22s:152 Applied Linear Regression

Ch. 14 (sec. 1) and Ch. 15 (sec. 1 & 4): Logistic Regression

Logistic Regression

- Used when the response variable is binary

- We model the log of the odds for $Y_i = 1$

$$ln\left(\frac{P(Y_i = 1)}{1 - P(Y_i = 1)}\right) = \beta_0 + \beta_1 X_{1i} + \cdots + \beta_k X_{ki}$$

- Which can be converted to

$$P(Y_i = 1) = \frac{exp(\beta_0 + \beta_1 X_{1i} + \cdots + \beta_k X_{ki})}{1 + exp(\beta_0 + \beta_1 X_{1i} + \cdots + \beta_k X_{ki})}$$

$$= \frac{1}{1 + exp[-(\beta_0 + \beta_1 X_{1i} + \cdots + \beta_k X_{ki})]}$$

- Unlike OLS regression, logistic regression does not assume...
  - linearity between the independent variables and the dependent
  - normally distributed errors
  - homoscedasticity

- It does assume...
  - we have independent observations
  - that the independent variables be linearly related to the logit of the dependent variable (somewhat difficult to check)

- Maximum likelihood estimation (MLE) is used to calculate the regression coefficient estimates
  - Ordinary Least Squares (OLS) minimizes the sum of the squared residuals
  - MLE finds the parameter estimates that maximize the log-likelihood function

- **Significance testing**
  - Testing individual coefficients $(H_0 : \beta_j = 0)$
    - Wald tests (i.e. Z-tests) based on asymptotic normality of $\hat{\beta}_j$'s are provided in the *summary* output from **R**.
  - Testing Full vs. Reduced (nested) models
    - Likelihood ratio tests, which are chi-squared tests (χ^2 tests).
    - We can use the *anova()* function in **R** to do these likelihood ratio nested tests.
    - We will use the option test="Chisq" here, or $anova(lm.red, lm.full, test = \text{``}Chisq\text{''})$

- $*$ The Global Null model (simplest possible model) has only an intercept and is the model:

$$logit(\pi_i) = c \quad \text{for all } i$$
$$\text{and some constant } c$$

[i.e. covariates don't affect $\pi_i = P(Y_i = 1)$]

- $*$ Full model vs. Global Null model has the flavor of an overall F-test from multiple regression (i.e. are any of the variables in the model useful).

- **Example**: Incidence of bird on islands

  Dichotomous response called *incidence*.

$$incidence = \begin{cases} 1 & \text{if island occupied by bird} \\ 0 & \text{if bird did not breed there} \end{cases}$$

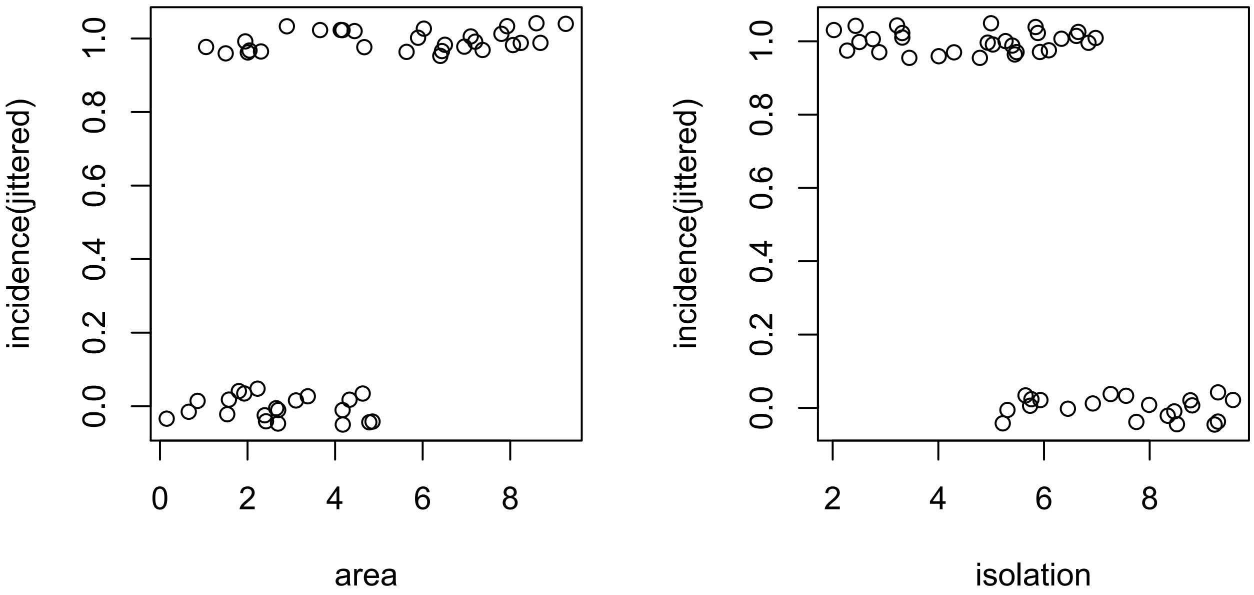
Two continuous predictor variables:
area - area of island in km^2
isolation - distance from mainland in km

```
> attach(iso.data)
> head(iso.data)

  incidence  area isolation
1         1 7.928     3.317
2         0 1.925     7.554
3         1 2.045     5.883
4         0 4.781     5.932
5         0 1.536     5.308
6         1 7.369     4.934
```

We expect *incidence* to be lower for high *isolation*, and incidence to be higher for high *area*.

Look at a (jittered) scatterplot of each covariate vs. the response.

```
> plot(jitter(incidence,factor=.25)~area,
                          ylab="incidence(jittered)")
> plot(jitter(incidence,factor=.25)~isolation,
                          ylab="incidence(jittered)")
```



Fit the full additive model (2 covariates):

```
> n=nrow(iso.data)
> n
[1] 50


> glm.out.full=glm(incidence ~ area + isolation,
                           family=binomial(logit))
> summary(glm.out.full)

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)   6.6417     2.9218   2.273  0.02302 *
area          0.5807     0.2478   2.344  0.01909 *
isolation    -1.3719     0.4769  -2.877  0.00401 **
---
Signif. codes:  0 *** 0.001 ** 0.01 * 0.05 . 0.1   1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 68.029  on 49  degrees of freedom
Residual deviance: 28.402  on 47  degrees of freedom
AIC: 34.402

Number of Fisher Scoring iterations: 6
```

Deviance(or residual deviance)

- This is used to assess the model fit.
- In logistic regression, the *deviance* has the flavor of RSS in ordinary regression.
- The smaller the deviance, the better the fit.

Null deviance - like RSS in ordinary regression when only an overall mean is fit
(see **R** output: n=50, and *df* are 49).

Residual deviance - like RSS from the full model fit
(see **R** output: n=50, and *df* are 47).

A comparison of the **Null deviance** and **Residual deviance** is used to test the global null hypothesis. In this case...

$$H_0 : \beta_1 = \beta_2 = 0$$
$$H_A : \text{At least one } \beta_j \text{ not equal to } 0$$

A <u>likelihood ratio test</u> is used for this nested test which follows a central χ^2_2 distribution under H_0 being true.

χ^2_q is a chi-squared distribution with q degrees of freedom, and q will be the number of restrictions being made in H_0 (or the number of covariates in the full model if doing global null hypothesis test).

$$\begin{aligned}\chi^2_q &= -2[log\ likelihood_{red} - log\ likelihood_{full}]\\ &= (-2LL_{red}) - (-2LL_{full})\\ &= (2LL_{saturated} - 2LL_{red}) - (2LL_{saturated} - 2LL_{full})\\ &= \text{Reduced model deviance} - \text{Full model deviance}\\ &= \text{Null deviance} - \text{Residual deviance}\end{aligned}$$

- Global null hypothesis test for *incidence* data:

From the *summary* output...

```
    Null deviance: 68.029  on 49  degrees of freedom
Residual deviance: 28.402  on 47  degrees of freedom
```

χ^2_2 test:

```
> chi.sq=68.029 - 28.402
> pchisq(chi.sq,2,lower.tail=FALSE)
[1] 2.483741e-09
```

This can also be done using the full vs. reduced likelihood ratio test (use test="Chisq"):

```
> glm.out.null=glm(incidence ~ 1,family=binomial(logit))
> anova(glm.out.null,glm.out.full,test="Chisq")
Analysis of Deviance Table

Model 1: incidence ~ 1
Model 2: incidence ~ area + isolation
  Resid. Df Resid. Dev Df Deviance P(>|Chi|)
1        49     68.029
2        47     28.402  2   39.627 2.484e-09
```

$\Rightarrow$ Reject H_0.

The *deviance* is saved in the model fit output, and it can be requested...

$$\chi^2_2 = \text{Reduced model deviance} - \text{Full model deviance}$$

```
> chi.sq=glm.out.null$deviance-glm.out.full$deviance
> pchisq(chi.sq,2,lower.tail=FALSE)
[1] 2.483693e-09
```

Same *p*-value as in previous page output.

- Individual tests for coefficients

After rejecting the *Global Null hypothesis*, we can consider individual Z-tests for the predictors.

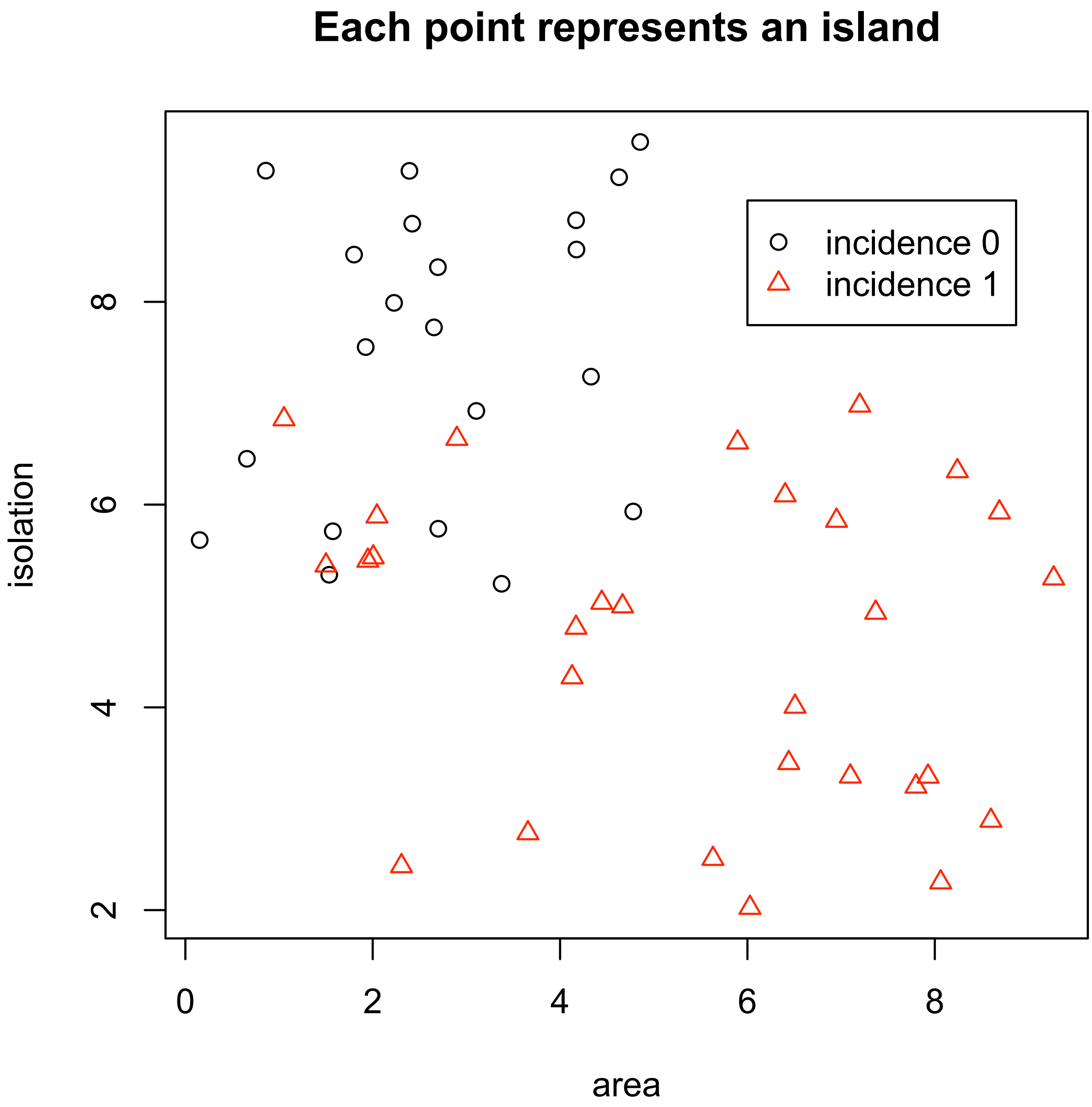
```
> summary(glm.out.full)

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)   6.6417     2.9218   2.273  0.02302 *
area          0.5807     0.2478   2.344  0.01909 *
isolation    -1.3719     0.4769  -2.877  0.00401 **
---
Signif. codes:  0 *** 0.001 ** 0.01 * 0.05 . 0.1   1
```

isolation is a significant predictor, given we've already accounted for *area*.

area is a significant predictor, given we've already accounted for *isolation*.

Another way to view the data:

```
plot(area,isolation,pch=(incidence+1),col=(incidence+1))
title("Each point represents an island")
legend(6,9,c("incidence 0","incidence 1"),
                                   col=c(1,2),pch=c(1,2))
```



- Interpretation of the parameters:

  $\hat{\beta}_{area} = 0.5807$

  or $e^{\hat{\beta}_{area}} = 1.7873$

  Holding *isolation* constant...

  A 1 km^2 increase in *area* is associated with an increase in the odds of seeing a bird by a factor of 1.7873.

  $e^{\hat{\beta}_{area}}$ represents the multiplicative effect (applied to the odds) of a 1-unit change in *area*.

  Increasing the area of an island by 1 km^2, increases the odds of seeing a bird by a multiplicative factor of 1.7873.

  It increases the odds by 78.73%

Another way to express it,

$$\text{Odds}_{[(\text{x}_1+1)\ km^2]} = 1.7872\times\ \text{Odds}_{[(\text{x}_1)\ km^2]}$$

$$\hat{\beta}_{isolation} = -1.3719$$

or $e^{\hat{\beta}_{isolation}} = 0.2536$

Holding *area* constant...

A 1 *km* increase in *isolation* is associated with an decrease in the odds of seeing a bird by a factor of 0.2536.

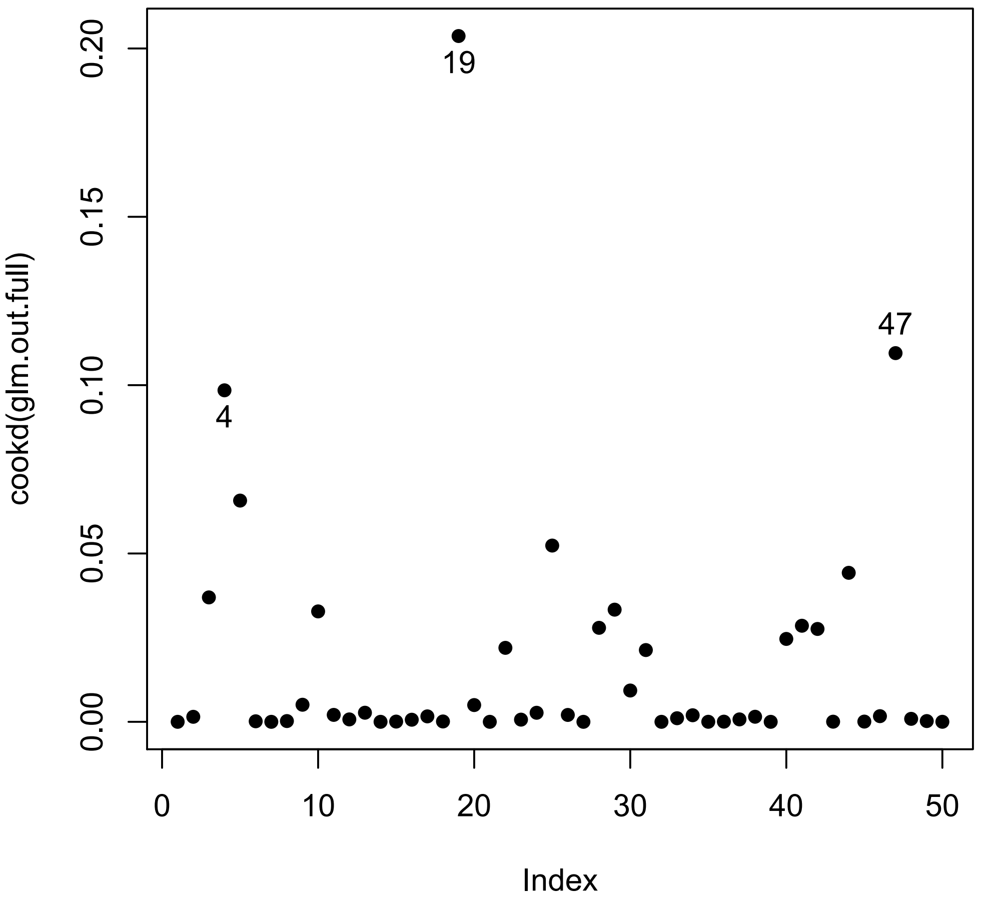
$$\text{Odds}_{[(\text{x}_2+1)\ km]} = 0.2536\times\ \text{Odds}_{[(\text{x}_2)\ km]}$$

- **Diagnostics**: Outliers, Influential data

  The *car* library diagnostics can also be used on generalized linear models...

  rstudent, hatvalues, cookd, vif, outlier.test, and *av.plots.*

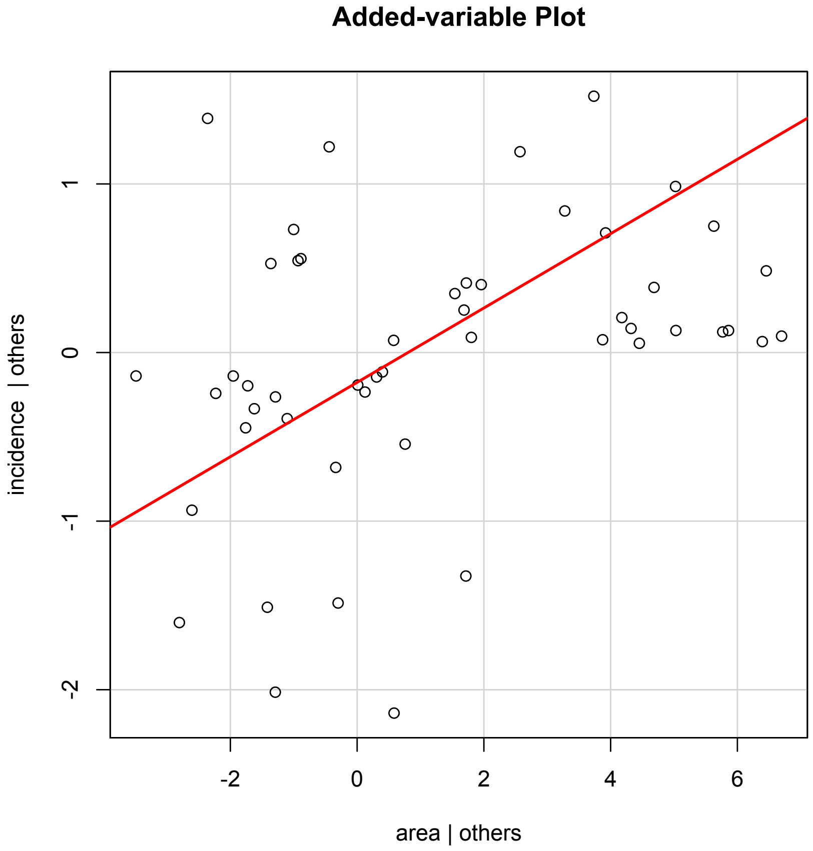
```
> plot(cooks.distance(glm.out.full),pch=16)
> identify(1:n,cooks.distance(glm.out.full))
```



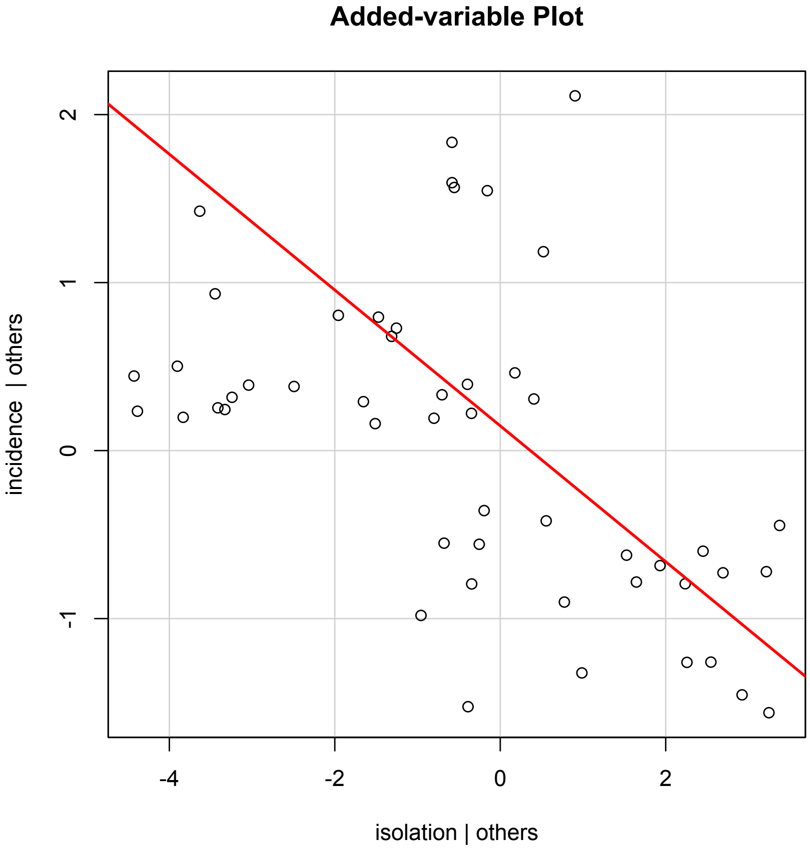
```
> vif(glm.out.full)
     area isolation
 1.040897  1.040897
```

```
> outlierTest(glm.out.full)

No Studentized residuals with Bonferonni p < 0.05
Largest |rstudent|:
   rstudent unadjusted p-value Bonferonni p
19 2.250205           0.024436           NA
```

```
> avPlot(glm.out.full,"area")
```



```
> avPlot(glm.out.full,"isolation")
```



- **Diagnostics**: Goodness of fit

  Since the responses are all 0's and 1's, it is more difficult to check how well the model fits our data (compared to ordinary regression).

  If you have data points fairly evenly spread across your x-values, you could try to check the fit using the Hosmer-Lemeshow Goodness of Fit Test.

  We will return to our original example data on lead levels in children's blood relative to soil lead levels to show how this test works.

The fitted value is a probability (or $\hat{p}$).

The logistic regression provides a $\hat{p}$ for every x-value.

To check the fit, we will partition the observations into 10 groups based on the x-values.

```
> break.points=quantile(soil,seq(0,1,0.1))
> group.soil=cut(soil,breaks=break.points)
> table(group.soil)

group.soil
          (40,89.4]          (89.4,151]
                 11                  14

          (151,239]           (239,361]
                 14                  14

          (361,527]           (527,750]
                 14                  13

          (750,891]          (891,1330]
                 14                  14

        (1330,1780]         (1780,5260]
                 14                  14
```

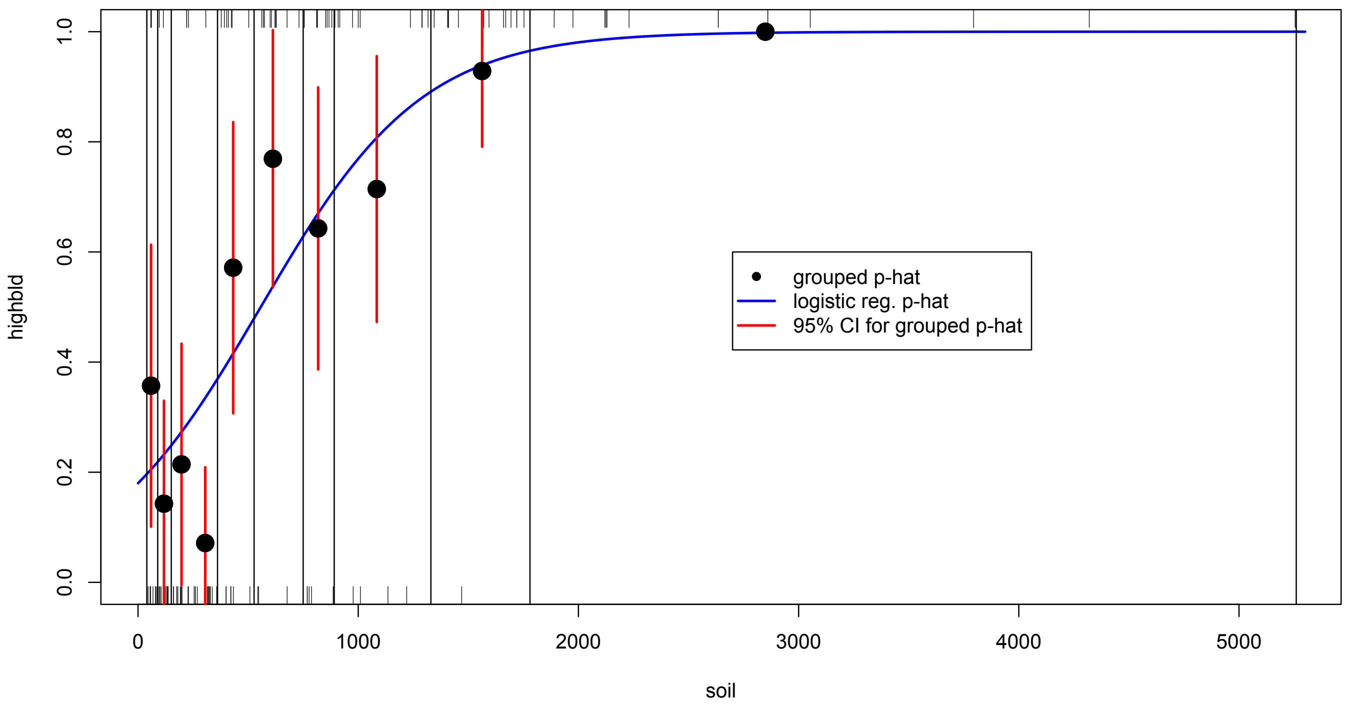
For each group g, we will estimate a $\hat{p}_g$.

This $\hat{p}_g$ does not consider the other fitted $\hat{p}$ values (unlike the logistic regression fitted values which all fall along a smooth curve).

```
> group.est.p=tapply(highbld,group.soil,mean)
> group.est.p=as.vector(group.est.p)
> round(group.est.p,4)
 [1] 0.2727 0.1429 0.2143 0.0714 0.5714
     0.7692 0.6429 0.7143 0.9286 1.0000
```

Now we will compare the 'freely fit' estimated probabilities, with the logistic regression (restricted) fitted probabilities.

The vertical lines represent the grouping structure of the observations.



If the dots fall close to the fitted logistic curve, it's a reasonably good fit.

The short red lines represent $+/-$ 2 standard errors of each $\hat{p}$.

The Hosmer-Lemeshow Test takes these values and tests the goodness of fit using a χ^2 test statistic.

H_0 : Fit is sufficient
H_A: Fit is not sufficient (the curve doesn't explain the data very well)

```
> hosmerlem(highbld, glm.out$fitted, g = 10)
       X^2          Df    P(>Chi)
12.2422056  8.0000000  0.1407200
```

The p-value=0.1407, so we do not reject null.

The logistic regression model describes the data reasonably well.

The Hosmer-Lemeshow Test function isn't in an **R** library, but it is shown below. To use it, just copy and paste it into the **R** interpreter window.

```
hosmerlem=function (y, yhat, g = 10) {
   ## y is the original response.
   ## yhat are the fitted values from the model.
   ## g is the number of groups requested.
   cutyhat = cut(yhat,
            breaks = quantile(yhat, probs = seq(0,1, 1/g)),
            include.lowest = T)
   obs = xtabs(cbind(1 - y, y) ~ cutyhat)
   expect = xtabs(cbind(1 - yhat, yhat) ~ cutyhat)
   chisq = sum((obs - expect)^2/expect)
   P = 1 - pchisq(chisq, g - 2)
   c("X^2" = chisq, Df = g - 2, "P(>Chi)" = P)
 }

 ## A function to do the Hosmer-Lemeshow test in R.
 ## R Function is due to Peter D. M. Macdonald,
    McMaster University.
```

One criticism of this test is that it depends on the chosen breakpoints for the group. See...

Hosmer, D.W., Hosmer, T.,Dessie, S.Le.,and S. Lemeshow (1998). A Comparison of Goodness-of-Fit Tests for the Logistic Regression Model. *Statistics in Medicine*, vol. 16, 965-980.

- Issues to consider
  - Influential observations

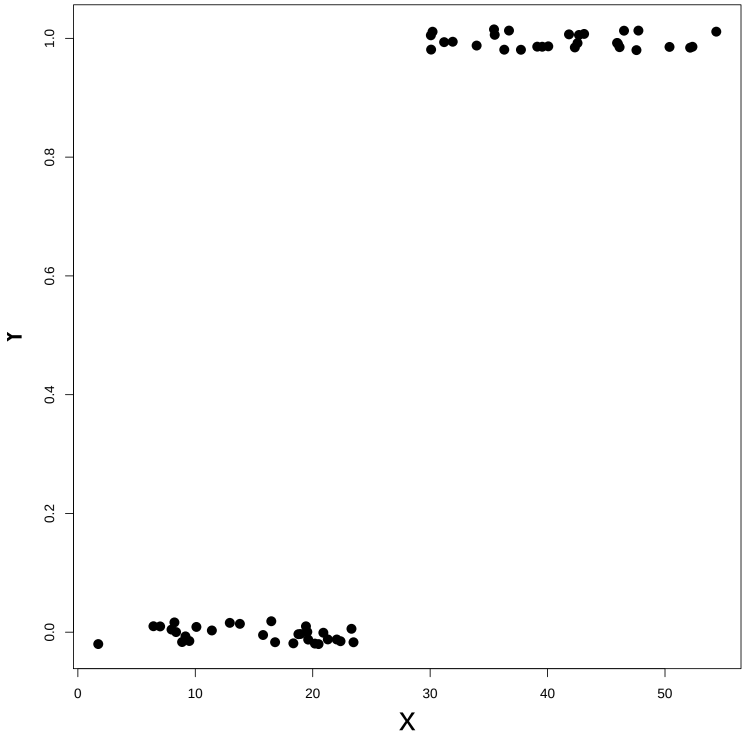
  - multicollinearity
    - When you reject H_0, but none of the individual regression coefficients are significant
    - high correlation among predictors
    - same solution as for linear regression

  - nonlinearity in the logit
    - awkward to check
    - no consensus on how to deal with

  - poor model fit
    - Can consider a goodness-of-fit test (Hosmer-Lemeshow χ^2 test)

  - High separation or discrimination...

- What is high separation?



If there's no overlap of the x's that lead to a 0 and the x's that lead to a 1.

Depending on the degree of separation, this can cause problems with fitting the model.

This inflates SE of regression coefficient.

If there's perfect separation, coefficients can not be estimated.

```
## Code for graphic of Hosmer-Lemeshow Test:

## Break the x-axis into 10 groups:
break.points=quantile(soil,seq(0,1,0.1))
group.soil=cut(soil,breaks=break.points)
table(group.soil)

## For each group, get the estimated p-hat:
group.est.p=tapply(highbld,group.soil,mean)
group.est.p=as.vector(group.est.p)

se=as.vector(sqrt(group.est.p*(1-group.est.p)/
                                    table(group.soil)))

## Get mean x-values for each group for plotting purposes:
group.x.means=tapply(soil,group.soil,mean)
group.x.means=as.vector(group.x.means)

## Overlay plots:
xvalues=seq(0,5300)
yvalues=predict(glm.out,list(soil=xvalues),type="response")

plot(highbld~soil,type="n")
rug(jitter(soil[highbld==0]))
rug(jitter(soil[highbld==1]),side=3)
lines(xvalues,yvalues,col="blue",lwd=2)

points(group.x.means,group.est.p,cex=2,pch=16)
vlines=c(group.x.means[1]/2,group.x.means[-10]
               +(group.x.means[-1]-group.x.means[-10])/2)
```

```
abline(v=vlines)
legend(2700,.6,c("grouped p-hat","logistic reg. p-hat",
          "95% CI for grouped p-hat"),
          col=c("black","blue","red"),lty=c(-1,1,1),
          pch=c(16,-1,-1),lwd=2)

up=group.est.p+2*se
down=group.est.p-2*se
for (i in 1:10){
          lines(c(group.x.means[i],group.x.means[i]),
          c(up[i],down[i]),col="red",lwd=2)
}
points(group.x.means,group.est.p,cex=2,pch=16)

hosmerlem=function (y, yhat, g = 10) {
   cutyhat = cut(yhat, breaks =
           quantile(yhat, probs = seq(0,1, 1/g)),
           include.lowest = T)
   obs = xtabs(cbind(1 - y, y) ~ cutyhat)
   expect = xtabs(cbind(1 - yhat, yhat) ~ cutyhat)
   chisq = sum((obs - expect)^2/expect)
   P = 1 - pchisq(chisq, g - 2)
   c("X^2" = chisq, Df = g - 2, "P(>Chi)" = P)
 }

hosmerlem(highbld, glm.out$fitted, g = 10)
```