Homework 3

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5.3

(a)

Construct the ROC curve for the toy example in Section 5.4.2. with complete separation.

```
# data import
x = c(1, 2, 3, 4, 5, 6)
y = c(1, 1, 1, 0, 0, 0)

# fit model
toy.model = glm(y~x, family = "binomial")

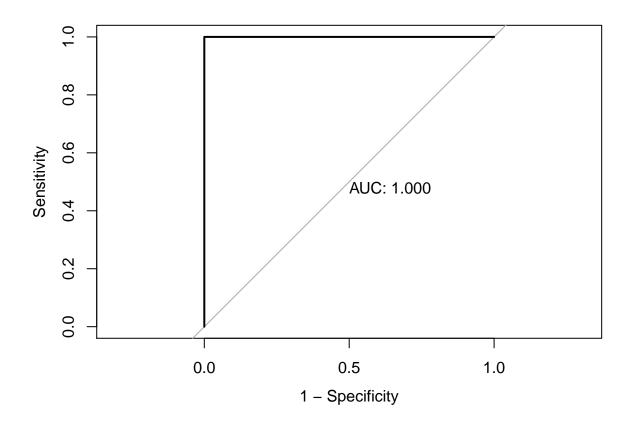
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

toy.pred = predict(toy.model, newdata = data.frame(x))
toy.roc = roc(y, toy.pred)

## Setting levels: control = 0, case = 1

## Setting direction: controls < cases

plot(toy.roc, legacy.axes = T, print.auc = T)</pre>
```



summary(toy.model)

```
##
   glm(formula = y ~ x, family = "binomial")
##
##
  Deviance Residuals:
##
                        2
    2.110e-08
                2.110e-08
                            1.052e-05 -1.052e-05 -2.110e-08 -2.110e-08
##
##
   Coefficients:
##
                Estimate Std. Error z value Pr(>|z|)
##
                  165.32
                          407521.43
                                           0
                                                    1
##
   (Intercept)
                  -47.23
                          115264.41
                                           0
##
##
   (Dispersion parameter for binomial family taken to be 1)
##
##
##
       Null deviance: 8.3178e+00 on 5
                                        degrees of freedom
## Residual deviance: 2.2152e-10
                                  on 4
                                        degrees of freedom
##
  AIC: 4
## Number of Fisher Scoring iterations: 25
```

From the result we could see that, when fitting the GLM, we have a warning message saying that fitted probabilities numerically 0 or 1 occurred. This implies complete/semi-complete separation occurred. We

could see that the AUC = 1. Therefore, in this case, we have complete separation. The standard error of the estimated coefficient for x is very large.

(b)

Add two observations at x = 0.5, one with y = 1 and one with 0.

```
x = c(1, 2, 3, 3.5, 3.5, 4, 5, 6)
y = c(1, 1, 1, 1, 0, 0, 0, 0)

toy.model2 = glm(y~x, family = "binomial")
```

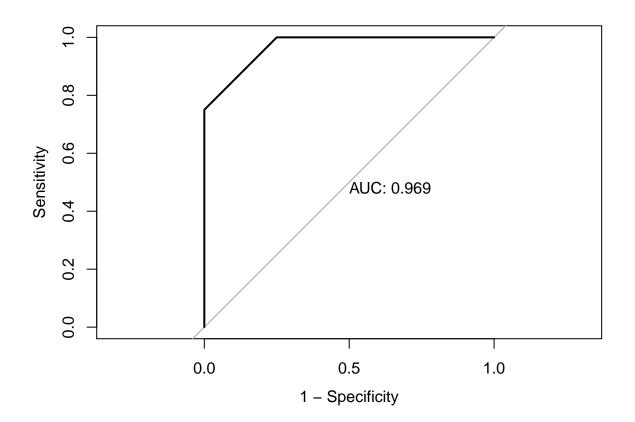
Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

```
toy.pred = predict(toy.model2, newdata = data.frame(x))
toy.roc = roc(y, toy.pred)
```

```
## Setting levels: control = 0, case = 1
```

Setting direction: controls < cases

```
plot(toy.roc, legacy.axes = T, print.auc = T)
```



summary(toy.model2)

```
##
## Call:
## glm(formula = y ~ x, family = "binomial")
##
## Deviance Residuals:
       Min
                  1Q
                        Median
                                      3Q
                                               Max
## -1.17741 -0.00002 0.00000
                                0.00002
                                           1.17741
##
## Coefficients:
##
              Estimate Std. Error z value Pr(>|z|)
## (Intercept) 137.32 54599.64 0.003
                                             0.998
                -39.23
                        15599.90 -0.003
                                             0.998
## x
##
## (Dispersion parameter for binomial family taken to be 1)
##
      Null deviance: 11.0904 on 7 degrees of freedom
## Residual deviance: 2.7726 on 6 degrees of freedom
## AIC: 6.7726
##
## Number of Fisher Scoring iterations: 21
```

In this case, we have AUC = 0.969.But we also have the warning message. So we are facing the semi-complete separation. The standard error for estimated coefficient for x is still very large.

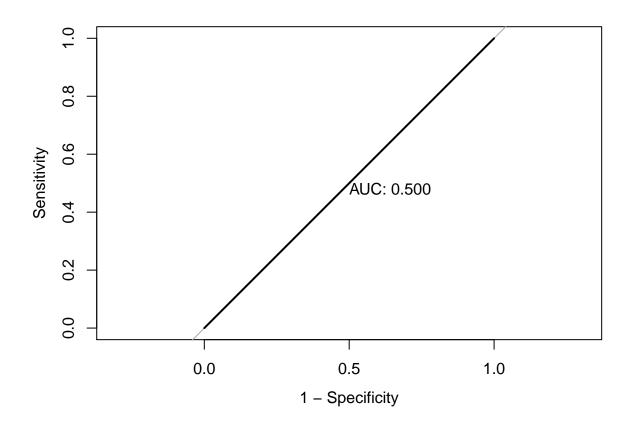
Then we want to construct a toy data set with n = 8 and the area under the ROC curve equals 0.5.

```
# construct new dataset
x.new = c(1, 1, 2, 2, 3, 3, 4, 4)
y.new = c(1, 0, 1, 0, 1, 0)

# fit new model for new dataset
toy.model3 = glm(y.new~x.new, family = "binomial")
toy.pred = predict(toy.model3, newdata = data.frame(x.new))
toy.roc = roc(y.new, toy.pred)
```

```
## Setting direction: controls < cases</pre>
```

Setting levels: control = 0, case = 1



summary(toy.model3)

```
##
## Call:
## glm(formula = y.new ~ x.new, family = "binomial")
## Deviance Residuals:
               1Q Median
                               3Q
                                      Max
## -1.177 -1.177
                    0.000
                                    1.177
                            1.177
##
## Coefficients:
                 Estimate Std. Error z value Pr(>|z|)
## (Intercept) -5.866e-16 1.732e+00
                                           0
## x.new
                1.404e-16 6.325e-01
                                           0
                                                    1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##
       Null deviance: 11.09 on 7 degrees of freedom
## Residual deviance: 11.09 on 6 degrees of freedom
## AIC: 15.09
##
## Number of Fisher Scoring iterations: 2
```

In this case, we have AUC = 0.5 exactly and the ROC looks like a straight line. In this case, the standard error of the estimated coefficient for x is reasonable.

5.5

We now know that $n_i y_i \sim Binomial(n_i, \pi_i)$ and $\mu_i = E(y_i) = \pi_i$. In addition, since $\pi_i = F(\sum_j \beta_j x_{ij})$, we also have $n_i = F^{-1}(\pi_i)$ (as F is absolutely continuous). Another equation is $n_i = \sum_j \beta_j x_{ij}$.

According to the likelihood equation, we have:

$$\begin{split} \frac{\partial L(\beta)}{\partial \beta_{j}} &= \sum_{i=1}^{N} \frac{n_{i}(y_{i} - \mu_{i})}{var(y_{i})} \cdot \frac{\partial \mu_{i}}{\partial n_{i}} \\ &= \sum_{i=1}^{N} \frac{n_{i}(y_{i} - \mu_{i})}{var(y_{i})} \cdot f(n_{i})[f(\cdot) is the pdf corresponding to F(\cdot)] \end{split}$$

Therefore, we obtain:

$$w_i = \left(\frac{\partial \mu_i}{\partial n_i}\right)^2 / var(y_i) = f^2(n_i) / var(y_i)$$

Then, let W be the diagonal matrix with w_i as the main diagonal elements. Hence the information matrix for MLE $\hat{\boldsymbol{\beta}}$ J = X'WX and $var(\hat{\boldsymbol{\beta}}) = J^{-1}$.

5.9

Use conditional logistic regression to test $H_0: \beta_1 = 0$ against $H_1: \beta_1 < 0$ for the toy example in Section 5.4.2.

5.14

Assuming $\pi_1 = \pi_2 = \cdots = \pi_N = \pi$, then the log likelihood would be

$$L(\pi) = \sum_{i=1}^{N} y_i log(\pi) + (n_i - y_i) log(1 - \pi)$$

Take the first derivative, we can get

$$L'(\pi) = \frac{\sum y_i}{\pi} - \frac{\sum n_i - y_i}{1 - \pi}$$

Set it equal to 0, we can get

$$\hat{\pi} = (\sum y_i)/(\sum n_i)$$

And the second derivative of $L(\pi)$ also confirms that $\hat{\pi}$ maximizes the likelihood function. Then the Pearson statistic for ungrouped data (when n = 1) is:

$$\begin{split} \chi^2 &= \sum \frac{(observed - fitted)^2}{fitted} \\ &= \sum_{i=1}^{N} \sum_{j=1}^{n_i} \frac{(y_{ij} - \hat{\pi})^2}{\hat{\pi}} + \frac{[1 - y_{ij} - (1 - \hat{\pi})]^2}{1 - \hat{\pi}} \\ &= \sum_{i=1}^{N} \sum_{j=1}^{n_i} \frac{(y_{ij} - \hat{\pi})^2}{\hat{\pi}(1 - \hat{\pi})} \\ &= \frac{N\hat{\pi}(1 - \hat{\pi})}{\hat{\pi}(1 - \hat{\pi})} = N \end{split}$$

Since the Pearson statistic $\chi^2 = N$, the statistic is not informative for us to test the goodness-of-fit of the null model.

5.15

The log likelihood is $\sum_{i} [y_i log \pi_i + (1 - y_i) log (1 - \pi_i)]$. For the saturated model, we have $\hat{\pi_i} = y_i$ and the value of the log likelihood of saturated model equals 0 (because y_i can only take value of 0 and 1).

$$\begin{split} D(y; \hat{\boldsymbol{\mu}}) &= -2 \sum observed \times log(observed/fitted) \\ &= -2 (\sum_i y_{ij} log(\frac{y_i}{\hat{\pi_i}}) + \sum_i (1 - y_i) log(\frac{1 - y_i}{1 - \hat{\pi}})) \\ &= -2 \sum_i [y_i log(\frac{\hat{\pi_i}}{1 - \hat{\pi_i}}) + log(1 - \hat{\pi_i})] \\ &= -2 \sum_i [y_i (\hat{\beta_0} + \hat{\beta_1} x_i) + log(1 - \hat{\pi_i})] \end{split}$$

From 5.14, we could know that $\sum_i y_i = \sum_i \hat{\pi_i}$ and so $\sum_i x_i = \sum_i x_i \hat{\pi_i}$. So the deviance would be:

$$\begin{split} D &= -2[\hat{\beta_0} \sum_i \hat{\pi_i} + \hat{\beta_1} \sum_i x_i \hat{\pi_i} + \sum_i \log(1 - \hat{\pi_i})] \\ &= -2[\sum_i \hat{\pi_i} (\hat{\beta_0} + \hat{\beta_1} x_i) + \sum_i \log(1 - \hat{\pi_i})] \\ &= -2 \sum_i \hat{\pi_i} \log(\frac{\hat{\pi_i}}{1 - \hat{\pi_i}}) - 2 \sum_i \log(1 - \hat{\pi_i}) \end{split}$$

Therefore, the deviance only depends on $\hat{\pi_i}$, and it is uninformative for checking model fit.