

Applied Logistic Regression

Week 7

1. Homework week 6: highlights
2. Assessing model calibration I
3. Assessing model calibration II
4. The Pearson chi-square statistic
5. The Hosmer-Lemeshow test
6. Statistical software for goodness of fit test I
7. Statistical software for goodness of fit test I
8. Assessing model discrimination (Area under the ROC curve) I
9. Assessing model discrimination (Area under the ROC curve) I
10. Homework

Stanley Lemeshow, Professor of Biostatistics
College of Public Health, The Ohio State University



THE OHIO STATE UNIVERSITY

Summary statistics may not be very specific about individual components

i.e.,

- a small value of one of these statistics does not rule out the possibility of some substantial deviation from fit for a few subjects.
- a large value for one of these statistics is a clear indication of a substantial problem with the model.

def: COVARIATE PATTERN - a single set of values for the covariates in a model

When developing models we assume that each subject is unique in their configuration of the covariates

- i.e., we assume # covariate patterns = n .

e.g.,

if AGE, RACE, SEX, WT were our variables, then the combination of these may well result in a unique set of values for each subject.

Once a final model is obtained there may be relatively few variables in the model, and the number of covariate patterns may be less than n .

e.g.,

if the final model contains only RACE and SEX, each coded at 2 levels, then there are only 4 possible covariate patterns.

The number of covariate patterns is not an issue in model development.

- The df for tests are based on the difference in the number of variables in competing models, not on the number of covariate patterns.
- They become an issue when assessing the fit of a model.

Suppose our fitted model contains p independent variables, x_1, x_2, \dots, x_p . Let J denote the number of distinct values of \underline{x} observed (i.e., covariate patterns).

- If some subjects have the same value of \underline{x} then $J < n$.

Denote the number of subjects with $\underline{x} = \underline{x}_j$ by m_j , $j = 1, 2, \dots, J$.

$$\text{Clearly, } \sum_{j=1}^J m_j = n.$$

Let y_j denote the number of positive responses, $y = 1$, among the m_j subjects with $\underline{x} = \underline{x}_j$.

Then $\sum_{j=1}^J y_j = n_1 =$ total number of subjects with $y = 1$.

- The distribution of the goodness-of-fit statistics is obtained by letting n get large
- If J , the number of covariate patterns, also increases with n , then each value of m_j will tend to be small.
- Distributional results obtained under the condition that only n becomes large are said to be based on “n-asymptotics”.

If we fix $J < n$ and let n become large, then each value of m_j will tend to become large.

- Distributional results based on each m_j becoming large are said to be based on " m – asymptotics".

Initially we will assume that $J \approx n$ as in the case most frequently occurring.

- We expect this to be the case whenever we have some continuous covariates in the model.

Let us now review several of the available methods.

Let $\hat{\pi}_i = \frac{e^{\hat{\beta}_0 + \sum_{j=1}^p \hat{\beta}_j x_j}}{1 + e^{\hat{\beta}_0 + \sum_{j=1}^p \hat{\beta}_j x_j}}$ be computed for all individuals, $i = 1, \dots, n$.

Given the values $\hat{\pi}_1, \hat{\pi}_2, \dots, \hat{\pi}_n$, an informally used approach is to rank order these n values and establish "deciles of risk".

i.e.,

1st decile contains the smallest $n/10$ values of $\hat{\pi}_i$

2nd decile contains the next smallest $n/10$ values of $\hat{\pi}_i$

⋮

10th decile contains the largest $n/10$ values of $\hat{\pi}_i$

If $n/10$ is not an integer, then the 10 groups may have slightly different numbers.

Now, if the model holds then those who actually develop the outcome should have high values for $\hat{\pi}_i$. Similarly, those who don't develop the outcome should have low values for $\hat{\pi}_i$.

Procedures have been developed for comparing the observed number with the expected number in each decile.

i.e., for the j^{th} decile

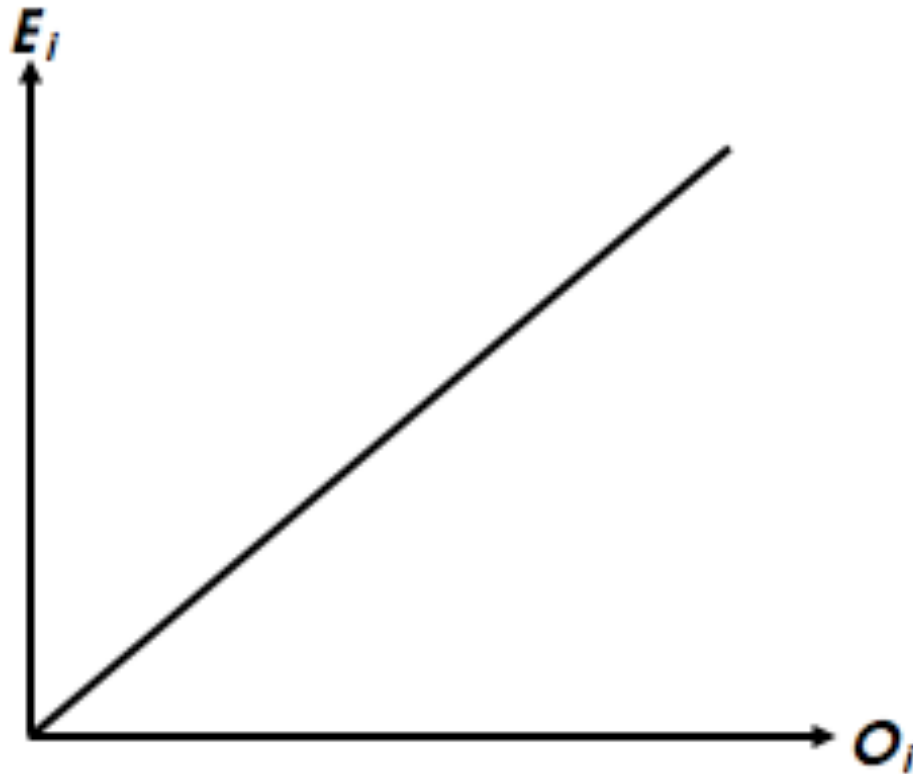
$$O_j = \sum_{i \in D_j} y_i$$

$$E_j = \sum_{i \in D_j} \hat{\pi}_i$$

where $j = 1, \dots, 10$ and where D_j denotes the $n/10$ individuals in the j^{th} decile of risk.

Consider the pairs $(O_1, E_1), \dots, (O_i, E_i), \dots, (O_{10}, E_{10})$.

One method used has been to plot these pairs:



If the observed and expected correspond, then the 10 points should fall on a line with slope = 1, intercept = 0.

This is an eye-ball method as there is no test statistic associated with it.

Pearson Chi-Square Statistic

In linear regression we were concerned with residuals of the form

$$y_i - \hat{y}_i$$

In logistic regression fitted values are calculated for each covariate pattern, and depend on the estimated probability for that covariate pattern.

We denote the fitted value, \hat{y}_i , as

$$m_j \hat{\pi}_j = m_j \left\{ \frac{e^{\hat{g}(\underline{x}_j)}}{1 + e^{\hat{g}(\underline{x}_j)}} \right\}$$

where $\hat{g}(\underline{x}_j)$ is the estimated logit.

For a particular covariate pattern the Pearson residual is defined as

$$r(y_j, \hat{\pi}_j) = \frac{(y_j - m_j \hat{\pi}_j)}{\sqrt{m_j \hat{\pi}_j (1 - \hat{\pi}_j)}}$$

The summary statistic based on these residuals is the Pearson chi-square statistic

$$X^2 = \sum_{j=1}^J r(y_j, \hat{\pi}_j)^2$$

and $X^2 \sim \chi^2(J - (p + 1))$ if the model holds.

Problem: when $J \approx n$, the distribution is obtained under n -asymptotics and hence the number of parameters is increasing at the same rate as the sample size.

Hence, p - values calculated for χ^2 are incorrect when $J \approx n$.

Although the p -value may be slightly off, X^2 is an effective way to compare observed to expected frequencies for each covariate pattern.

This statistic is routinely produced by many software packages.

The Pearson Chi Square Statistic can be thought of as arising from the following $2 \times J$ table:

		Covariate Pattern				
		1	2	3		J
$y = 0$		O_{01}	O_{02}	O_{03}		O_{0J}
$y = 1$		O_{11}	O_{12}	O_{13}		O_{1J}
		m_1	m_2	m_3		m_J

$E_{11} = m_1 \hat{\pi}_1$

$E_{03} = m_3 (1 - \hat{\pi}_3)$

When chi-square tests are computed from a contingency table the p -values are correct under the hypothesis when the estimated expected values are “large” in each cell.

- This condition will hold under m -asymptotics.

In the previous table the expected values will always be quite small since the number of columns, J , \uparrow as $n \uparrow$.

One way to avoid these difficulties under n -asymptotics is to group the data in such a way that m -asymptotics can be used.

e.g., we may collapse the columns into a fixed number of groups, g , and then calculate the observed and expected frequencies.

By fixing the number of columns, the estimated expected frequencies will become large as n becomes large.

- Thus m -asymptotics hold.

The Hosmer-Lemeshow Tests

Let us suppose that $J = n$. Two grouping strategies are proposed:

- (1) Collapse the table based on percentiles of the estimated probabilities.
- (2) Collapse the table based on fixed values of the estimated probabilities.

With method (1), use of $g = 10$ groups results in the first group containing the $n'_1 = n/10$ subjects having the smallest estimated probabilities, and the last group containing the $n'_{10} = n/10$ subjects having the largest estimated probabilities.

		Decile of Risk										
Outcome		1	2	3	...						10	
Present ($y = 1$)		O_{11}	O_{12}	O_{13}	...						$O_{1,10}$	n_1
Absent ($y = 0$)		O_{01}	O_{02}	O_{03}	...						$O_{0,10}$	n_0
		$n/10$	$n/10$	$n/10$...						$n/10$	n

E_{11} E_{03}

Where

$$O_{1j} = \sum_{i \in D_j} y_i \quad O_{0j} = \sum_{i \in D_j} (1 - y_i)$$

$$E_{1j} = \sum_{i \in D_j} \hat{\pi}_i \quad E_{0j} = \sum_{i \in D_j} (1 - \hat{\pi}_i)$$

Then we compute

$$\hat{C} = \sum_{k=0}^1 \sum_{j=1}^{10} \frac{(O_{kj} - E_{kj})^2}{E_{kj}}$$

This is the Pearson chi-square statistic from the $2 \times g$ table of observed and expected frequencies.

If the 2nd grouping strategy is used, $g = 10$ groups results in cutpoints defined at the values $k/10$, $k = 1, 2, \dots, 9$ and the groups contain all subjects with estimated probabilities between adjacent cutpoints.

$$\begin{aligned} \text{e.g., } 1^{\text{st}} \text{ group} &= 0 = \hat{\pi}_i < .1 \\ 2^{\text{nd}} \text{ group} &= .1 = \hat{\pi}_i < .2 \\ &\vdots \\ 10^{\text{th}} \text{ group} &= .9 = \hat{\pi}_i < 1.0 \end{aligned}$$

Based on extensive simulations, it has been demonstrated that, when $J = n$ and the fitted logistic model is the correct model, the distribution of \hat{C} is well approximated by $\chi^2(g - 2)$.

The grouping method based on deciles of risk is preferable to the one based on fixed cutpoints in the sense of better adherence to the $\chi^2 (g - 2)$ distribution

- this is especially true when many of the estimated probabilities are small (i.e., $<.02$).

Assessing the fit of the model for the low birth weight data follows.

SYSTAT LOGIT

```
>model low=constant+lwt+race
```

```
>dc # smart=10
```

```
=====
```

DECILES OF RISK

```
=====
```

RECORDS PROCESSED: 189

SUM OF WEIGHTS = 189.00000

		STATISTIC	P-VALUE	DOF		
HOSMER-LEMESHOW		7.04419	0.53187	8.00000		
PEARSON		188.30343	0.41865	185.00000		
DEVIANCE		223.25909	0.02869	185.00000		
CAT.		0.16785	0.22266	0.25301	0.27064	0.29538
RESP	OBS	2.00000	4.00000	5.00000	4.00000	5.00000
	EXP	2.19847	3.52513	4.66830	4.72146	4.48439
REF	OBS	16.00000	14.00000	15.00000	14.00000	11.00000
	EXP	15.80153	14.47487	15.33170	13.27854	11.51561
AV. PROB.		0.12214	0.19584	0.23341	0.26230	0.28027
CAT.		0.33324	0.36796	0.40774	0.47690	1.00000
RESP	OBS	7.00000	6.00000	4.00000	12.00000	10.00000
	EXP	6.58226	6.28696	8.38347	8.30865	9.84091
REF	OBS	14.00000	12.00000	18.00000	7.00000	9.00000
	EXP	14.41774	11.71304	13.61653	10.69135	9.15909
AV. PROB.		0.31344	0.34928	0.38107	0.43730	0.51794

>dc

=====
DECILES OF RISK
=====

RECORDS PROCESSED: 189
SUM OF WEIGHTS = 189.00000

	STATISTIC	P-VALUE	DOF
HOSMER-LEMESHOW	2.34774	0.67209	4.00000
PEARSON	188.30343	0.41865	185.00000
DEVIANCE	223.25909	0.02869	185.00000

CAT.	0.10000	0.20000	0.30000	0.40000	0.50000
------	---------	---------	---------	---------	---------

RESP	OBS	0.00000	4.00000	19.00000	14.00000	16.00000
	EXP	0.30527	3.51225	17.55645	17.45570	13.74300
REF	OBS	4.00000	19.00000	50.00000	36.00000	15.00000
	EXP	3.69473	19.48775	51.44355	32.54430	17.25700

AV. PROB.	0.07632	0.15271	0.25444	0.34911	0.44332
-----------	---------	---------	---------	---------	---------

CAT.	0.60000	0.70000	0.80000	0.90000	1.00000
------	---------	---------	---------	---------	---------

RESP	OBS	6.00000	0.00000	0.00000	0.00000	0.00000
	EXP	6.42734	0.00000	0.00000	0.00000	0.00000
REF	OBS	6.00000	0.00000	0.00000	0.00000	0.00000
	EXP	5.57266	0.00000	0.00000	0.00000	0.00000

AV. PROB.	0.53561	0.00000	0.00000	0.00000	0.00000
-----------	---------	---------	---------	---------	---------

>quit

STOP

STATA

```
. xi:logit low lwt i.race
```

i.race **_Irace_1-3**

(naturally coded; `_Irace_1` omitted)

Iteration 0: log likelihood = -117.336

Iteration 1: log likelihood = -111.7491

Iteration 2: log likelihood = -111.62983

Iteration 3: log likelihood = -111.62955

Logit estimates

Number of obs = 189

LR chi2(3) = 11.41

Prob > chi2 = 0.0097

Log likelihood = -111.62955

Pseudo R2 = 0.0486

low	Coef.	Std. Err.	z	P> z	[95% Conf. Interval]	
lwt	-.0152231	.0064393	-2.36	0.018	-.0278439	-.0026023
_Irace_2	1.081066	.4880512	2.22	0.027	.1245034	2.037629
_Irace_3	.4806033	.3566733	1.35	0.178	-.2184636	1.17967
_cons	.8057535	.8451625	0.95	0.340	-.8507345	2.462241

```
. lfit, group(10) table
```

Logistic model for low, goodness-of-fit test

(Table collapsed on quantiles of estimated probabilities)

Group	Prob	Obs_1	Exp_1	Obs_0	Exp_0	Total
1	0.1681	2	2.4	17	16.6	19
2	0.2228	4	4.2	17	16.8	21
3	0.2531	5	4.0	12	13.0	17
4	0.2708	4	5.0	15	14.0	19
5	0.2955	8	5.4	11	13.6	19
6	0.3334	6	6.1	13	12.9	19
7	0.3681	6	8.2	17	14.8	23
8	0.4078	3	5.8	12	9.2	15
9	0.4770	12	8.9	8	11.1	20
10	0.5975	9	8.9	8	8.1	17

```

number of observations =      189
      number of groups =       10
Hosmer-Lemeshow chi2(8) =       7.61
      Prob > chi2 =      0.4728

```

```
. lfit
```

Logistic model for low, goodness-of-fit test

```

number of observations =      189
number of covariate patterns =    109
      Pearson chi2(105) =    111.22
      Prob > chi2 =      0.3204

```

```
. logit STA AGE CAN ISYSGP 4 TYP LOCD
```

```
Iteration 0:    log likelihood = -100.08048
Iteration 1:    log likelihood = -70.385527
Iteration 2:    log likelihood = -67.395341
Iteration 3:    log likelihood = -66.763511
Iteration 4:    log likelihood = -66.758491
Iteration 5:    log likelihood = -66.758489
```

Logistic regression

Number of obs = 200

LR chi2 (5) = 66.64

```
Prob > chi2      =      0.0000
```

Log likelihood = -66.758489

Pseudo R2 = 0.3330

STA	Coef.	Std. Err.	z	P> z	[95% Conf. Interval]
AGE	.040628	.0128617	3.16	0.002	.0154196 .0658364
CAN	2.078751	.8295749	2.51	0.012	.4528141 3.704688
_ISYSGP_4	-1.51115	.7204683	-2.10	0.036	-2.923242 -.0990585
TYP	2.906679	.9257469	3.14	0.002	1.092248 4.72111
LOCD	3.965535	.9820316	4.04	0.000	2.040788 5.890281
_cons	-6.680532	1.320663	-5.06	0.000	-9.268984 -4.09208

```
. lfit, group(10) table
```

Logistic model for STA, goodness-of-fit test

(Table collapsed on quantiles of estimated probabilities)

Group	Prob	Obs_1	Exp_1	Obs_0	Exp_0	Total
1	0.0105	0	0.1	20	19.9	20
2	0.0290	0	0.4	20	19.6	20
3	0.0492	2	1.0	21	22.0	23
4	0.0666	0	1.0	17	16.0	17
5	0.1083	2	1.8	19	19.2	21
6	0.1674	2	2.6	17	16.4	19
7	0.2254	5	3.9	15	16.1	20
8	0.3171	4	5.5	16	14.5	20
9	0.4554	8	7.6	12	12.4	20
10	0.9623	17	16.1	3	3.9	20

```

number of observations =      200
number of groups      =       10
Hosmer-Lemeshow chi2(8) =      4.00
Prob > chi2           =     0.8570

```

```
. lfit
```

Logistic model for STA, goodness-of-fit test

```

number of observations =      200
number of covariate patterns =    135
Pearson chi2(129) =     79.23
Prob > chi2           =     0.9998

```

Because the distribution of \hat{C} depends on m - asymptotics, the appropriateness of the p - value will depend on the estimated expected frequencies being large enough to employ this theory.

If one is concerned about the magnitude of the expected frequencies, selected adjacent columns may be combined to increase the size of the expected frequencies. Unfortunately, when this is done the power of the test is reduced since the degrees of freedom are reduced.

When \hat{C} is calculated from fewer than 6 groups, it will almost always indicate that the model fits. Thus, try to use with as many groups as possible.

WEEK 7: AREA UNDER THE ROC CURVE

Some researchers have proposed using the 2×2 classification table as a measure of fit.

This table is the result of cross-classifying $y(0,1)$ with

$$\bar{y} = \begin{cases} 0 & \text{if } \hat{\pi} < c \\ 1 & \text{if } \hat{\pi} \geq c \end{cases} \quad \text{and } c \text{ is often taken to } = .5.$$

This table is, unfortunately, a measure of $|\hat{\beta}|$ not the correctness of the model. We know in the normal theory discriminant function situation that:

(1) The logistic model is the correct model for $\Pr(y = 1 | \underline{x})$

(2) Classification is a function of the separation of the 2 groups

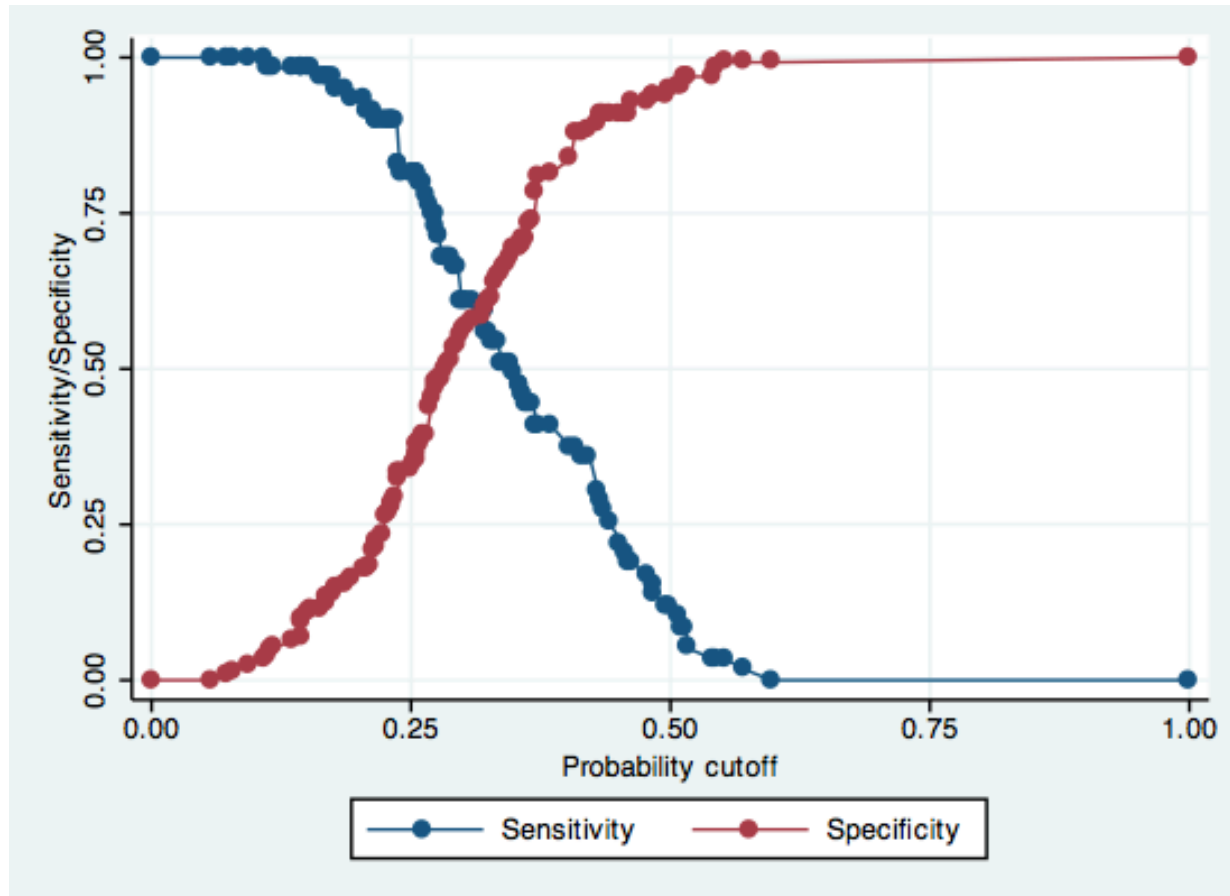
$$\Delta^2 = (\underline{\mu}_1 - \underline{\mu}_0)' \Sigma^{-1} (\underline{\mu}_1 - \underline{\mu}_0) = \underline{\beta}' (\underline{\mu}_1 - \underline{\mu}_0)$$

This is a function of $\underline{\beta}$... not the correctness of the model assumptions.

*Classification should not be used as a criterion for model adequacy unless it is a stated goal of the analysis.

STATA produces a graph of sensitivity and specificity versus probability cutoff:

`.lsens`



Area Under The ROC Curve (a measure of *discrimination*)

Consider the model for estimating the probability of low birth weight.

- suppose we were interested in *predicting* the outcome for each patient.
- One rule we might try is as follows:
 - predict baby will be low birth weight if $\Pr(\text{LOW}) \geq .50$
 - predict baby will be normal birth weight if $\Pr(\text{LOW}) < .50$

(Choice of .50 is traditional rather than optimal.)

This would result in the following 2 × 2 classification table:

. lstat

Logistic model for low

Classified	True		Total
	D	~D	
+	6	6	12
-	53	124	177
Total	59	130	189

Classified + if predicted $\text{Pr}(D) \geq .5$

True D defined as low != 0

Sensitivity	$\text{Pr}(+ D)$	10.17%
Specificity	$\text{Pr}(- \sim D)$	95.38%
Positive predictive value	$\text{Pr}(D +)$	50.00%
Negative predictive value	$\text{Pr}(\sim D -)$	70.06%

False + rate for true ~D	$\text{Pr}(+ \sim D)$	4.62%
False - rate for true D	$\text{Pr}(- D)$	89.83%
False + rate for classified +	$\text{Pr}(\sim D +)$	50.00%
False - rate for classified -	$\text{Pr}(D -)$	29.94%

Correctly classified 68.78%

Suppose that, instead of a cutpoint of .5, .6 had been used:

```
. lstat, cutoff(.6)
```

Logistic model for low

Classified	True		Total
	D	~D	
+	0	0	0
-	59	130	189
Total	59	130	189

Classified + if predicted $\Pr(D) \geq .6$

True D defined as low != 0

Sensitivity	$\Pr(+ D)$	0.00%
Specificity	$\Pr(- \sim D)$	100.00%
Positive predictive value	$\Pr(D +)$.%
Negative predictive value	$\Pr(\sim D -)$	68.78%

False + rate for true ~D	$\Pr(+ \sim D)$	0.00%
False - rate for true D	$\Pr(- D)$	100.00%
False + rate for classified +	$\Pr(\sim D +)$.%
False - rate for classified -	$\Pr(D -)$	31.22%

Correctly classified 68.78%

Summarizing results for all cutpoints between .1 and .6 in steps of .05, we have:

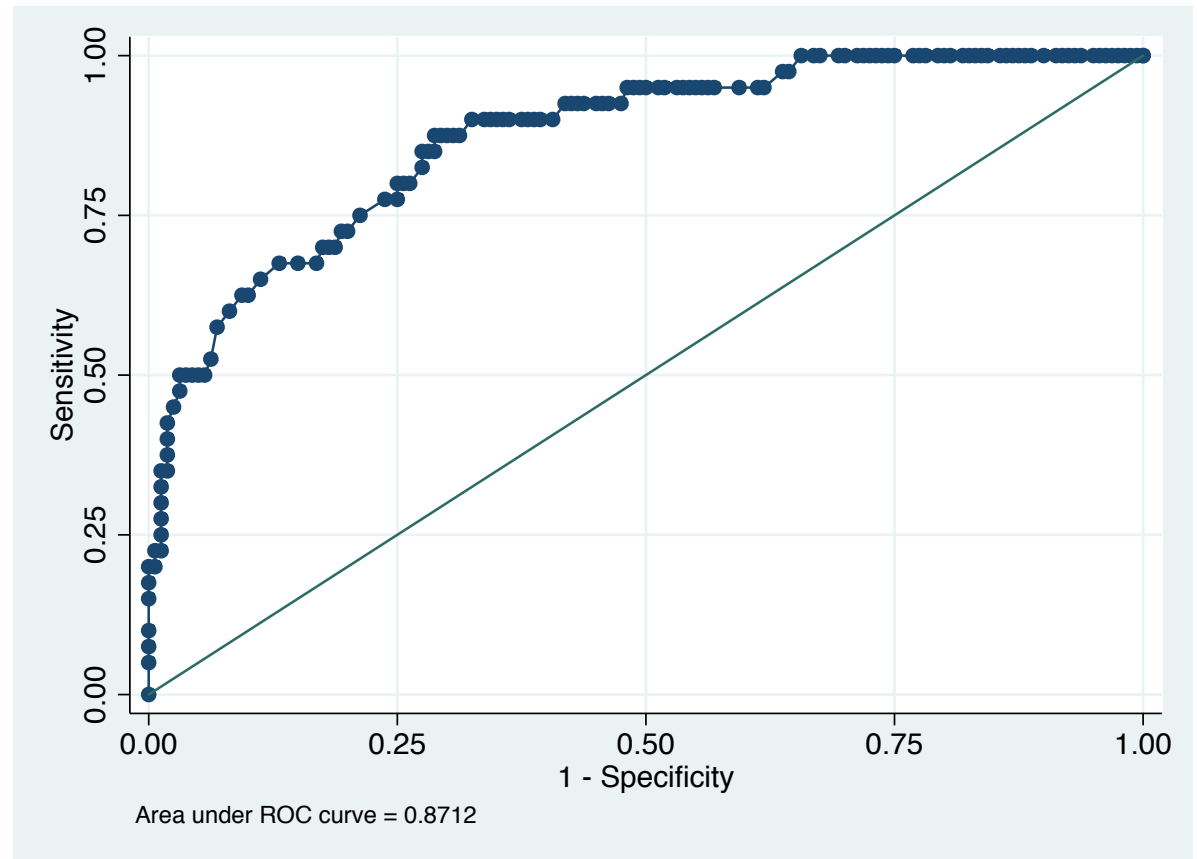
<u>Cutpoint</u>	Sensitivity	Specificity	1 - Specificity
0.1	100.00	3.08	96.92
0.15	98.31	11.54	88.46
0.2	93.22	17.69	82.31
0.25	81.36	33.85	66.15
0.3	61.02	56.15	43.85
0.35	49.15	69.23	30.77
0.4	37.29	83.85	16.15
0.45	22.03	90.77	9.23
0.5	10.17	95.38	4.62
0.55	3.39	99.23	0.77
0.6	00.00	100.00	0.00

Plotting sensitivity vs (1 - specificity) we have the ROC Curve:

```
. lroc
```

Logistic estimates for LOW

Area under ROC curve = 0.6473



The area under the ROC curve is a measure of discrimination.

- It is a measure of the likelihood that a patient who has a low birth weight baby will have a higher $\text{Pr}(\text{LOW})$ than a patient with a normal birth weight baby.

As a general rule:

- $ROC = .5$: no discrimination (might as well just flip a coin)
- $ROC \geq .7$: considered acceptable discrimination
- $ROC \geq .8$: excellent discrimination
- $ROC \geq .9$: outstanding discrimination (very unusual)

note: a poorly fitting model (i.e., poorly calibrated as assessed by goodness-of-fit, Pearson χ^2 , etc) may still have good discrimination.

- e.g., simply add .25 to every probability in a good fitting logistic model.
 - the calibration will fall apart
 - the discrimination will not be affected at all

Another way to get the area under the ROC Curve is as follows:

- let n_1 = no. of patients who have low birthweight babies
- let n_2 = no. of patients who have normal birthweight babies
- create $n_1 \times n_2$ pairs
i.e., each patient who gave birth to a low birthweight baby is paired with each patient who had a normal birthweight baby
- of these $n_1 \times n_2$ pairs, determine proportion of the time that the woman who had the low birthweight baby had the higher of the two probabilities
 - This proportion is the area under the ROC Curve

This can be done easily by running the nonparametric Mann-Whitney U Test:

```
. ranksum pihat, by(LOW)
```

Test: Equality of medians (Two-Sample Wilcoxon Rank-Sum)

Sum of Ranks: 6735 (LOW == 1)

Expected Sum: 5605

z-statistic 3.24

Prob > |z| 0.0012

Wilcoxon Rank-sum test

```
. tabulate LOW
```

LOW	Freq.	Percent	Cum.
0	130	68.78	68.78
1	59	31.22	100.00
Total	189	100.00	

Converts Wilcoxon Rank-sum test to Mann-Whitney U

$$U = mn + \frac{m(m+1)}{2} - T$$

$$m = \min\{n_1, n_2\}$$

$$n = \max\{n_1, n_2\}$$

```
. display 59*130+((59*60)/2)-6735
```

2705

```
. display 2705/(59*130)
```

.35267275

Area Under ROC Curve

$$= 1 - .3527 = .6473$$

Suppose you need the confidence intervals for the area under the ROC curve. Stata 13 now has the option to perform nonparametric analysis of the ROC curve using bootstrap. To do this:

(1) Run the logistic regression

(2) Estimate the logit, and

(3) Run the nonparametric ROC regression command on the logit.

Logistic regression, generation of the logit, and lroc

```
. logit LOW LWT i.RACE, nolog
```

Logistic regression

Number of obs = 189

LR chi2(3) = 11.41

Prob > chi2 = 0.0097

Log likelihood = -111.62955

Pseudo R2 = 0.0486

LOW	Coef.	Std. Err.	z	P> z	[95% Conf. Interval]	
LWT	-.0152231	.0064394	-2.36	0.018	-.027844	-.0026022
RACE						
2	1.081066	.4880522	2.22	0.027	.1245015	2.037631
3	.4806033	.3566737	1.35	0.178	-.2184644	1.179671
_cons	.8057535	.8451667	0.95	0.340	-.8507428	2.46225

```
. predict logit, xb
```

```
. lroc, nograph all
```

Logistic model for LOW

number of observations = 189

area under ROC curve = 0.6473

Nonparametric ROC regression of low birth weight on the predicted logit with a random seed, 500 replications, and correction for ties

- the **nodots** option suppresses some of the Stata output

```
. rocreg LOW logit, bseed(04062012) breps(500) tiecorrected nodots
```

```
Bootstrap results                                Number of obs    =      189
                                                Replications    =      500
```

Nonparametric ROC estimation

```
Control standardization: empirical, corrected for ties
ROC method                : empirical
```

Area under the ROC curve

```
Status      : LOW
Classifier: logit
```

```
-----
AUC |      Observed      |      Bias      |      Bootstrap      |      [95% Conf. Interval]
    |      Coef.         |                |      Std. Err.      |
-----+-----
    |      .6473272      |      .002192    |      .0427415       |      .5635555      .731099 (N)
    |                    |                |                    |      .5724257      .7336735 (P)
    |                    |                |                    |      .5720991      .7292663 (BC)
```

Note:

(N) normal confidence interval; (P) percentile confidence interval
(BC) bias-corrected confidence interval