return(value)
        }
        else{
            return(paste0("[", value, "]"))
        }
    }
    new_values <- sapply(values, put_value_in_parentheses)
    return(new_values)
}

mytheme <- list(# round large p-values to two places
    "pkgwide-fn:pvalue_fun" = function(x) style_pvalue(x, digits = 2, prepend_p = TRUE))

set_gtsummary_theme(mytheme)

full <- tbl_regression(nb.mod.full, exponentiate = TRUE) %>%
    modify_table_body(~ .x %>% dplyr::mutate(ci = put_vector_in_parentheses(ci))) %>%
  add_global_p() %>%
  bold_p(t = 0.05) %>%
  bold_labels() %>%
  add_glance_table(
    label = list(nobs ~ "Num. Obs.", AIC ~ "AIC"),
    include = c(nobs, AIC))
```

```
## Warning: glm.fit: algorithm did not converge
```

```r
main <- tbl_regression(nb.mod.main, exponentiate = TRUE) %>%
    modify_table_body(~ .x %>% dplyr::mutate(ci = put_vector_in_parentheses(ci))) %>%
  add_global_p() %>%
  bold_p(t = 0.05) %>%
  bold_labels() %>%
  add_glance_table(
```

```
    label = list(nobs ~ "Num. Obs.", AIC ~ "AIC"),
    include = c(nobs, AIC))
```

Warning: glm.fit: algorithm did not converge

```
reduced <- tbl_regression(nb.mod.red, exponentiate = TRUE) %>%
    modify_table_body(~ .x %>% dplyr::mutate(ci = put_vector_in_parentheses(ci))) %>%
  add_global_p() %>%
  bold_p(t = 0.05) %>%
  bold_labels() %>%
  add_glance_table(
    label = list(nobs ~ "Num. Obs.", AIC ~ "AIC"),
    include = c(nobs, AIC))
```

```
merge <- tbl_merge(
    tbls = list(full, main, reduced),
    tab_spanner = c("**Full Model**", "**Main Effects Model**","**Reduced Model**")
  )
```

```
merge %>%
  as_gt() %>%
  tab_options(table.align='left')
```

Characteristic	Full Model IRR[1]	Full Model 95% CI[1]	Full Model p-value	Main Effects Model IRR[1]	Main Effects Model 95% CI[1]	Main Effects Model p-value	Reduced Model IRR[1]	Reduced Model 95% CI[1]	Reduced Model p-value
Treatment			p<0.001			p<0.001			p<0.001
Control	—	—		—	—		—	—	
Vaccine	97.0	[10.2, 1,045]		37.5	[7.87, 175]		40.7	[8.78, 181]	
Sex			p=0.47			p=0.70			
Female	—	—		—	—				
Male	2.50	[0.20, 36.0]		0.76	[0.19, 3.30]				
Treatment * Sex			p=0.26						
Vaccine * Male	0.19	[0.01, 3.54]							
Num. Obs.	10			10			10		
AIC	86.3			85.5			83.7		

[1]IRR = Incidence Rate Ratio, CI = Confidence Interval