HW_3

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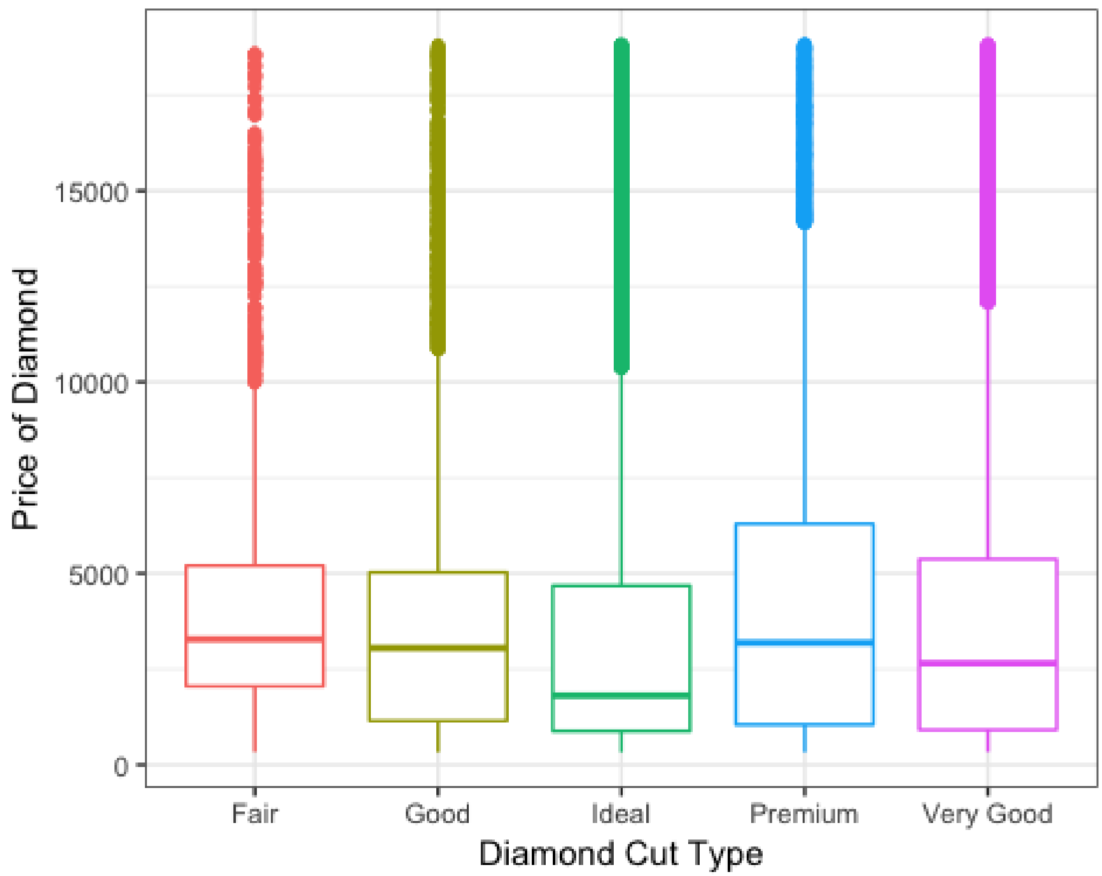
Question 1: What is the effect of cut quality on diamond price?

```
diamonds <- read.csv("Data/diamond.csv")
head(diamonds[1:3, ])

##   price     cut carat
## 1   326   Ideal  0.23
## 2   326 Premium  0.21
## 3   327    Good  0.23

dia_mod <- glm(diamonds$price ~ diamonds$cut, family = "poisson")
coef(dia_mod)

##          (Intercept)      diamonds$cutGood     diamonds$cutIdeal
##            8.3799424            -0.1038367            -0.2316292
##   diamonds$cutPremium diamonds$cutVery Good
##            0.0504411            -0.0904632

exp(8.3799424)

## [1] 4358.758

exp(8.3799424 + -0.1038367) - exp(8.3799424)  #Good effect from fair

## [1] -429.8935

exp(8.3799424 + -0.2316292) - exp(8.3799424)  #Ideal effect from fair

## [1] -901.2159

exp(8.3799424 + 0.0504411) - exp(8.3799424)  #Premium effect from fair

## [1] 225.5

exp(8.3799424 + -0.0904632) - exp(8.3799424)  #Very_Good effect from fair

## [1] -376.9979

confint(dia_mod)  # None overlap zero = signficicant; 95% interval is very
narrow = highly confident

##                             2.5 %      97.5 %
## (Intercept)            8.37920242  8.38068216
## diamonds$cutGood      -0.10470072 -0.10297248
```

```
## diamonds$cutIdeal      -0.23240302 -0.23085517
## diamonds$cutPremium     0.04966133  0.05122103
## diamonds$cutVery Good -0.09125511 -0.08967112
```

```
ggplot(diamonds, aes(x = cut, y = price, colour = cut)) + geom_boxplot(notch
= FALSE) +
    labs(x = "Diamond Cut Type", y = "Price of Diamond") + theme_bw() +
    theme(legend.position = "none")
```



The cut quality of diamonds effects the price of diamonds. The basline price of diamonds cut at fair quality is $4358.76. The price of diamonds cut at fair quality is higher than diamonds cut at good quality by $429.89, ideal quality by $901.22, and very good quality by $377.00. The price of diamonds cut at fair quality diamond is lower than a premium cut quality diamond by $225.50.

Question 2: Does education have an impact on contraception use?

```
cont <- read.csv("Data/contraception.csv")
head(cont[1:3, ])
```

```
##   age education notUsing using Total
## 1 <25       low       53     6    59
```

```
## 2 <25       low       10     4    14
## 3 <25      high      212    52   264
```

```
# Ho: increased education does not effect contraception use
# Ha: increased education promotes contraception use
cont$prop_use <- cont$using/cont$Total
cont_success <- cbind(cont$using, cont$notUsing)
head(cont_success)
```

```
##      [,1] [,2]
## [1,]    6   53
## [2,]    4   10
## [3,]   52  212
## [4,]   10   50
## [5,]   14   60
## [6,]   10   19
```

```
cont_mod <- glm(cont_success ~ cont$education, family = "binomial")
summary(cont_mod)  #no signifcance between groups
```

```
## 
## Call:
## glm(formula = cont_success ~ cont$education, family = "binomial")
## 
## Deviance Residuals: 
##     Min       1Q   Median       3Q      Max  
## -4.0868  -2.6566  -0.5529   2.1121   5.6674  
## 
## Coefficients:
##                   Estimate Std. Error z value Pr(>|z|)    
## (Intercept)       -0.81020    0.06871  -11.79   <2e-16 ***
## cont$educationlow  0.09249    0.11011    0.84    0.401    
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## (Dispersion parameter for binomial family taken to be 1)
## 
##     Null deviance: 165.77  on 15  degrees of freedom
## Residual deviance: 165.07  on 14  degrees of freedom
## AIC: 240.58
## 
## Number of Fisher Scoring iterations: 4
```

```
coef(cont_mod)
```

```
##       (Intercept) cont$educationlow 
##       -0.81020374        0.09248529
```

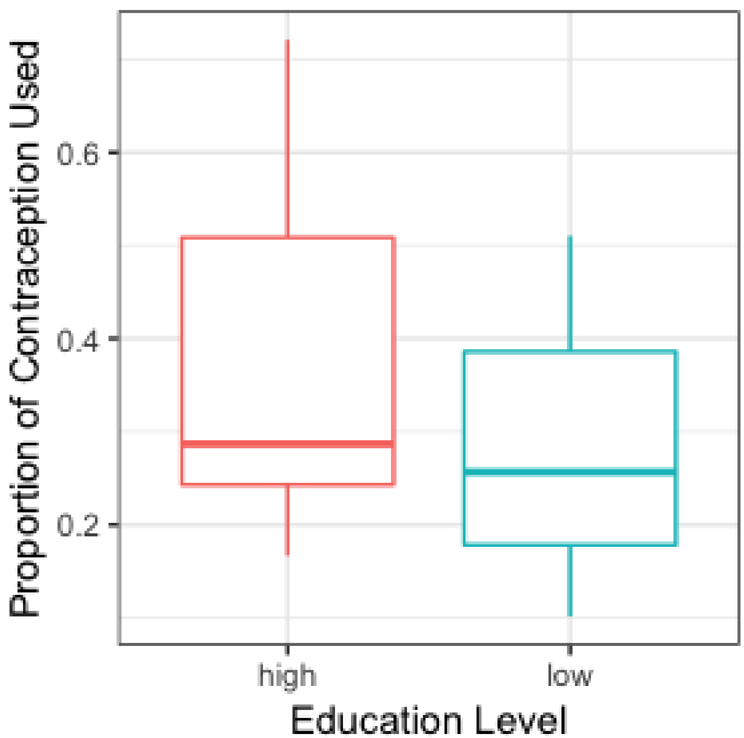
```
plogis(-0.81020374 + 0.09248529) - plogis(-0.81020374)  # 2% effect size 
between high and low education
```

```
## [1] 0.02004851
```

```r
confint(cont_mod)  # no significance because effect of education overlaps zero
```

```
##                        2.5 %     97.5 %
## (Intercept)       -0.9460962 -0.6766394
## cont$educationlow -0.1239481  0.3078275
```

```r
ggplot(cont, aes(x = education, y = prop_use, colour = education)) +
    geom_boxplot(notch = FALSE) + labs(x = "Education Level",
    y = "Proportion of Contraception Used") + theme_bw() +
theme(legend.position = "none")
```



Women with a higher education is 2% more likely to use contraception. However, here is no significant effect that an increased education promotes contraception use.

Question 3: Hurricanes vs Himmicanes

```r
canes <- read.csv("Data/Hurricane Dataset.csv")
head(canes)
```

```
##   Year     Name  MasFem MinPressure_before Minpressure_Updated.2014
## 1 1950     Easy 6.77778                958                      960
## 2 1950     King 1.38889                955                      955
## 3 1952     Able 3.83333                985                      985
## 4 1953  Barbara 9.83333                987                      987
## 5 1953 Florence 8.33333                985                      985
## 6 1954    Carol 8.11111                960                      960
```

```
##   Gender_MF Category alldeaths  NDAM Elapsed.Yrs Source  ZMasFem
## 1         F        3         2  1590          63    MWR -0.00094
## 2         M        3         4  5350          63    MWR -1.67076
## 3         M        1         3   150          61    MWR -0.91331
## 4         F        1         1    58          60    MWR  0.94587
## 5         F        1         0    15          60    MWR  0.48108
## 6         F        3        60 19321          59    MWR  0.41222
##   ZMinPressure_A    ZNDAM
## 1       -0.35636 -0.43913
## 2       -0.51125 -0.14843
## 3        1.03765 -0.55047
## 4        1.14091 -0.55758
## 5        1.03765 -0.56090
## 6       -0.25310  0.93174
```

```
canes <- na.omit(canes)
canes_mod <- glm(canes$alldeaths ~ canes$Gender_MF, family = "poisson")
summary(canes_mod)
```

```
##
## Call:
## glm(formula = canes$alldeaths ~ canes$Gender_MF, family = "poisson")
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -6.8932  -5.3945  -3.7551  -0.3653  27.4348
##
## Coefficients:
##                    Estimate Std. Error z value Pr(>|z|)
## (Intercept)         3.16792    0.02606 121.584   <2e-16 ***
## canes$Gender_MFM -0.51234    0.05496  -9.322   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 4031.9  on 91  degrees of freedom
## Residual deviance: 3937.1  on 90  degrees of freedom
## AIC: 4266
##
## Number of Fisher Scoring iterations: 6
```

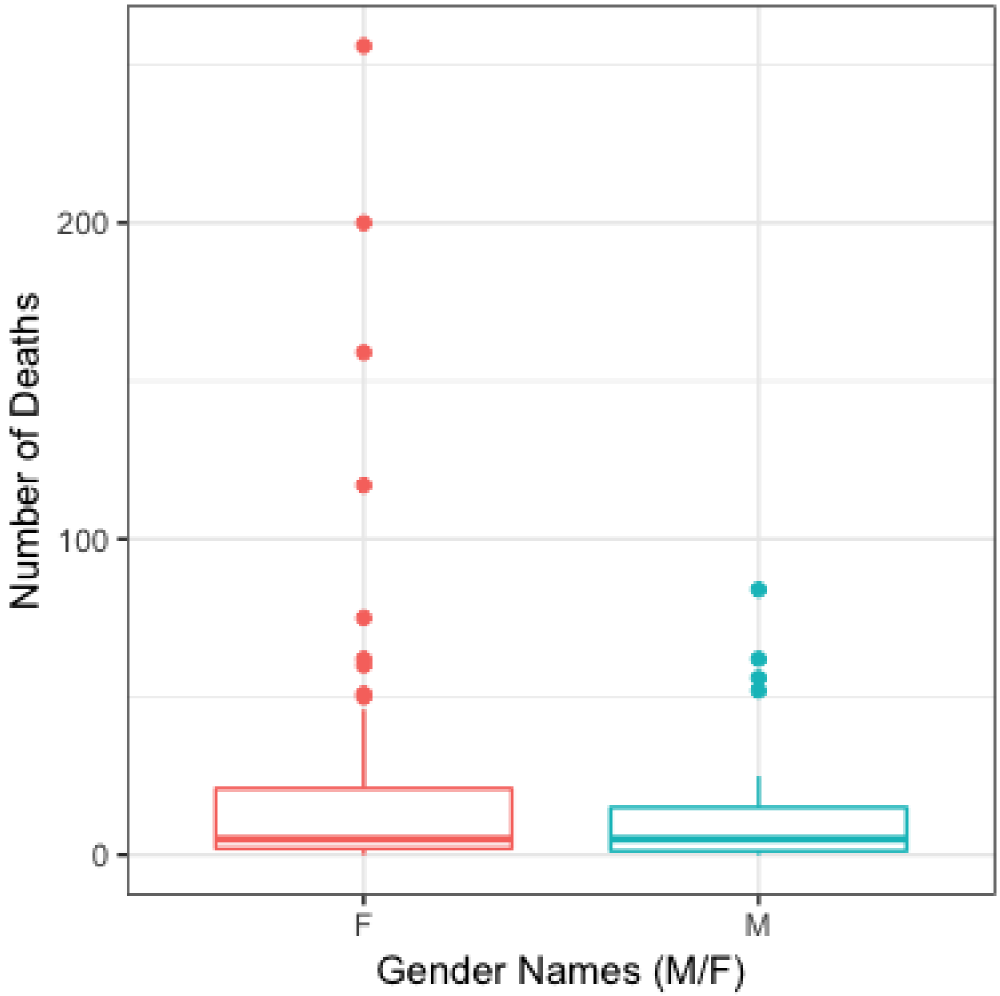
```
coef(canes_mod)
```

```
##      (Intercept) canes$Gender_MFM
##        3.1679220       -0.5123354
```

```
exp(3.167922 + -0.5123354) - exp(3.167922)
```

```
## [1] -9.524731
```

```r
confint(canes_mod)

##                       2.5 %     97.5 %
## (Intercept)       3.1164152  3.2185581
## canes$Gender_MFM -0.6211542 -0.4056501

# negative binomial
canes_negbin <- glm.nb(canes$alldeaths ~ canes$Gender_MF)
coef(canes_negbin)

##      (Intercept) canes$Gender_MFM
##        3.1679220       -0.5123354

confint(canes_negbin)

##                      2.5 %    97.5 %
## (Intercept)       2.816448 3.5640722
## canes$Gender_MFM -1.149166 0.1720959

ggplot(canes, aes(x = Gender_MF, y = alldeaths, colour = Gender_MF)) +
    geom_boxplot(notch = FALSE) + labs(x = "Gender Names (M/F)",
    y = "Number of Deaths") + theme_bw() + theme(legend.position = "none")
```



The hurricanes with a female names has 9.5 more deahts than male names. The poisson generalized linear model shows signficances that hurricanes have more deaths than himmicanes. The results of the poisson glm states that the gender names of hurricanes has significances on the total number of deaths, this is similar to Jung et al.'s conclusion. However, the poisson glm is not the best glm to use for this data set due to the overdispersed toward the female names. The negative binomial results indicate there is no significant differences (95% CI overlap zero) between female and male hurricane names and total deaths.

Question 4:

```
## 'data.frame':    48 obs. of  3 variables:
##  $ Study_Area: chr  "NCA" "NCA" "NCA" "NCA" ...
##  $ Array_ID  : Factor w/ 48 levels "FD1","FD2","FD3",..: 12 13 14 15 16 17
18 19 20 21 ...
##  $ Richness  : num  1 2 1 3 2 1 1 2 3 2 ...

hist(rich$Richness)
```


```
rich_mod <- glm(rich$Richness ~ rich$Study_Area, family = "poisson")
summary(rich_mod)
```

```
##
## Call:
## glm(formula = rich$Richness ~ rich$Study_Area, family = "poisson")
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -2.3214  -0.4435  -0.1260   0.7414   1.7308
##
## Coefficients:
##                        Estimate Std. Error z value Pr(>|z|)
## (Intercept)              0.4055     0.2357   1.720   0.0854 .
## rich$Study_AreaOCTC      0.5857     0.2566   2.282   0.0225 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 50.145  on 47  degrees of freedom
## Residual deviance: 44.215  on 46  degrees of freedom
## AIC: 167.92
```

```
##
## Number of Fisher Scoring iterations: 5
```

```r
coef(rich_mod)
```

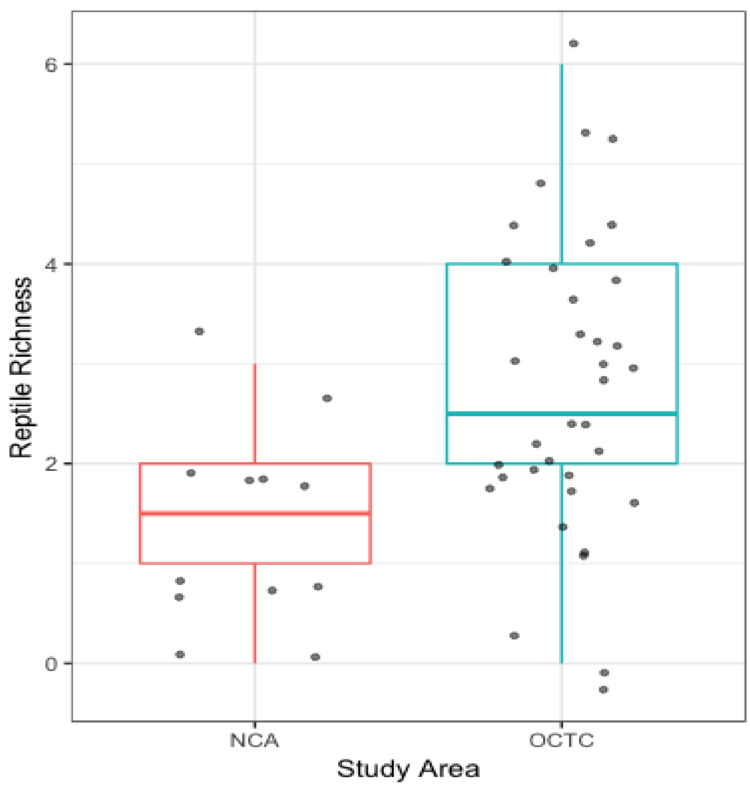
```
##         (Intercept) rich$Study_AreaOCTC
##           0.4054651           0.5857269
```

```r
exp(0.4054651 + 0.5857269) - exp(0.4054651)
```

```
## [1] 1.194444
```

```r
confint(rich_mod)
```

```
##                           2.5 %    97.5 %
## (Intercept)         -0.09503459 0.8343866
## rich$Study_AreaOCTC  0.10879789 1.1209811
```



The reptile richness is significantly different between two study areas. There is a 119% difference in reptile richness between study areas. The 95% CI does not overlap zero; however, the interval is wide for the effect size suggesting low confindence in the significance. The reptile richness data set is does not fit normal or binomial regression; however, the poisson regression is not a good fit either due to the overdispersion of the data. A negative binomial to account for the overdispersion would be a better fit, but the theta is too large causing errors.