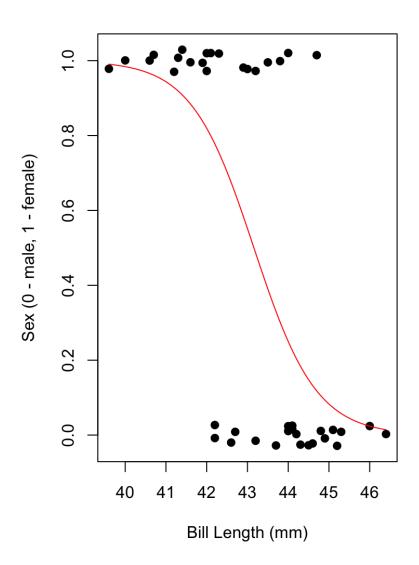
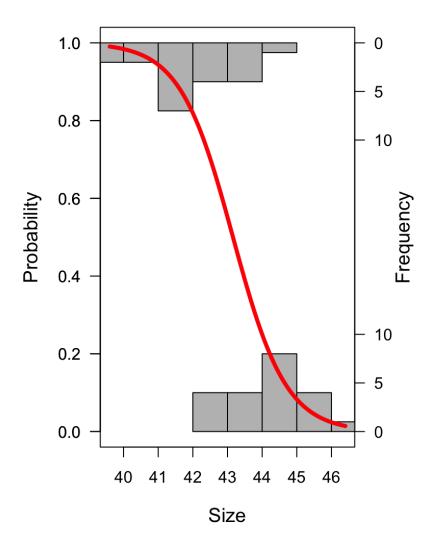
Homework 3

Code: # Load necessary libraries install.packages("popbio") library(popbio) # Load the dataset data(puffinbill) # Display column names and a preview of the dataset names(puffinbill) print(puffinbill) # Assign features to variables sex <- puffinbill\$sex curlen <- puffinbill\$curlen # Apply encoding on the categorical column 'sex' sexcode <- ifelse(sex == "F", 1, 0) print(sexcode) # Plot the observations plot(curlen, jitter(sexcode, 0.15), pch = 19, xlab = "Bill Length (mm)", ylab = "Sex (0 - male, 1 female)") # Fit a generalized logistic regression model model <- glm(sexcode ~ curlen, binomial) summary(model) # Explore the range of 'curlen' values xv <- seq(min(curlen), max(curlen), 0.01) summary(xv) # Predict probabilities using the model yv <- predict(model, list(curlen = xv), type = "response")</pre> summary(yv) # Plot the logistic regression curve lines(xv, yv, col = "red") # Display a frequency distribution of each category logi.hist.plot(curlen, sexcode, boxp = FALSE, type = "count", col = "gray", xlabel = "Size")

Results:

Plots:





Console:

> names(puffinbill)

[1] "bird" "sex" "curlen"

> print(puffinbill)

bird sex curlen

- M 44.1 1 1
- 2 2 M 44.0
- 3 3 M 44.1
- 4 M 42.6 4
- 5 5 M 46.4
- 6 M 42.2 6
- 7 7 M 44.5
- 8 8 M 44.2
- M 43.7 9 9
- 10 M 44.0 10
- M 45.3 11 11
- 12 12 M 44.3
- 13 13 M 46.0
- 14 14 M 45.2
- 15 15 M 43.2
- 16 16 M 45.1
- 17 17 M 44.6
- M 42.2 18 18
- 19 19 M 42.7
- 20 20 M 44.9
- 21 21 M 44.8
- 22 22 F 43.0
- 23 23 F 42.0
- 24 24 F 43.2
- 25 25 F 42.9
- 26 26 F 40.0
- 27 27 F 40.6
- 28 28 F 42.1
- 29 29 F 42.0
- 30 30 F 43.5
- 31 31 F 41.4
- 32 32 F 41.6
- 33 33 F 44.7
- 34 34 F 41.3
- 35 35 F 40.7
- 36 36 F 41.2 37 37 F 42.3
- 38 38 F 44.0
- 39 39 F 39.6
- 40 40 F 43.8
- 41 41 F 41.9

```
> # Assign features to variables
> sex <- puffinbill$sex
> curlen <- puffinbill$curlen
> # Apply encoding on the categorical column 'sex'
> sexcode <- ifelse(sex == "F", 1, 0)
> print(sexcode)
> # Plot the observations
> plot(curlen, jitter(sexcode, 0.15), pch = 19, xlab = "Bill Length (mm)", ylab = "Sex (0 - male, 1 -
female)")
> # Fit a generalized logistic regression model
> model <- glm(sexcode ~ curlen, binomial)
> summary(model)
Call:
glm(formula = sexcode ~ curlen, family = binomial)
Coefficients:
      Estimate Std. Error z value Pr(>|z|)
(Intercept) 56.3369 16.7506 3.363 0.00077 ***
         curlen
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
(Dispersion parameter for binomial family taken to be 1)
  Null deviance: 56.814 on 40 degrees of freedom
Residual deviance: 35.161 on 39 degrees of freedom
AIC: 39.161
Number of Fisher Scoring iterations: 5
> # Explore the range of 'curlen' values
> xv <- seq(min(curlen), max(curlen), 0.01)
> summary(xv)
 Min. 1st Qu. Median Mean 3rd Qu. Max.
 39.6 41.3 43.0 43.0 44.7 46.4
> # Predict probabilities using the model
> yv <- predict(model, list(curlen = xv), type = "response")
> summary(yv)
 Min. 1st Qu. Median Mean 3rd Qu. Max.
0.01433 0.11795 0.55160 0.52276 0.91880 0.99048
> # Plot the logistic regression curve
> lines(xv, yv, col = "red")
```

- > # Display a frequency distribution of each category
- > logi.hist.plot(curlen, sexcode, boxp = FALSE, type = "count", col = "gray", xlabel = "Size")

>