Logistic Regression Model

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Model Selection

Logistic regression is a part of a category of statistical models called generalized linear models(GLM). The GLM is a unification of both linear and nonlinear regression models that also allows the incorporation of nonnormal response distributions. In GLM, the response variable distribution must be a member of exponential family which includes normal, poisson, binomial, exponential, gamma etc. This broad class of models includes ordinary regression and ANOVA, as well as multivariate statistics such as ANCOVA and loglinear regression.
Logistic regression allows one to predict a discrete outcome, such as group membership, from a set of variables that may be continuous, discrete, dichotomous, or a mix of any of these. Generally, the dependent or response variable is dichotomous, such as presence/absence or success/failure. Discriminant analysis is also used to predict group membership with only two groups. However, discriminant analysis can only be used with continuous independent variables. Thus, in instances where the independent variables are a categorical, or a mix of continuous and categorical, logistic regression is preferred.

Logistic Regression

The dependent variable in logistic regression is usually dichotomous, that is, the dependent variable can take the value 1 with a probability of success π, or the value 0 with probability of failure $1 - \pi$. This type of variable is called a Bernoulli (or binary) variable. Although not as common, applications of logistic regression have also been extended to cases where the dependent variable is of more than two cases, known as multinomial or polytomous [Tabachnick and Fidell (1996) use the term polychotomous].

As mentioned previously, the independent or predictor variables in logistic regression can take any form. That is, logistic regression makes no assumption about the distribution of the independent variables. They do not have to be normally distributed, linearly related or of equal variance within each group.The relationship between the predictor and response variables is not a linear function in logistic regression, instead, the logistic regression function is used, which is the logit transformation of π:

Sigmoidal Response Functions for Binary Responses

The three response functions which can be used for modeling binary responses from zero-one coding are the following:

- Probit mean Response Function
- Logistic mean response function
- Complementary log log response function.

Note that all of these response functions have the following properties:

- Bounded between 0 and 1.
- They are sigmoidal means S-shaped
- Approaches asymptotically to 0 and 1.

Simple Logistic Regression

When the response variable is binary, taking 1 and 0 with probabilities π and $1-\pi$, respectively, y is a Bernoulli random variable with parameter $E(y) = \pi$.
The simple logistic regression model is given by

$$\pi_i = \frac{e^{\beta_0+\beta_1 x_i}}{1+e^{\beta_0+\beta_1 x_i}}$$

We know that $E(y_i) = 1(\pi_i) + 0(1-\pi_i) = \pi_i \Longrightarrow \pi_i = E(y_i)$
Straightforward algebra yields

$$E(y_i) = \pi_i = [1+\exp(-\beta_0 - \beta_1 x_i)]^{-1}$$

The x observations are assumed to be known constants. If x observations are random, $E(y_i)$ is viewed as a conditional mean given the value of x_i. The parameter π defines the mean of the distribution: $E(y_i) = \pi$. The logistic regression models the success probability as a function of the severity(x). That is, $\pi = \pi(x)$ so that for case i with severity x_i, $\pi_i = \pi(x_i)$.

Simple Logistic Regression

Once the MLE b_0 and b_1 are found, we substitute these values in the response function

$$\pi_i = \frac{e^{\beta_0+\beta_1 x_i}}{1+e^{\beta_0+\beta_1 x_i}}$$

to obtain the response function

$$\widehat{\pi}_i = \frac{e^{b_0+b_1 x_i}}{1+e^{b_0+b_1 x_i}}$$

Hence, the logistic response function will be

$$\widehat{\pi} = \frac{e^{b_0+b_1 x}}{1+e^{b_0+b_1 x}}$$

Considering the logit transformation we can rewrite the response function as

$$\widehat{\pi}' = b_0 + b_1 x$$

where $\widehat{\pi}' = \ln\left(\frac{\widehat{\pi}}{1-\widehat{\pi}}\right)$.

Remark: The logarithm of the odds $\ln\left[\frac{\pi}{1-\pi}\right]$, is referred to as the log odds or the logit. It is clear that the logistic regression model assumes a linear model for the logit; that is,

What is b_1 in a logistic regression?

In the case of a linear regression the estimated regression coefficient b_1 represent the slope of the fitted line but in case of the logistic regression it represents the the logarithm of the ratio of odds of two consecutive observations. This means

$$b_1 = \log\left(\frac{odds_2}{odds_1}\right)$$

where $\log(odds_1)$ is the logarithm of the estimated odds when $x = x_j$ and $\log(odds_2)$ is the logarithm of the estimated odds when $x = x_{j+1}$
Hence on taking the antilog in the above expression we have the estimated ratio of odds, called the odds ratio denoted by $\widehat{OR}$ is equal to $\exp(b_1)$.
Therefore

$$\widehat{OR} = \frac{odds_2}{odds_1} = \exp(b_1)$$

For example, a regression coefficient $b_1 = -0.2$ with $\exp(b_1) = 0.82$ indicates that a change from x to $x + 1$ reduces the odds of occurrence by the multiplicative factor 0.82; it reduces the odds of occurrence by 18%. A value of $b_1 = 0$ and $\exp(b_1) = 1$ a change in the explanatory variable has no effect on the odds of occurrence.

Example

The board of directors of professionals association conducted a random sample survey of 30 members to assess the effects of several possible amount os dues increase. The table below is the result of the survey. X denotes the dollar increase in annual dues posited in the survey interview and $Y = 1$ if the interviewee indicated the membership will not be renewed at the amount of the dues increase and 0 denotes if the membership will be renewed.

y	x	y	x	y	x
0.0	30.0	1.0	30.0	0.0	30.0
0.0	31.0	0.0	32.0	0.0	33.0
1.0	34.0	0.0	35.0	0.0	35.0
1.0	35.0	1.0	36.0	0.0	37.0
0.0	38.0	1.0	39.0	0.0	40.0
1.0	40.0	1.0	40.0	0.0	41.0
1.0	42.0	1.0	43.0	1.0	44.0
0.0	45.0	1.0	45.0	1.0	45.0
0.0	46.0	1.0	47.0	1.0	48.0
0.0	49.0	1.0	50.0	1.0	50.0

Assuming logistic regression is appropriate we have the following maximum likelihood parameter estimates: $\hat{\beta}_0 = -4.8075$ and $\hat{\beta}_1 = 0.1251$. Hence the fitted response function is given by

$$\hat{\pi} = [1 + \exp(4.8075 - 0.1251 x_i)]^{-1}$$

Example

```
> data=read.table("C://STAT4001//membership.txt", header=T)
> y<-data$y
> x<-data$x
> model=glm(y~x,family=binomial(logit))
> model
Call:  glm(formula = y ~ x, family = binomial(logit))
Coefficients:
(Intercept)            x
    -4.8075       0.1251
Degrees of Freedom: 29 Total (i.e. Null);  28 Residual
Null Deviance:      41.46
Residual Deviance: 37.46        AIC: 41.46
```

We can display the fitted model using R code below

```
> plot(x,y)
> curve(predict(model,data.frame(x=x),type="resp"),add=TRUE)
> points(x,fitted(model),pch=20)
```

Multiple Logistic Regression

The simple logistic regression model

$$\pi_i = [1 + \exp(-\beta_0 - \beta_1 x_i)]^{-1}$$

can be extended to more than one predictor variable. The multiple logistic regression model for $x_1, x_2, ..., x_{p-1}$ predictor variables can be expressed as

$$E(y) = \frac{exp(\mathbf{x}'\boldsymbol{\beta})}{1 + exp(\mathbf{x}'\boldsymbol{\beta})}$$

equivalently

$$E(y) = \left[1 + \exp(-\mathbf{x}'\boldsymbol{\beta})\right]^{-1}$$

where,

$$\boldsymbol{\beta} = \begin{pmatrix} \beta_0 \\ \beta_1 \\ \beta_2 \\ \vdots \\ \beta_{p-1} \end{pmatrix}, \mathbf{x} = \begin{pmatrix} 1 \\ x_1 \\ x_2 \\ \vdots \\ x_{p-1} \end{pmatrix}, \mathbf{x}_i = \begin{pmatrix} 1 \\ x_{i1} \\ x_{i2} \\ \vdots \\ x_{i,p-1} \end{pmatrix}$$

The fitted logistic response function and the fitted values can be expressed as

$$\widehat{\pi} = \frac{\exp(\mathbf{x}'\mathbf{b})}{1 + exp(\mathbf{x}'\mathbf{b})} = [1 + \exp(-\mathbf{x}'\mathbf{b})]^{-1}$$

Example-Market Data

A marketing research firm was investigating whether a family will purchase a new car during next year using logistic regression. A random sample of 33 suburban families was selected. Data on annual family income(x_1 in thousand dollars) and the current age of the oldest family automobile (x_2, in years) was collected. A follow up interview conducted 12 months later was to determine whether the family actually purchased a new car $y = 1$ or didn't purchase a new car $y = 0$ during the year. The data is as below:

y	x_1	x_2	y	x_1	x_2
0.0	32.0	3.0	0.0	45.0	2.0
1.0	60.0	2.0	0.0	53.0	1.0
0.0	25.0	4.0	1.0	68.0	1.0
1.0	82.0	2.0	1.0	38.0	5.0
0.0	67.0	2.0	1.0	92.0	2.0
1.0	72.0	3.0	0.0	21.0	5.0
0.0	26.0	3.0	1.0	40.0	4.0
0.0	33.0	3.0	0.0	45.0	1.0
1.0	61.0	2.0	0.0	16.0	3.0
1.0	18.0	4.0	0.0	22.0	6.0
0.0	27.0	3.0	1.0	35.0	3.0
1.0	40.0	3.0	0.0	10.0	4.0
0.0	24.0	3.0	1.0	15.0	4.0
0.0	23.0	3.0	0.0	19.0	5.0
1.0	22.0	2.0	0.0	61.0	2.0
0.0	21.0	3.0	1.0	32.0	5.0
0.0	17.0	1.0			

Example- Market Data

Considering that a multiple logistic regression model fits the data we have the maximum likelihood estimates of the parameters β_0, β_1 and β_2 are

$$\begin{aligned} b_0 &= \hat{\beta}_0 = -4.7393 \\ b_1 &= \hat{\beta}_1 = 0.0677 \\ b_2 &= \hat{\beta}_2 = 0.5986 \end{aligned}$$

Therefore the estimated regression model is

$$\hat{\pi} = [1 + exp(4.7393 - 0.0677x_1 - 0.5986x_2)]^{-1}$$

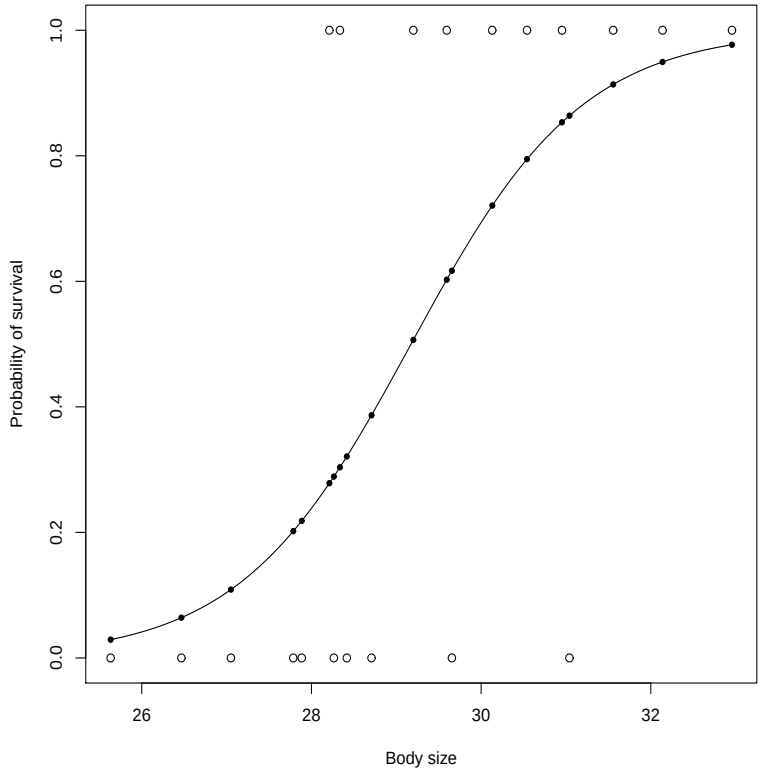
```
> data=read.table("C://STAT4001//market.txt", header=T)
> y<-data$y
> x1<-data$x1
> x2<-data$x2
> x1
 [1] 32 45 60 53 25 68 82 38 67 92 72 21 26 40 33 45 61 16 18 22 27 35 40 10 24  15 23 19 22 61 21 32 17
> x2
 [1] 3 2 2 1 4 1 2 5 2 2 3 5 3 4 3 1 2 3 4 6 3 3 3 4 3 4 3 5 2 2 3 5 1
> y
 [1] 0 0 1 0 0 1 1 1 0 1 1 0 0 1 0 0 1 0 1 0 0 1 1 0 0 1 0 0 1 0 0 1 0
> model=glm(y~x1+x2, family=binomial(logit))
> summary(model)
Call:
glm(formula = y ~ x1 + x2, family = binomial(logit))
Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) -4.73931    2.10195  -2.255   0.0242 *
x1           0.06773    0.02806   2.414   0.0158 *
x2           0.59863    0.39007   1.535   0.1249
Signif. codes:  0 *** 0.001 ** 0.01 * 0.05 . 0.1   1
```

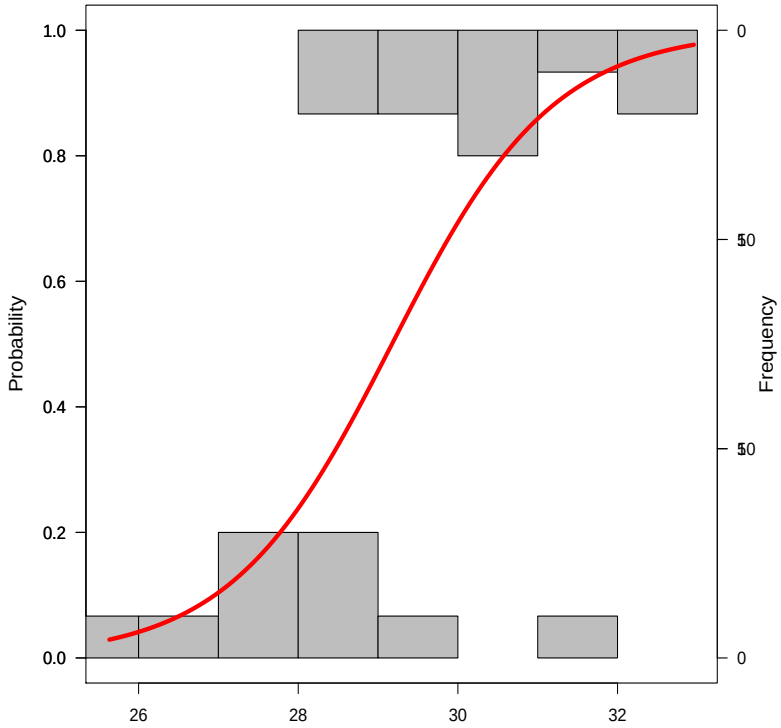
Example- Ecological Data

The survival response and body size conducted in a ecological study

```
> data
   bodysize survive
1  25.63320       0
2  26.46724       0
3  27.05107       0
4  27.78609       0
5  27.88550       0
6  28.21167       1
7  28.26452       0
8  28.33589       1
9  28.41717       0
10 28.70792       0
11 29.20096       1
12 29.59447       1
13 29.65526       0
14 30.13143       1
15 30.54080       1
16 30.95309       1
17 31.04085       0
18 31.55717       1
19 32.13806       1
20 32.95669       1
> bodysize=data$bodysize
> survive=data$survive
> plot(bodysize,survive,xlab="Body size",ylab="Probability of survival")
> g=glm(survive~bodysize,family=binomial)
> curve(predict(g,data.frame(bodysize=x),type="resp"),add=TRUE)
> points(bodysize,fitted(g),pch=20)
```

Example- Ecological Data





We can draw the logistic curve along with the histogram (displayed in the right above) with R code

```
>library(popbio)
>logi.hist.plot(bodysize,survive,boxp=FALSE,type="hist",col="gray")
```

Example-Prostate Cancer

Treatment for protest cancer changes depending on whether or not the lymphatic nodes surrounding the protest are affected. In order to avoid an invasive investigation procedure (opening the abdominal cavity), a certain number of variables are considered as explanatory variables for the binary variable y: if y=0 the cancer has not reached the lymphatic system and if y=1 the cancer has reached the lymphatic system. A sample of 53 observations is available in

http://www.agrocampus-ouest.fr/igagrocampus-ouest.fr/math/RforStat/prostate.txt

The variables include
age: Age of the patient at the time of diagnosis
acid: Serum acid phosphate level
Xray: X-ray analysis, 0=negative, 1=positive
size: Tumor size
grade: State of the tumor as determined by biopsy, 0=medium, 1=serious
log.acid: Logarithm of the acidity level

```
> data=read.table("http://www.agrocampus-ouest.fr/igagrocampus-ouest.fr/math/RforStat/prostate.txt", header=T)
> head(data,5)
  age acid Xray size grade Y   log.acid
1  66 0.48    0    0     0 0 -0.7339692
2  68 0.56    0    0     0 0 -0.5798185
3  66 0.50    0    0     0 0 -0.6931472
4  56 0.52    0    0     0 0 -0.6539265
5  58 0.50    0    0     0 0 -0.6931472
```

Example-Prostate Cancer

Fitting logistic regression with different regressor variable

```
> prostate=read.table("http://www.agrocampus-ouest.fr/igagrocampus-ouest.fr/math/RforStat/prostate.txt", header=T)
> model1=glm(Y~log.acid,data=prostate,family=binomial)
> summary(model1)
Call:
glm(formula = Y ~ log.acid, family = binomial, data = prostate)
Deviance Residuals:
    Min       1Q   Median       3Q      Max
-1.9802  -0.9095  -0.7266   1.1951   1.7302
Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)    0.404      0.509   0.794   0.4274
log.acid       2.245      1.040   2.159   0.0309 *
---
Signif. codes:  0 *** 0.001 ** 0.01 * 0.05 . 0.1   1
(Dispersion parameter for binomial family taken to be 1)
    Null deviance: 70.252  on 52  degrees of freedom
Residual deviance: 64.813  on 51  degrees of freedom
AIC: 68.813
```

Hence, the fitted model is

$$\log\left(\frac{\pi(x)}{1-\pi(x)}\right) = 0.404 + 2.245x$$

Equivalently,

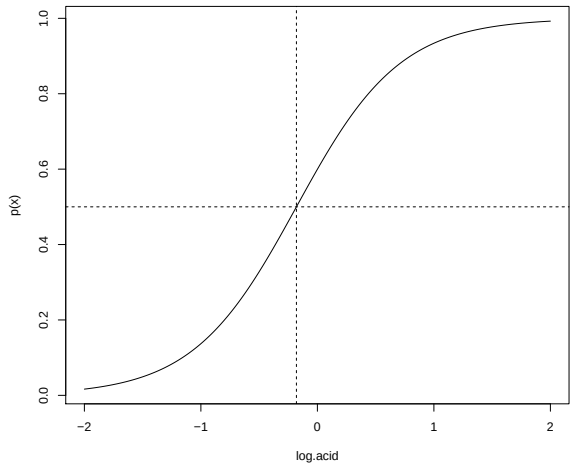
$$\pi(x) = \frac{\exp(0.404 + 2.245x)}{1 + \exp(0.404 + 2.245x)}.$$

Note that the p-value for testing the hypothesis $\beta_1 = 0$ Vs $\beta_1 \neq 0$ is 0.0309. Therefore the variable log.acid is retained in the model.

Example-Prostate Cancer

Fitting logistic regression with different regressor variable

```
> prostate=read.table("http://www.agrocampus-ouest.fr/igagrocampus-ouest.fr/math/RforStat/prostate.txt", header=T)
> model1=glm(Y~log.acid,data=prostate,family=binomial)
> beta<-coef(model1)
> x<-seq(-2,2,0.01)
> y<- exp(beta[1]+beta[2]*x)/(1+exp(beta[1]+beta[2]*x))
> plot(x,y, type="l", xlab="log.acid", ylab="p(x)")
> abline(h=0.5, lty=2)
> xlim<--beta[1]/beta[2]
> abline(v=xlim, lty=2)
```



Observe that

$$\hat{p}(x) = \begin{cases} \leq 0.5 & \text{for} \quad x \leq -0.18 \\ > 0.5 & \text{for} \quad x > -0.18 \end{cases}$$

Example-Prostate Cancer

Fitting logistic regression with different regressor variable

```
> prostate=read.table("http://www.agrocampus-ouest.fr/igagrocampus-ouest.fr/math/RforStat/prostate.txt", header=T)
> model2=glm(Y~size,data=prostate,family=binomial)
> summary(model2)
Call:
glm(formula = Y ~ size, family = binomial, data = prostate)
Deviance Residuals:
    Min       1Q   Median       3Q      Max
-1.2735  -0.6536  -0.6536   1.0842   1.8158
Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  -1.4351     0.4976  -2.884  0.00393 **
size          1.6582     0.6306   2.630  0.00855 **
---
Signif. codes:  0 *** 0.001 ** 0.01 * 0.05 . 0.1   1
(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 70.252  on 52  degrees of freedom
Residual deviance: 62.553  on 51  degrees of freedom
AIC: 66.553
```

Note that in case of binary response variable like size the parameters are estimated with the level 1 of the variable. Hence

$$\log\left(\frac{\pi(x)}{1-\pi(x)}\right) = \begin{cases} = -1.435 & \text{if} \quad x = 0 \\ = -1.435 + 1.658 = 0.223 & \text{if} \quad x = 1 \end{cases}$$

Example-Prostate Cancer

Logistic regression with all explanatory variables can expressed as

```
> prostate=read.table("http://www.agrocampus-ouest.fr/igagrocampus-ouest.fr/math/RforStat/prostate.txt", header=T)
> model3=glm(Y~.,data=prostate,family=binomial)
> summary(model3)

Call:
glm(formula = Y ~ ., family = binomial, data = prostate)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-2.0960  -0.6102  -0.2863   0.4834   2.2000

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) 10.08672    7.83450   1.287   0.1979
age         -0.04289    0.06166  -0.696   0.4867
acid        -8.48006    7.63305  -1.111   0.2666
Xray         2.06673    0.85469   2.418   0.0156 *
size         1.38415    0.79546   1.740   0.0819 .
grade        0.85376    0.81247   1.051   0.2933
log.acid     9.60912    6.21652   1.546   0.1222
---
Signif. codes:  0 *** 0.001 ** 0.01 * 0.05 . 0.1   1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 70.252  on 52  degrees of freedom
Residual deviance: 44.768  on 46  degrees of freedom
AIC: 58.768

Number of Fisher Scoring iterations: 5
```

Choosing the Model

The anova function can be used to compare two models using the deviance statistic to test the nullity of the coefficients of the bigger model.
For example in the prostate cancer data

```
> prostate=read.table("http://www.agrocampus-ouest.fr/igagrocampus-ouest.fr/math/RforStat/prostate.txt", header=T)
> model1=glm(Y~log.acid,data=prostate,family=binomial)
> model3=glm(Y~.,data=prostate,family=binomial)
> anova(model1,model3, test="Chisq")
Analysis of Deviance Table

Model 1: Y ~ log.acid
Model 2: Y ~ age + acid + Xray + size + grade + log.acid
  Resid. Df Resid. Dev Df Deviance Pr(>Chi)
1        51     64.813
2        46     44.768  5   20.044 0.001226 **
---
Signif. codes:  0 *** 0.001 ** 0.01 * 0.05 . 0.1   1
```

As the p-value of the test is 0.001226, the null hypothesis is rejected. Thus the model 1 is rejected and at least one of the supplementary variable in model 3 (full model) is considered to be relevant. Like in the multiple linear regression model we can use step function to choose the best model.

```
> choose<-step(model, direction="backward")
```

Making a Prediction

Once a best logistic regression has been selected it can be used for prediction using the function `predict`.

```
> prostate=read.table("http://www.agrocampus-ouest.fr/igagrocampus-ouest.fr/math/RforStat/prostate.txt", header=T)
```

```
> model=glm(Y~., data=prostate,family="binomial")
> bestmodel=step(model, direction="backward")
> xnew<-matrix(c(61,0.60,1,0,1,-0.51),nrow=1)
> colnames(xnew)<-c("age","acid","Xray","size","grade","log.acid")
> xnew=as.data.frame(xnew)
> predict(bestmodel,xnew, type="response")
        1
0.4835626
```

Since the predicted probability is less than 0.5 we therefore predict $\hat{Y} = 0$. that is to say the cancer has not reached the lymphatic system.