ST346 Generalized Linear Models for Regression and Classification - Coursework 1

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Contents

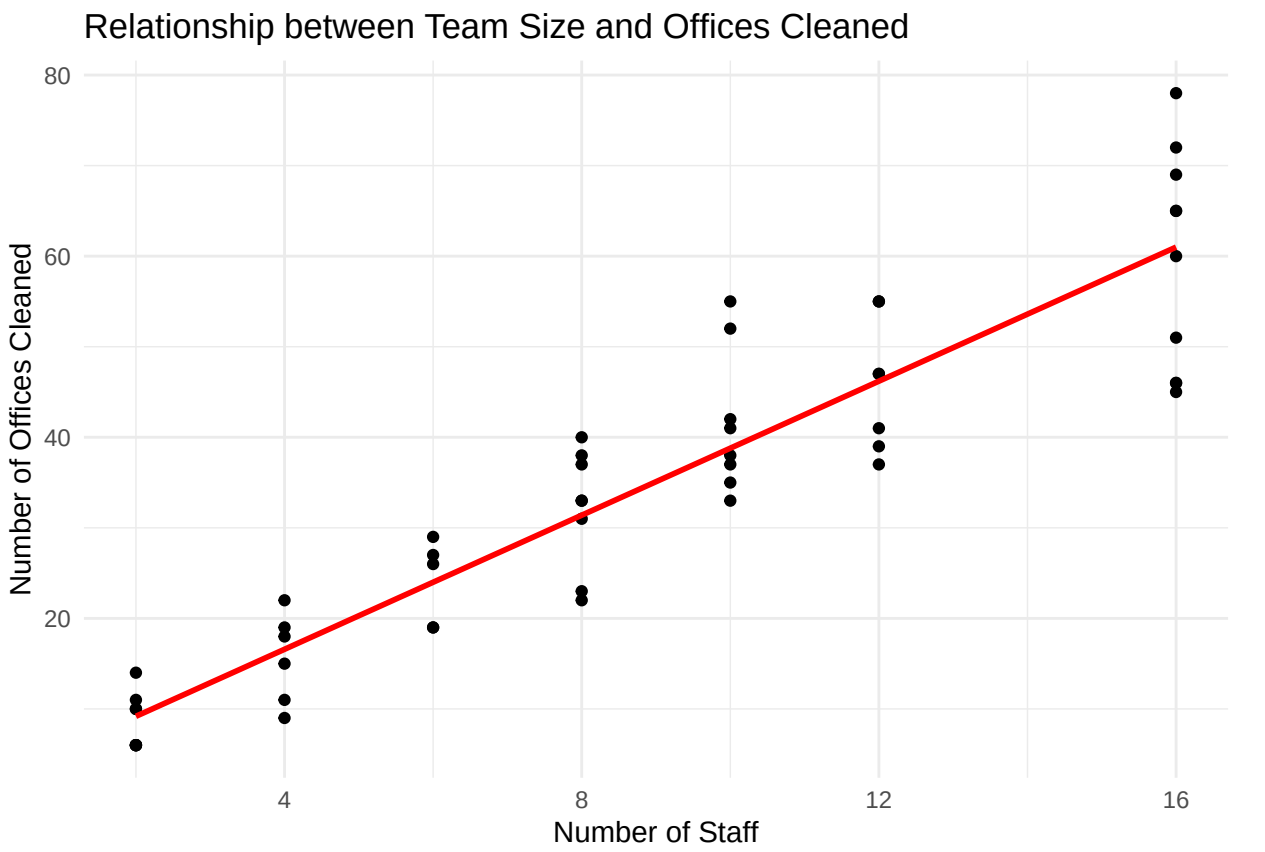
1 Data Loading and Exploration

```
# Load the dataset
load("CourseworkData1.rda")
```

2 Question 1: Weighted Regression

2.1 Part a: Data Visualization

```
# Visualize the relationship between team size and offices cleaned
plot <- ggplot(data=cleaners, aes(x = Staff, y = Offices)) +
  geom_point() +
  geom_smooth(method = "lm", se = FALSE, color = "red") +
  labs(title = "Relationship between Team Size and Offices Cleaned",
       x = "Number of Staff",
       y = "Number of Offices Cleaned") +
  theme_minimal()
print(plot)
```




```
# Calculate correlation
correlation <- cor(cleaners$Staff, cleaners$Offices)
print(paste("Correlation coefficient:", round(correlation, 3)))
```

```
## [1] "Correlation coefficient: 0.926"
```

```
summary(cleaners)
```

```
##      Staff           Offices
##  Min.   : 2.000   Min.   : 6.00
##  1st Qu.: 4.000   1st Qu.:19.00
##  Median : 8.000   Median :35.00
##  Mean   : 8.679   Mean   :33.91
##  3rd Qu.:12.000   3rd Qu.:46.00
##  Max.   :16.000   Max.   :78.00
```

The scatter plot shows a positive correlation between team size and offices cleaned. As the number of staff increases, the number of offices cleaned also increases. The correlation coefficient is 0.926, very close to 1, showing a strong positive relation. It is reasonable to assume a linear relationship.

2.2 Part b: Linear Model Fitting

```
# Fit a normal linear model and interpret the slope coefficient
model <- lm(Offices ~ Staff, data = cleaners)
summary(model)
```

```
##
```

```
## Call:
## lm(formula = Offices ~ Staff, data = cleaners)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -15.9990  -4.9901   0.8046   4.0010  17.0010
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   1.7847     2.0965   0.851    0.399
## Staff         3.7009     0.2118  17.472   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 7.336 on 51 degrees of freedom
## Multiple R-squared:  0.8569, Adjusted R-squared:  0.854
## F-statistic: 305.3 on 1 and 51 DF,  p-value: < 2.2e-16
```

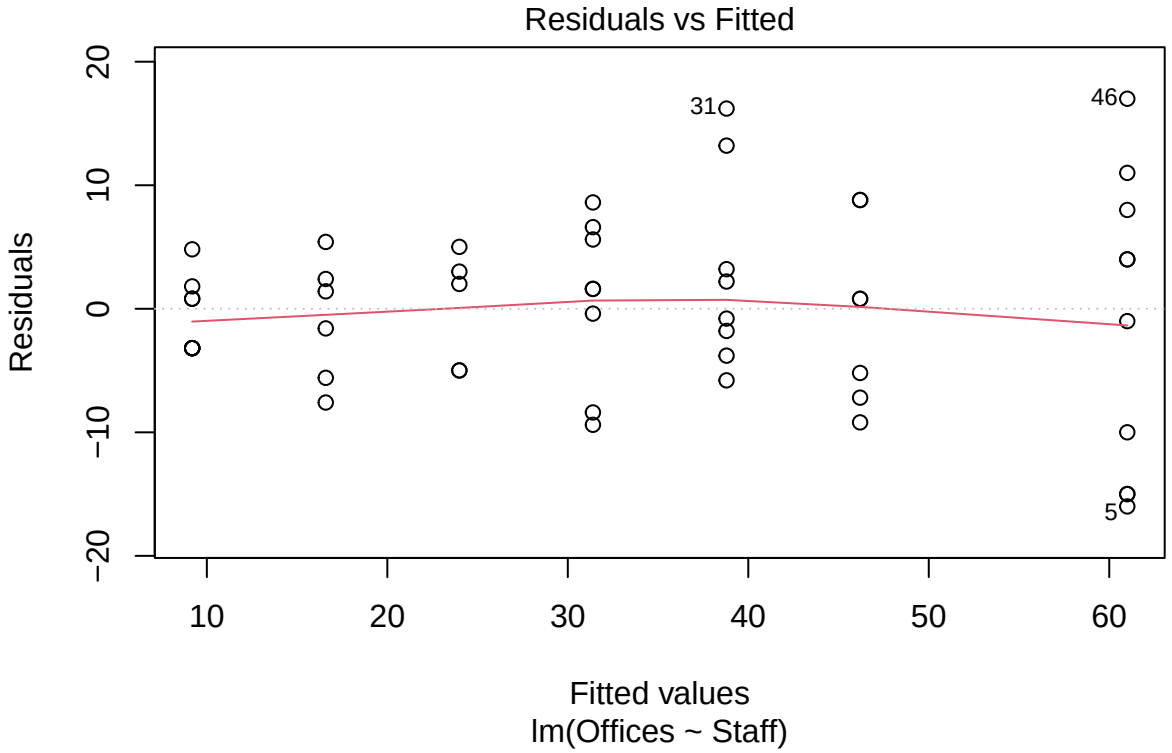
```
slope <- coef(model)["Staff"]
print(paste("Slope coefficient:", round(slope, 3)))
```

```
## [1] "Slope coefficient: 3.701"
```

The slope coefficient is 3.7, meaning on average for each additional cleaner, 3.7 offices can be cleaned.

2.3 Part c: Residual Analysis

```
# Produce and evaluate a residuals versus fitted values plot
plot(model, which=1)
```



The smoother resembles a horizontal line at zero. However, the residual plot resembles a 'right-opening

megaphone'. The variation of the residuals is increasing with fitted value. It violates the assumption of homoscedasticity.

2.4 Part d: Variance Estimation Table

```
variance_table <- aggregate(Offices ~ Staff, data = cleaners, FUN = var)
names(variance_table) <- c("Team_size_x", "Variance")
variance_table$Variance <- round(variance_table$Variance, 2)
print(variance_table)
```

```
##   Team_size_x Variance
## 1           2     9.00
## 2           4    24.67
## 3           6    22.00
## 4           8    44.12
## 5          10    62.84
## 6          12    53.14
## 7          16   144.01
```

This produces the same variance estimates as given in the question.

2.5 Part e: Weight Calculation

Derivation of weight expression:

Since we assume that $w_i = 1$ for $x_i = 2$ and $Var(Y_i|x_i) = Var(Y_j|x_j)$ if $x_i = x_j$,

$$Var(Y_i|x_i) = \phi/w_i$$
$$w_i = \phi/Var(Y_i|x_i)$$
$$Var(Y_i|x = 2) = \phi/1 = \phi$$
$$w_i = \frac{\phi/\text{Var}(Y_i|x_i)}{\phi/\text{Var}(Y|x = 2)} = \frac{\text{Var}(Y|x = 2)}{\text{Var}(Y_i|x_i)}$$

```
# Use the derived expression to compute estimates
base_variance <- variance_table$Variance[variance_table$Team_size_x == 2]
variance_table$Weight <- base_variance / variance_table$Variance
print(variance_table)
```

```
##   Team_size_x Variance     Weight
## 1           2     9.00 1.00000000
## 2           4    24.67 0.36481557
## 3           6    22.00 0.40909091
## 4           8    44.12 0.20398912
## 5          10    62.84 0.14322088
## 6          12    53.14 0.16936394
## 7          16   144.01 0.06249566
```

```
assign_weight <- function(staff_size) {
  weight <- variance_table$Weight[variance_table$Team_size_x == staff_size]
  return(weight)
}

cleaners$Weight <- sapply(cleaners$Staff, assign_weight)
head(cleaners)
```

```
##   Staff Offices     Weight
## 1    16      51 0.06249566
## 2    10      37 0.14322088
## 3    12      37 0.16936394
## 4    16      46 0.06249566
## 5    16      45 0.06249566
## 6     4      11 0.36481557
```

```
summary(cleaners$Weight)
```

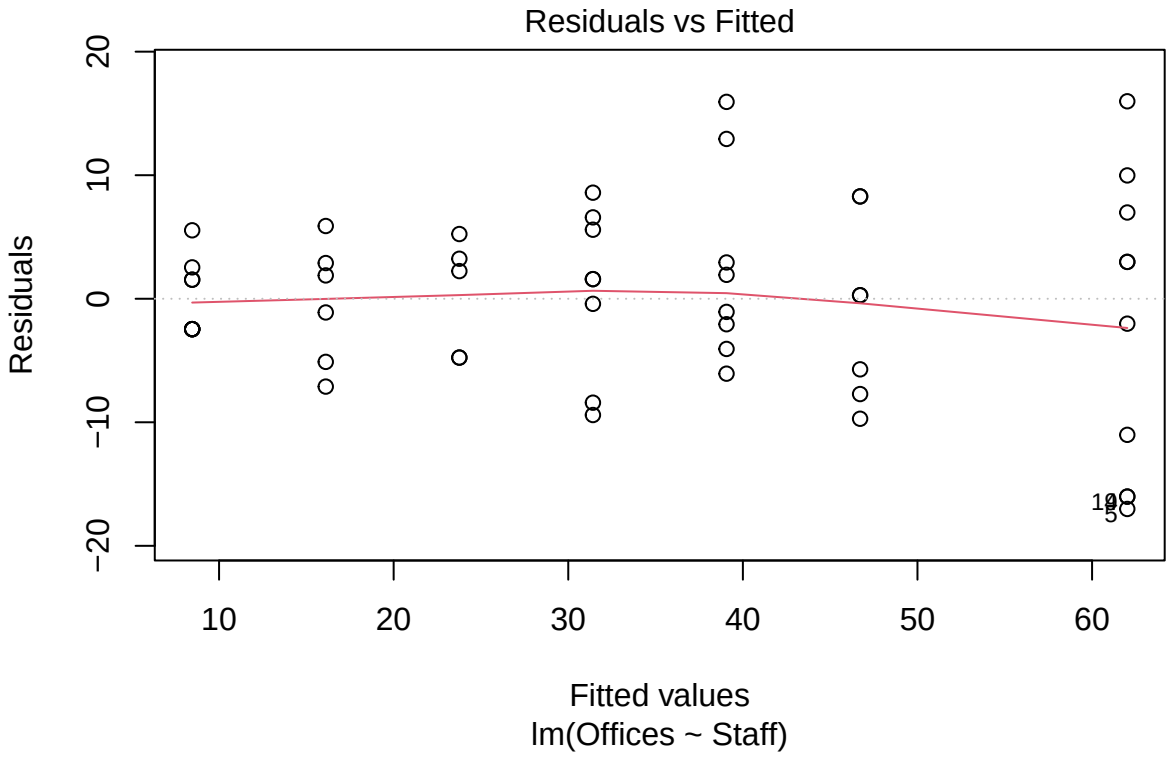
```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##  0.0625  0.1432  0.2040  0.3363  0.4091  1.0000
```

2.6 Part f: Weighted Linear Model

```
# Model summary
weighted_model <- lm(Offices ~ Staff, data = cleaners, weights = Weight)
summary(weighted_model)
```

```
##
## Call:
## lm(formula = Offices ~ Staff, data = cleaners, weights = Weight)
##
## Weighted Residuals:
##     Min      1Q  Median      3Q     Max
## -4.2952 -2.4604  0.1173  2.0709  6.0309
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   0.8095     1.1158   0.725    0.471
## Staff         3.8255     0.1788  21.400   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.894 on 51 degrees of freedom
## Multiple R-squared:  0.8998, Adjusted R-squared:  0.8978
## F-statistic:   458 on 1 and 51 DF,  p-value: < 2.2e-16
```

```
# Weighted residual plot
plot(weighted_model, which=1)
```



The smoother resembles a horizontal line at zero. No clear 'right-opening megaphone' pattern. The variation of the residuals is rather stable with fitted value. It follows the assumption of homoscedasticity and linearity. The slope coefficient is 3.826, meaning on average for each additional cleaner, 3.826 offices can be cleaned. It is higher than that of the unweighted model, suggesting the unweighted model underestimates the impact of staff number. Overall, the weighted model is more suitable for this dataset.

2.7 Part g: Transformed Model

```r
# Transform the model
cleaners$Y_star <- cleaners$Offices * sqrt(cleaners$Weight)
cleaners$x_star <- cleaners$Staff * sqrt(cleaners$Weight)
cleaners$intercept_star <- sqrt(cleaners$Weight)
transformed_model <- lm(Y_star ~ 0 + intercept_star + x_star, data = cleaners)

# Report model summary
summary(transformed_model)
```

```
##
## Call:
## lm(formula = Y_star ~ 0 + intercept_star + x_star, data = cleaners)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -4.2952 -2.4604  0.1173  2.0709  6.0309
##
## Coefficients:
##                Estimate Std. Error t value Pr(>|t|)
## intercept_star   0.8095     1.1158   0.725    0.471
## x_star           3.8255     0.1788  21.400   <2e-16 ***
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.894 on 51 degrees of freedom
## Multiple R-squared:  0.9617, Adjusted R-squared:  0.9602
## F-statistic: 639.6 on 2 and 51 DF,  p-value: < 2.2e-16
```

```
cat("Transformed model coefficients:\n")
```

```
## Transformed model coefficients:
```

```
print(coef(transformed_model))
```

```
## intercept_star         x_star
##      0.8094971      3.8254605
```

```
cat("\nWeighted model coefficients:\n")
```

```
##
## Weighted model coefficients:
```

```
print(coef(weighted_model))
```

```
## (Intercept)       Staff
##   0.8094971   3.8254605
```

```
cat("\nTransformed model standard errors:\n")
```

```
##
## Transformed model standard errors:
```

```
print(sqrt(diag(vcov(transformed_model))))
```

```
## intercept_star         x_star
##      1.1157924      0.1787589
```

```
cat("\nWeighted model standard errors:\n")
```

```
##
## Weighted model standard errors:
```

```
print(sqrt(diag(vcov(weighted_model))))
```

```
## (Intercept)       Staff
##   1.1157924   0.1787589
```

2.8 Part h: Residual Comparison

```
# Verify that the weighted and transformed model residuals are the same
weighted_residuals <- residuals(weighted_model, type = "response") * sqrt(cleaners$Weight)
transformed_residuals <- residuals(transformed_model)
residual_difference <- weighted_residuals - transformed_residuals
cat("Summary of residual differences:\n")
```

```
## Summary of residual differences:
```

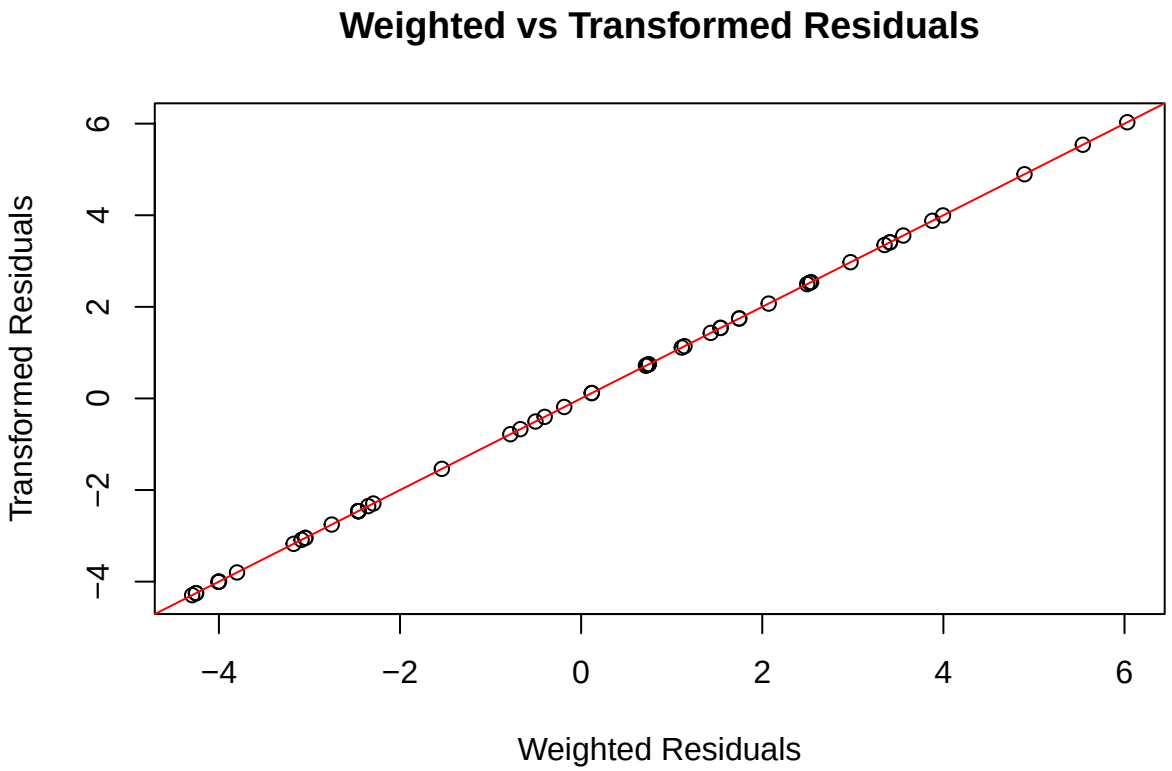
```
print(summary(residual_difference))
```

```
##       Min.    1st Qu.     Median       Mean    3rd Qu.       Max.
## -2.220e-16  0.000e+00  0.000e+00  8.903e-18  0.000e+00  4.441e-16
```

```r
all_same <- all(abs(residual_difference) < 1e-10)
cat("\nAre all residuals essentially the same? ", all_same)
```

```
##
## Are all residuals essentially the same?  TRUE
```

```r
plot(weighted_residuals, transformed_residuals,
     main = "Weighted vs Transformed Residuals",
     xlab = "Weighted Residuals", ylab = "Transformed Residuals")
abline(0, 1, col = "red")
```




```r
residual_correlation <- cor(weighted_residuals, transformed_residuals)
cat("\nCorrelation between residuals: ", residual_correlation)
```

```
##
## Correlation between residuals:  1
```

3 Question 2: Logistic Regression

3.1 Part a: Logistic Regression Model

Use logistic function to turn linear predictor into probability:

$$P(Poisonous|Cup \quad Diameter_i) = h(\eta_i) = \frac{1}{1 + exp(-\alpha - \beta * Diameter_i)}$$

3.2 Part b: Odds Ratio Calculation

$$odds \quad ratio = odds(Diameter = 10)/odds(Diameter = 5) = exp(\beta * (10 - 5)) = exp(5\beta)$$

The odds ratio for a mushroom with 10 cm cap diameter vs 5 cm cap diameter is 0.8042

```r
model <- glm(Class ~ Diameter, data = mushrooms, family = binomial)
summary(model)
```

```
##
## Call:
## glm(formula = Class ~ Diameter, family = binomial, data = mushrooms)
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  0.08027    0.08145   0.986    0.324
## Diameter    -0.04358    0.01056  -4.128 3.66e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 2752.2  on 1999  degrees of freedom
## Residual deviance: 2734.6  on 1998  degrees of freedom
## AIC: 2738.6
##
## Number of Fisher Scoring iterations: 4
```

```r
beta <- coef(model)["Diameter"]
odds_ratio <- exp(beta * 5)
print(odds_ratio)
```

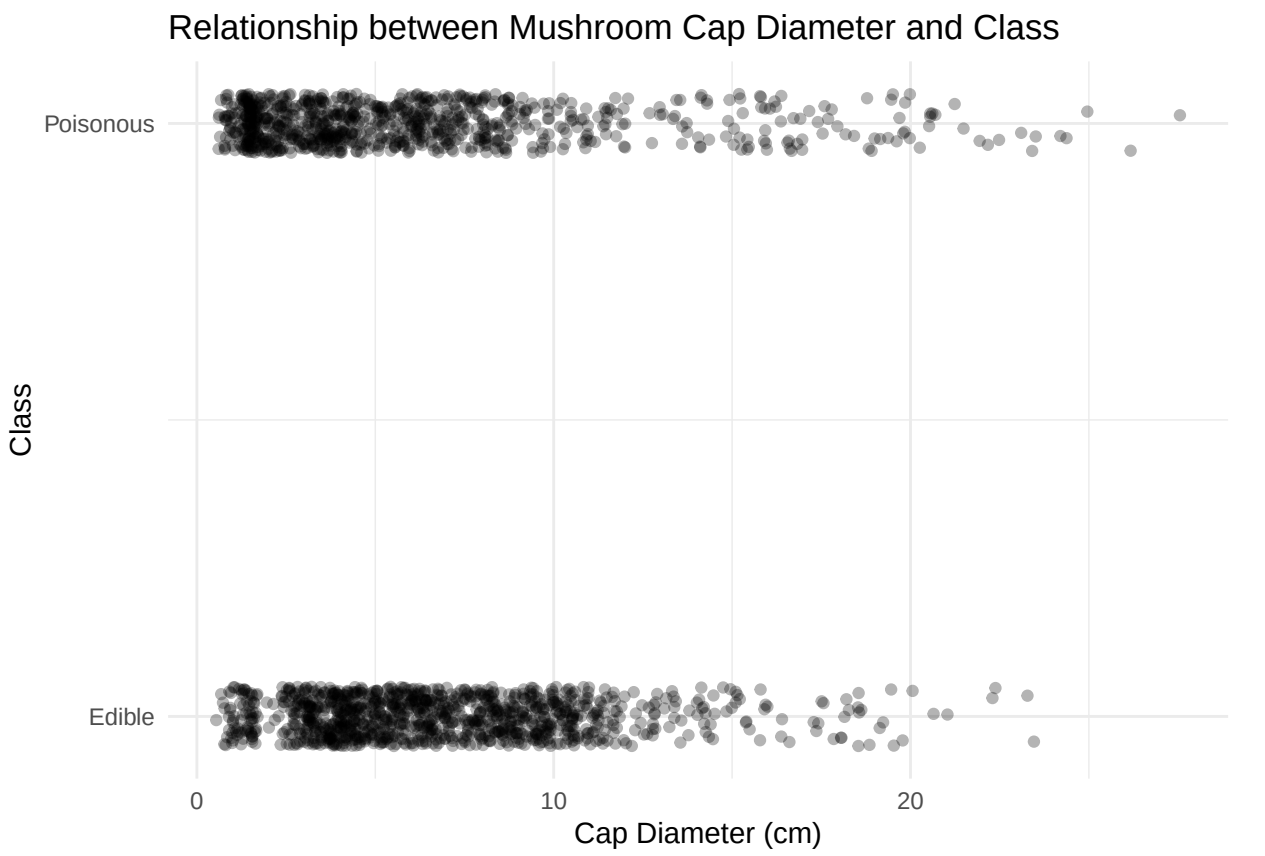
```
##  Diameter
## 0.8042195
```

3.3 Part c: Empirical Relationship Plot

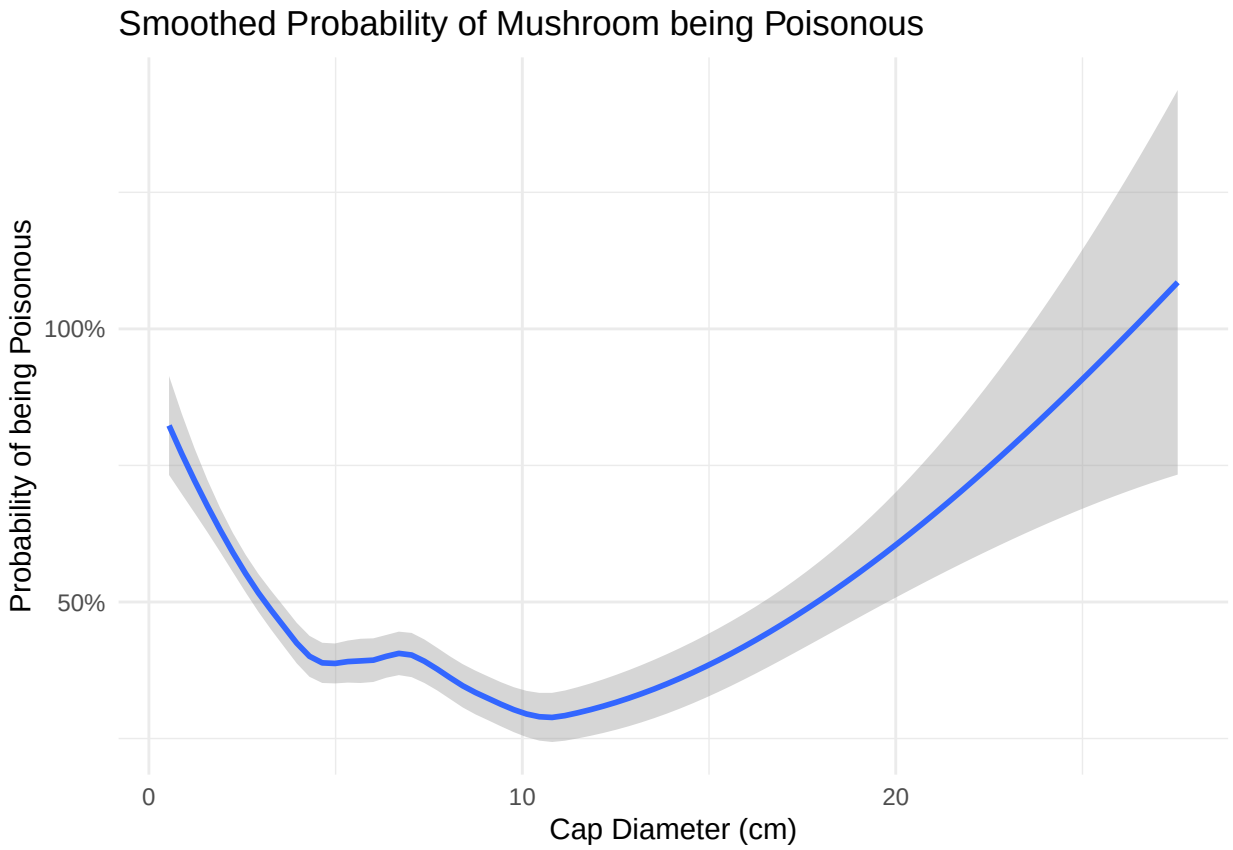
```r
p1 <- ggplot(mushrooms, aes(x = Diameter, y = as.numeric(Class) - 1)) +
  geom_jitter(alpha = 0.3, height = 0.05) +
  scale_y_continuous(breaks = c(0, 1), labels = c("Edible", "Poisonous")) +
  labs(title = "Relationship between Mushroom Cap Diameter and Class",
       x = "Cap Diameter (cm)", y = "Class") +
  theme_minimal()

p2 <- ggplot(mushrooms, aes(x = Diameter, y = as.numeric(Class) - 1)) +
  geom_smooth(method = "loess", se = TRUE) +
  scale_y_continuous(labels = scales::percent) +
  labs(title = "Smoothed Probability of Mushroom being Poisonous",
       x = "Cap Diameter (cm)", y = "Probability of being Poisonous") +
  theme_minimal()

print(p1)
```


Relationship between Mushroom Cap Diameter and Class
Poisonous
Edible
Class
0
10
20
Cap Diameter (cm)

```
print(p2)
```




```
summary_data <- mushrooms %>%
  group_by(Diameter) %>%
  summarise(prob_poisonous = mean(Class == "poisonous"))
head(summary_data)
```

```
## # A tibble: 6 x 2
##   Diameter prob_poisonous
##      <dbl>          <dbl>
## 1     0.54            0
## 2     0.61            1
## 3     0.62            1
## 4     0.63            1
## 5     0.65            1
## 6     0.68            0.5
```

The probability of being poisonous is higher in the smaller diameter range and decreases with increasing diameter. A minimum is reached in the medium diameter range (about 10-12 cm); thereafter, the toxic probability rises slowly again as the diameter continues to increase. Overall, the smoother is not an s-shaped trend,which is typical shape of logistic regression,indicating the relationship assumed in (a) is not fitted enough.

3.4 Part d: Quadratic Logistic Regression

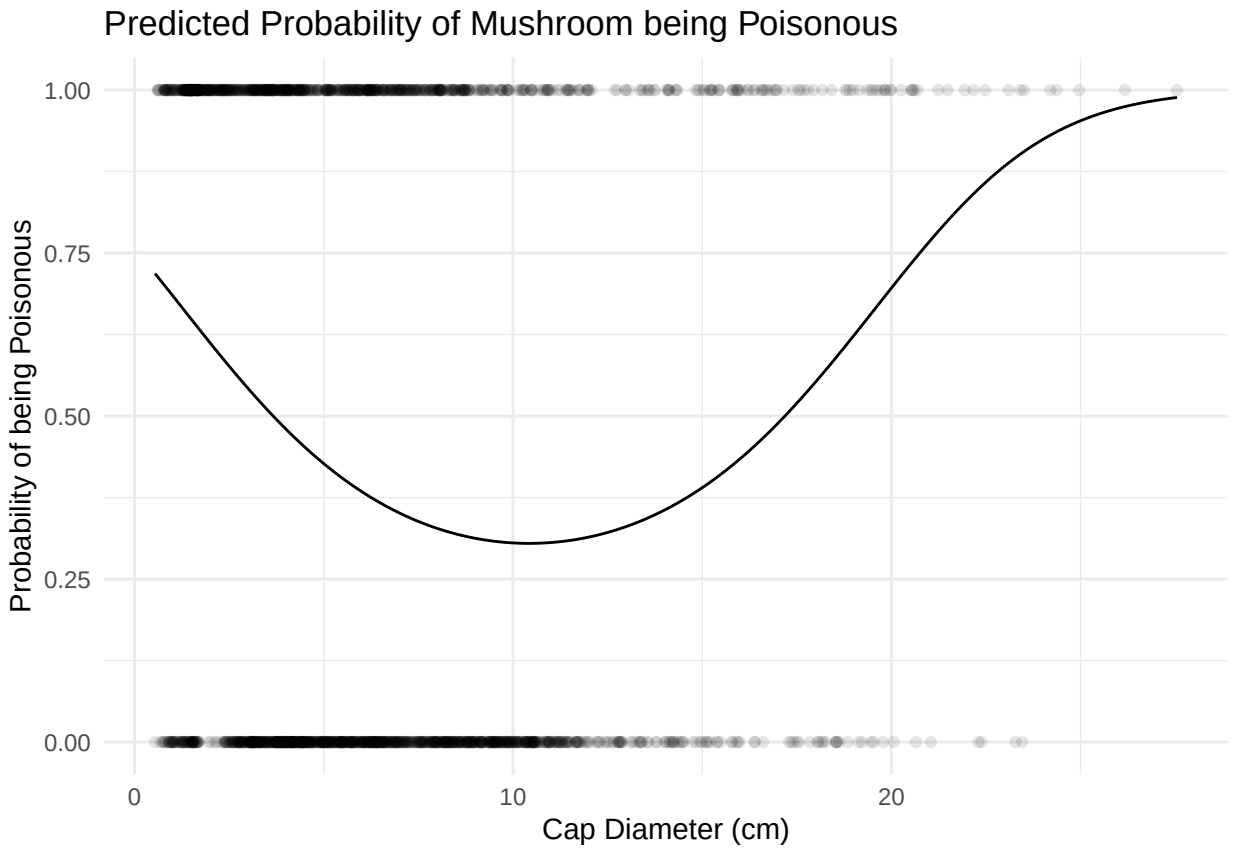
```
#fit a new quadratic regression model
quadratic_model <- glm(Class ~ Diameter + I(Diameter^2), data = mushrooms, family = binomial)

#predict probability of a mushroom being poisonous
```

```r
new_data <- data.frame(Diameter = seq(min(mushrooms$Diameter), max(mushrooms$Diameter), length.out = 200
new_data$Probability <- predict(quadratic_model, newdata = new_data, type = "response")

#plot
p <- ggplot(new_data, aes(x = Diameter, y = Probability)) +
  geom_line() +
  geom_point(data = mushrooms, aes(y = as.numeric(Class) - 1), alpha = 0.1) +
  labs(title = "Predicted Probability of Mushroom being Poisonous",
       x = "Cap Diameter (cm)",
       y = "Probability of being Poisonous") +
  theme_minimal()

print(p)
```




```r
summary(quadratic_model)
```

```
##
## Call:
## glm(formula = Class ~ Diameter + I(Diameter^2), family = binomial,
##     data = mushrooms)
##
## Coefficients:
##                Estimate Std. Error z value Pr(>|z|)
## (Intercept)    1.135480   0.132419   8.575   <2e-16 ***
## Diameter      -0.376103   0.034742 -10.826   <2e-16 ***
## I(Diameter^2)  0.018040   0.001847   9.770   <2e-16 ***
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 2752.2  on 1999  degrees of freedom
## Residual deviance: 2618.8  on 1997  degrees of freedom
## AIC: 2624.8
##
## Number of Fisher Scoring iterations: 4
```

The Quadratic Logistic Regression shows a clear non-linear relationship between the cap diameter of a mushroom and its probability of being poisonous. From the S-shaped curve in the plot we know: small diameter mushrooms have a higher probability of being poisonous, and as the diameter increases, the probability drops rapidly to a low point in the medium diameter range and then rises again. This model fits the trend of the data in the scatterplot better, suggesting it captures the characteristics of the data more accurately than simple linear logistic regression.

3.5 Part e: Predict

```
#round diameters to the nearest half cm
diameters <- seq(round(min(mushrooms$Diameter) * 2) / 2,
                 round(max(mushrooms$Diameter) * 2) / 2,
                 by = 0.5)

#use the rounded diameters to fit a new model.
pred_data <- data.frame(Diameter = diameters)

#predicted probability of a mushroom being poisonous fall below 50%
pred_data$Probability <- predict(quadratic_model, newdata = pred_data, type = "response")
safe_diameters <- pred_data[pred_data$Probability < 0.5, ]

cat("Cap diameters (to nearest 0.5 cm) where predicted probability of being poisonous is below 50%:\n")
```

```
## Cap diameters (to nearest 0.5 cm) where predicted probability of being poisonous is below 50%:
```

```
print(safe_diameters$Diameter)
```

```
##  [1]  4.0  4.5  5.0  5.5  6.0  6.5  7.0  7.5  8.0  8.5  9.0  9.5 10.0 10.5 11.0
## [16] 11.5 12.0 12.5 13.0 13.5 14.0 14.5 15.0 15.5 16.0 16.5 17.0
```