

## Regression Diagnostics for Binary Outcome Models

- As in the case of ordinary least squares regression, post-model diagnostics can be used to
  - check model assumptions
  - check (indirectly) for omitted predictors, functional form of predictors
  - identify unusual data observations - that do not fit the model well
  - other aspects
- For binary regression models, one useful quantity is the *residual* - difference between observed and predicted. This quantity is most relevant for predicted proportions (recall all individual cases have a 0/1 outcome), but can be computed for each individual case

## Regression Diagnostics for Binary Outcome Models

**Before specific diagnostics, one overarching issue in binary outcome data is *sparseness* or *sparse tables***

- if for a given level of a discrete covariate, all responses are zero, then the odds ratio against a reference category is 0. If baseline category has zero events, then  $OR = \infty$
- sparse tables can occur when many covariates are considered together, leading to a high-dimensional layout of the covariate combinations cross-classified with outcome.
- In multiway tables, main effects of each covariate may be estimated, but interaction effects will become not estimable. This may not be a problem in many analyses, since high-level interactions are difficult to interpret or verify

## Zeros in Tables

### The Donner Party data - females under 25

```
. cc dstat sexcode if AGE < 25
```

	sexcode		Proportion	
	Exposed	Unexposed	Total	exposed
Cases	4	0	4	1.0000
Controls	3	6	9	0.3333
Total	7	6	13	0.5385
	Point estimate		[95% conf. interval]	
Odds ratio	.		1.416577	. (Cornfield)
Attr. frac. ex.	.		.2940729	. (Cornfield)
Attr. frac. pop	.			
chi2(1) = 4.95 Pr>chi2 = 0.0261				

Note: Exact confidence levels not possible with zero count cells.

```
. logit dstat sexcode if AGE < 25
```

```
note: sexcode != 1 predicts failure perfectly;
      sexcode omitted and 6 obs not used.
```

```
Iteration 0: Log likelihood = -4.7803567
```

```
Iteration 1: Log likelihood = -4.7803567
```

```
Logistic regression
```

```
Number of obs =      7
```

```
LR chi2(0)      =    0.00
```

```
Prob > chi2     =      .
```

```
Log likelihood = -4.7803567
```

```
Pseudo R2      = 0.0000
```

-----						
dstat		Coefficient	Std. err.	z	P> z	[95% conf. interval]
-----+-----						
sexcode		0 (omitted)				
_cons		.2876821	.7637626	0.38	0.706	-1.209265 1.784629
-----						

## Zeros in Tables

**Note:** main effects model in all subjects is estimable:

```
. logit dstat sexcode age25plus
```

```
. . . .
```

dstat	Coefficient	Std. err.	z	P> z	[95% conf. interval]	
sexcode	1.280376	.6992295	1.83	0.067	-.0900883	2.650841
age25plus	1.348034	.7356685	1.83	0.067	-.0938496	2.789918
_cons	-1.581687	.7804491	-2.03	0.043	-3.111339	-.0520348

	female	male
under 25	1.00	3.60
25+	3.85	13.85

## Zeros in Tables

**Note:** main with interactions effects model not estimable:

```
. logit dstat sexcode age25plus agebysex  
. . .
```

-----						
dstat	Coefficient	Std. err.	z	P> z	[95% conf. interval]	
-----+-----						
sexcode	17.63652	2388.794	0.01	0.994	-4664.313	4699.586
age25plus	34.60506	4777.587	0.01	0.994	-9329.294	9398.504
agebysex	-17.03307	2388.794	-0.01	0.994	-4698.983	4664.917
_cons	-17.34885	2388.794	-0.01	0.994	-4699.298	4664.601
-----						

Sub-tables do not all have OR estimates

## Zeros in Tables

Reclassifying age into 25 or under and 26+:

```
. logit dstat sexcode age26plus
```

dstat	Coefficient	Std. err.	z	P> z	[95% conf. interval]	
sexcode	1.355987	.6763103	2.00	0.045	.0304436	2.681531
age26plus	.5395536	.6381147	0.85	0.398	-.7111282	1.790235
_cons	-.9569176	.6412532	-1.49	0.136	-2.213751	.2999156

	female	male
under 25	1.00	3.88
25+	1.72	6.66

## Zeros in Tables

Reclassifying age into  $\leq 25$  and 26+, interaction added:

```
. logit dstat sexcode age26plus age26bysex
```

dstat	Coefficient	Std. err.	z	P> z	[95% conf. interval]	
sexcode	2.75684	1.226364	2.25	0.025	.3532114	5.160469
age26plus	2.233592	1.313846	1.70	0.089	-.341498	4.808682
age26bysex	-2.438387	1.531299	-1.59	0.111	-5.439678	.5629047
_cons	-1.94591	1.069045	-1.82	0.069	-4.0412	.1493795

	female	male
under 25	1.00	15.75
25+	9.33	12.83

Age effect within sex different here - present in women only



## Zeros in Tables and Sparse Tables Generally

- How predictor variables are grouped or partitioned may need to be considered for estimable effects.
- Zero is a valid value for an odds ratio.
- Methods for *sparse contingency tables* is a large area in statistical methodology and application. These methods are needed when there are a lot of covariates (and combinations) relative to number of failures - for example, genomic variant data

## Logistic Regression - Back to Residuals

### Two types of residuals:

- Pearson residuals are defined to be the standardized difference between the observed frequency (proportion) and the predicted frequency . These measure the relative deviations between the observed and fitted values.

$$r_i = \frac{y_i - \hat{u}_i}{\sqrt{\hat{u}_i(n_i - \hat{u}_i)/n_i}} \quad (1)$$

- Equals square root of the  $i^{th}$  component of the Pearson Chi-square statistic.

## Logistic Regression Residuals

### Two types of residuals (cont.):

- Deviance residuals are components of the deviance statistic, which measure the disagreement between the maxima of the observed and the fitted log likelihood functions.

$$d_i = \sqrt{2\{y_i \log(\frac{y_i}{\hat{\mu}_i}) + (n_i - y_i) \log(\frac{n_i - y_i}{n_i - \hat{\mu}_i})\}} \quad (2)$$

- Equals square root of  $i^{th}$  component of the deviance statistic (with sign re-attached).
- Analogous to the raw residual in OLS regression, where the goal is to minimize the sum of squared residuals. Logistic regression estimation minimizes the sum of the deviance residuals (using maximum likelihood to solve)

## **Logistic Regression Residuals**

- These quantities can be listed, plotted to identify unusual values
- In grouped data, can approximately normally distributed, zero-centered random variable (i.e., Z-statistic)
- Thus, values greater than  $\pm 2$  may be of interest ('extreme' values on the Z scale)

### Ex/ Logistic Regression Residuals

- Outcome (survival) of root cuttings may be related to cutting time and length

Table 1: Survival rate of plum root-stock cuttings

Length	Planting	Surviving	Proportion
Short	Immediate	107	0.45
	In spring	31	0.13
Long	Immediate	156	0.65
	In spring	84	0.35

## Ex/ Logistic Regression Residuals

```
. glm number length time, family(binomial total)
```

```
.
```

Generalized linear models	No. of obs	=	4
Optimization : ML	Residual df	=	1
	Scale parameter	=	1
Deviance = 2.293839315	(1/df) Deviance	=	2.293839
Pearson = 2.270478953	(1/df) Pearson	=	2.270479
Variance function: $V(u) = u \cdot (1 - u / \text{total})$	[Binomial]		
Link function : $g(u) = \ln(u / (\text{total} - u))$	[Logit]		
	AIC	=	7.758987
Log likelihood = -12.51797425	BIC	=	.907545

		OIM				
number		Coef.	Std. Err.	z	P> z	[95% Conf. Interval]
length		1.017691	.14548	7.00	0.000	.7325559 1.302827
time		-1.427542	.1464624	-9.75	0.000	-1.714603 -1.140481
_cons		-.3039203	.1171647	-2.59	0.009	-.533559 -.0742816

## Ex/ Logistic Regression Residuals

### Model output and and residuals

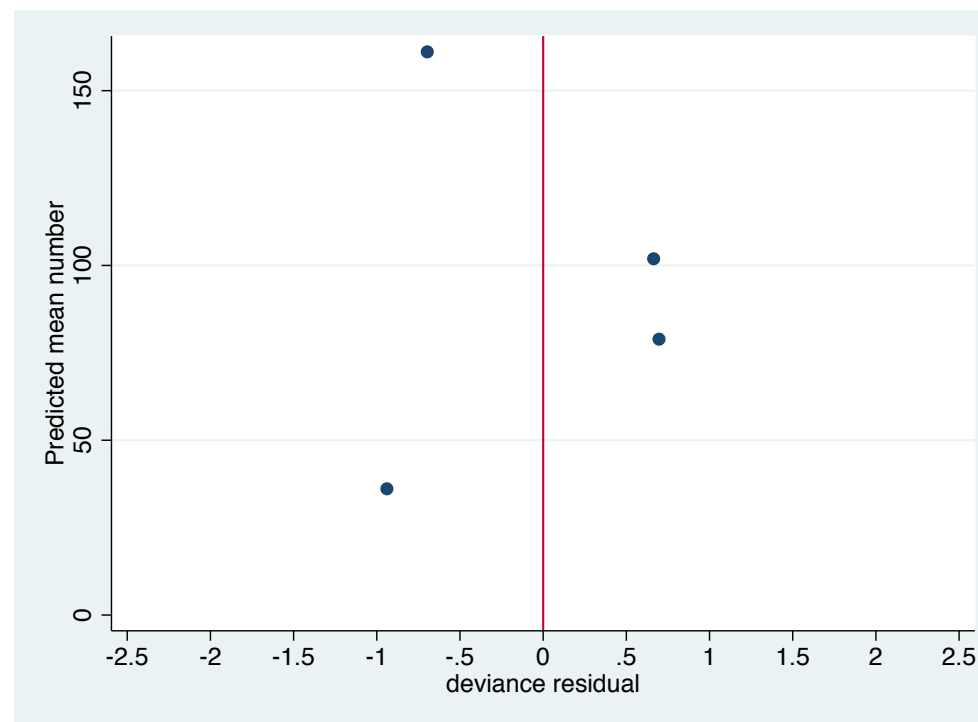
```
. predict yhat  
(option mu assumed; predicted mean number)  
. predict dres, d  
. predict pres, p  
. list
```

	length	time	number	total	yhat	pres	dres
1.	0	0	107	240	101.9039	.6655197	.6641749
2.	0	1	31	240	36.09614	-.9202459	-.9392965
3.	1	0	156	240	161.0961	-.7002535	-.6965749
4.	1	1	84	240	78.90386	.7002535	.6965749

## Ex/ Logistic Regression Residuals

plot the residuals:

```
, twoway (scatter yhat dres), xlabel(-2.5(.5)2.5) xline(0)
```



Not very exciting - but these indicate reasonable fit. Residuals are more interesting for larger models and/or continuous predictors



## **Logistic Regression - another model**

### **Example: Biomarkers in localized, high risk prostate cancer**

- Men with localized prostate cancer deemed 'high risk' based on clinical and pathologic features may undergo radiation therapy and long-term androgen deprivation. For some, this is too aggressive an intervention, while for others, even this approach does not sufficiently decrease risk of eventual metastatic disease and death
- Using data from subset of clinical trial RTOG 9202, we investigated tumor biomarkers for relationship to distant metastasis event to identify and explain heterogeneity in distant mets risk (Pollack et al *Clin Cancer Res* 2014)

## Logistic Regression -

```
. tab distant_met if all_markers
```

distant_met	Freq.	Percent	Cum.
-----+-----			
0	1,056	81.48	81.48
1	240	18.52	100.00
-----+-----			
Total	1,296	100.00	

```
. list distant_met ki67_acis10_index_percent p16_index_percent mdm2_intensity cox2_intensity
```

	distan~t	ki67_a~t	p16_~ent	mdm2_i~y	cox2_i~y
2.	0	8.6	100	211	159
7.	0	7.6	94.7	178	149
8.	0	7.7	61.1	187	131
16.	0	6.9	87.7	178	156
21.	1	21.4	38.4	159	166
23.	1	13.8	71.3	194	158
25.	0	28	90.8	152	128
35.	0	22.5	92.1	186	149
36.	0	43.5	96.3	178	161
38.	0	1.5	89.2	144	200

```
.  
.
```

## Logistic Regression - Goodness of Fit

```
. logistic distant_met ki67_acis10_index_percent p16_index_percent mdm2_intensity cox2_intensity
```

```
Logistic regression                Number of obs    =          372
                                   LR chi2(4)        =          34.05
                                   Prob > chi2        =          0.0000
Log likelihood = -174.01005         Pseudo R2      =          0.0891
```

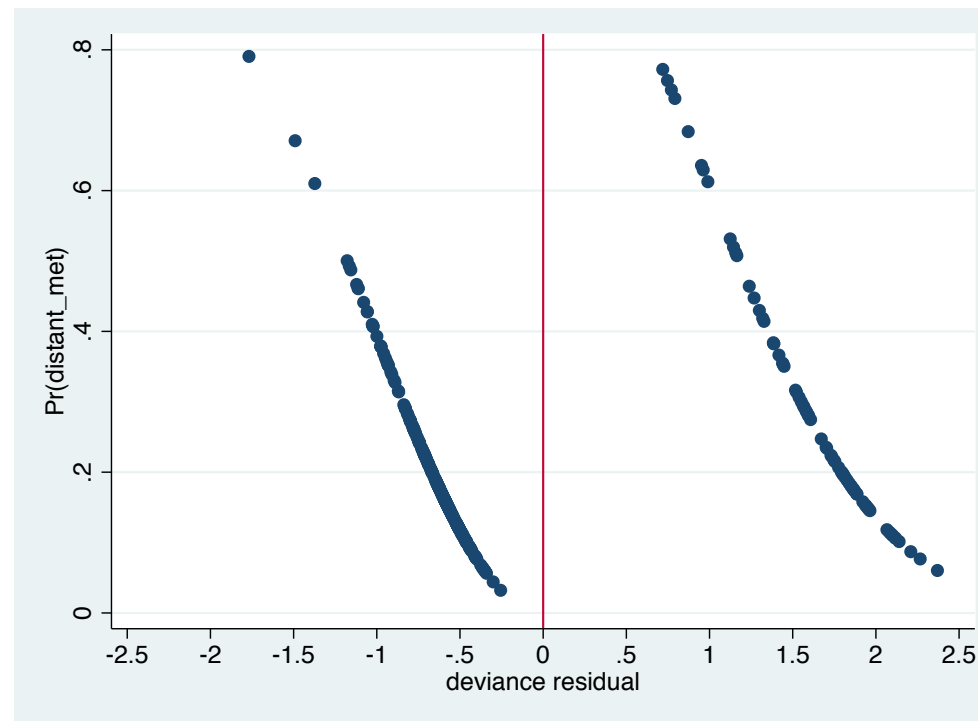
```
-----+-----
              distant_met | Odds Ratio   Std. Err.      z    P>|z|     [95% Conf. Interval]
-----+-----
ki67_acis10_index_percent | 1.064318     .0163019     4.07   0.000   1.032842     1.096754
      p16_index_percent   | .9867829     .0056341    -2.33   0.020   .9758019     .9978876
      mdm2_intensity      | 1.004605     .0032227     1.43   0.152   .9983081     1.010941
      cox2_intensity      | 1.012377     .0069322     1.80   0.072   .9988811     1.026056
               _cons       | .0296984     .028565     -3.66   0.000   .0045083     .1956366
-----+-----
```

```
. estat gof, group(10)
```

```
Logistic model for distant_met, goodness-of-fit test
(Table collapsed on quantiles of estimated probabilities)
      number of observations =          372
      number of groups      =          10
Hosmer-Lemeshow chi2(8) =          11.79
      Prob > chi2 =          0.1610
```

## Logistic Regression - Examining Residuals

```
predict yhat  
(option pr assumed; Pr(distant_met))  
(1149 missing values generated)  
  
. predict dres, dev  
(1,149 missing values generated)  
  
. twoway (scatter yhat dres), xlabel(-2.5(.5)2.5) xline(0)
```



## - Residuals

```
. list cn distant_met yhat dres if dres > 2.0 & dres ~=., noobs clean
```

cn	distan <sup>~</sup> t	yhat	dres
101	1	.1182092	2.066543
673	1	.0869857	2.209983
826	1	.0602835	2.370104
881	1	.0766417	2.266545
996	1	.1068749	2.114756
1006	1	.1013688	2.139621
1098	1	.1148568	2.080418
1250	1	.1131486	2.087608
1337	1	.1060305	2.118504
1486	1	.110245	2.100024
1495	1	.1104176	2.099279

**These cases had low predicted probability of distant mets yet had distant mets - may be worth further examination**

## - Logistic Model - add more predictors

We add some important clinical/pathologic predictors to the model

```
. logistic distant_met ki67_acis10_index_percent p16_index_percent mdm2_intensity
      cox2_intensity psahigh age gleason_d2
```

```
Logistic regression              Number of obs      =           343
                                LR chi2(7)          =           65.42
                                Prob > chi2          =           0.0000
Log likelihood = -136.68406      Pseudo R2        =           0.1931
```

```
-----+-----
              distant_met | Odds Ratio Std. Err.      z    P>|z|    [95% Conf. Interval]
-----+-----
ki67_acis10_index_percent | 1.05912    .0180011    3.38   0.001    1.02442    1.09499
      p16_index_percent |  .98398    .0060536   -2.62   0.009    .972189    .995919
      mdm2_intensity | 1.00355    .003444    1.03   0.301    .996829    1.01033
      cox2_intensity | 1.022      .0081364    2.73   0.006    1.00617    1.03807
          psahigh | 3.31139    2.132884    1.86   0.063    .9370218   11.70236
              age |  .957837    .0215753   -1.91   0.056    .9164707    1.001072
          gleason_d2 | 5.11480    1.648314    5.06   0.000    2.719684    9.619226
              _cons | .109938    .1999009   -1.21   0.225    .0031146    3.880518
-----+-----
```

These factors contribute based on beta values, also can possibly drop mdm2 intensity as a predictor

## Final Model

```
. logistic distant_met ki67_acis10_index_percent p16_index_percent cox2_intensity
    psahigh age gleason_d2
```

Logistic regression	Number of obs	=	392
	LR chi2(6)	=	75.42
	Prob > chi2	=	0.0000
Log likelihood = -149.23974	Pseudo R2	=	0.2017

	distant_met	Odds Ratio	Std. Err.	z	P> z	[95% Conf. Interval]	
-----+-----							
ki67_acis10_index_percent		1.063578	.0173017	3.79	0.000	1.030202	1.098035
p16_index_percent		.9859311	.0055475	-2.52	0.012	.975118	.9968641
cox2_intensity		1.02084	.0072459	2.91	0.004	1.006737	1.035141
psahigh		3.971405	2.331307	2.35	0.019	1.256809	12.54929
age		.9510925	.0206622	-2.31	0.021	.9114453	.9924643
gleason_d2		6.013003	1.854401	5.82	0.000	3.285353	11.00527
_cons		.2621869	.4488802	-0.78	0.434	.0091475	7.514857
-----							

## Logistic Regression - Variability Explained

In logistic regression, several analogues to the  $R^2$  have been suggested. One simple one is

$$R_{pseud}^2 = 1 - \frac{\log L(\hat{\beta})}{\log \hat{L}_0}$$

where  $\log L(\hat{\beta})$  is the log likelihood for the current model and  $\log \hat{L}_0$  is the null model.

- additionally, an  $R^2$  adjusted for the number of parameters may be used
- Generally, these measures are not as reliable as fits measures as in the linear regression setting
- For the prostate model, the value was about .20, or 20% of the variation in risk of distant mets is explained by covariates.



## Logistic Regression - Prediction

Several other post-model outputs relating to prediction are available. One of these uses assessment of classification performance:

- Cross-classifying to compare agreement between predicted and observed outcomes under some assignment rule such as - 'any case with  $> .50$  predicted probability of being an event (1) will be classified as an event' - Use familiar measures of sensitivity, specificity, PPV, NPV to summarize rule
- The receiver operating characteristic (ROC) curve - plot of sensitivity vs 1 - specificity - evaluation of prediction rule over all possible cut-points of probability. This can be shown to equal to probability of correctly determining among two random cases, which will be an event.

Results can look encouraging, but true test of model performance must be assessed on *independent* data - not use to build the model

## Logistic Regression - Prediction

. estat classification

Logistic model for distant\_met

		----- True -----		
Classified		D	~D	Total
-----+-----+-----+-----				
+		19	9	28
-		53	311	364
-----+-----+-----+-----				
Total		72	320	392

Classified + if predicted  $\Pr(D) \geq .5$  -True D defined as distant\_met != 0

Sensitivity	Pr( +  D)	26.39%
Specificity	Pr( -  ~D)	97.19%
Positive predictive value	Pr( D  +)	67.86%
Negative predictive value	Pr( ~D  -)	85.44%

False + rate for true ~D	Pr( +  ~D)	2.81%
False - rate for true D	Pr( -  D)	73.61%
False + rate for classified +	Pr( ~D  +)	32.14%
False - rate for classified -	Pr( D  -)	14.56%

Correctly classified 84.18%

## Logistic Regression - Prediction

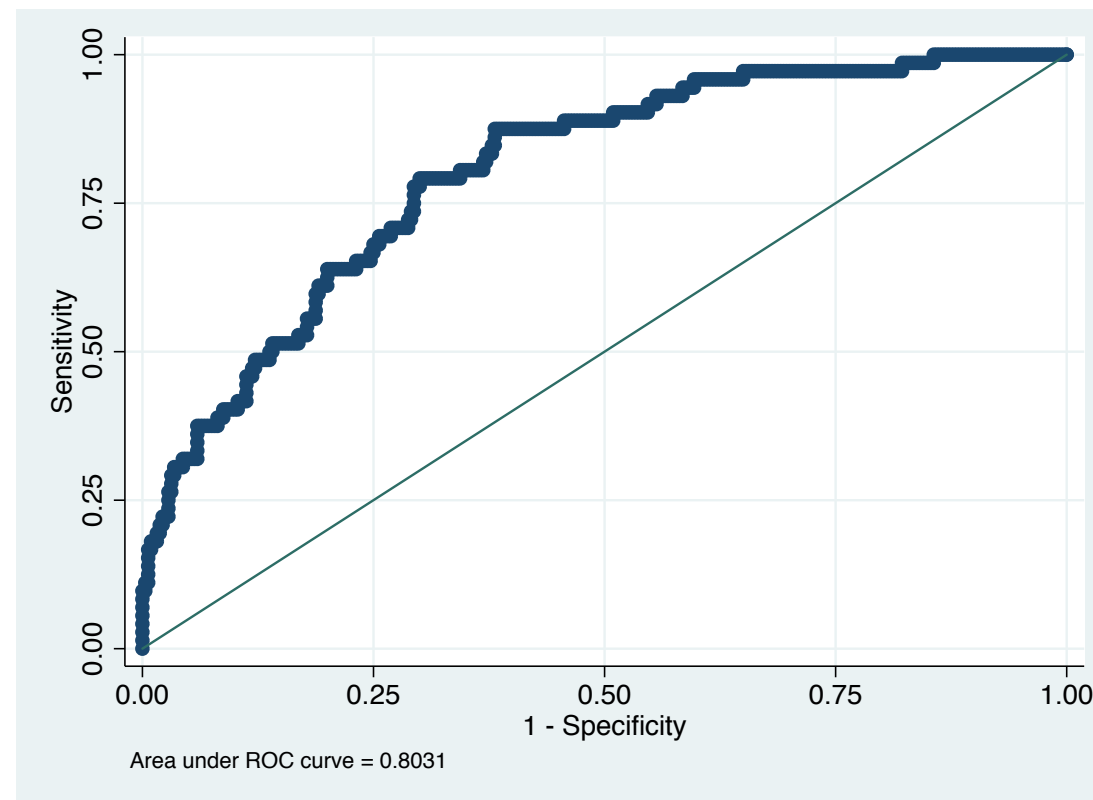
Curve Based on 6-predictor model for distant mets:

```
. lroc
```

Logistic model for distant\_met

number of observations = 392

area under ROC curve = 0.8031



Changing the cutpoint will change the performance:

```
. estat classification, cutoff(.35)
```

Logistic model for distant\_met

----- True -----				
Classified		D	~D	Total
-----+-----+-----				
+		33	36	69
-		39	284	323
-----+-----+-----				
Total		72	320	392

Classified + if predicted Pr(D) >= .35 -True D defined as distant\_met != 0

Sensitivity	Pr( +  D)	45.83%
Specificity	Pr( -  ~D)	88.75%
Positive predictive value	Pr( D  +)	47.83%
Negative predictive value	Pr( ~D  -)	87.93%

False + rate for true ~D	Pr( +  ~D)	11.25%
False - rate for true D	Pr( -  D)	54.17%
False + rate for classified +	Pr( ~D  +)	52.17%
False - rate for classified -	Pr( D  -)	12.07%

Correctly classified 80.87%

## **Model Assessment**

- Diagnostic tools follow those of linear regression models, but may be a bit more difficult to interpret. These are nonetheless useful.
- There are many more diagnostics covered in other texts, including identifying influential observations, outliers, assumptions about the distribution (ie link function), etc.
- Post-model classification tools assess the utility of the model in prediction. Developing such models further requires independent validation.