Logistic Regression - Exercise 3
Solutions

1. Assessment of overall fit

First, fit the model

```
. logit sepsis i.post umb c.age_ct##c.age_ct

..output omitted

Logistic regression                                     Number of obs   =        240
                                                        LR chi2(5)      =      46.87
                                                        Prob > chi2     =     0.0000
Log likelihood = -123.17402                             Pseudo R2       =     0.1598

------------------------------------------------------------------------------
      sepsis |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
        post |
     sternal |   1.594338   .4175655     3.82   0.000     .7759249    2.412752
     lateral |   1.838978   .4345141     4.23   0.000     .9873464    2.690611
             |
         umb |   1.078453   .3577357     3.01   0.003     .3773043    1.779602
      age_ct |  -.0823109   .0289085    -2.85   0.004    -.1389705   -.0256513
             |
c.age_ct#c.age_ct |   .0086873   .0033643     2.58   0.010     .0020934    .0152812
             |
       _cons |  -2.768343   .4018875    -6.89   0.000    -3.556028   -1.980658
------------------------------------------------------------------------------

. estat gof /*Pearson X2 statistic*/

Logistic model for sepsis, goodness-of-fit test

       number of observations =       240
 number of covariate patterns =        95
             Pearson chi2(89) =       114.86
                  Prob > chi2 =         0.0339
```

The Pearson's chi-square goodness of fit test is highly significant which might appear to say that the model does not fit the data very well at all. However, there are on average only 2.5 (=240/95) observations per covariate pattern, and this is too small for the P-value obtained from the chi-square reference distribution to be valid. This is because there will be many covariate patterns (CPs) with few records (and some with only one record), and they will have a large influence on the chi-square statistic.

You could carry out a Hosmer-Lemeshow goodness-of-fit test with 10 groups in order to increase the number of observations per group.

```
 estat gof, g(10) table /*Hosmer-Lemeshow*/

Logistic model for sepsis, goodness-of-fit test

  (Table collapsed on quantiles of estimated probabilities)
  +--------------------------------------------------------+
  | Group |   Prob | Obs_1 | Exp_1 | Obs_0 | Exp_0 | Total |
  |-------+--------+-------+-------+-------+-------+-------|
  |     1 | 0.0580 |     2 |   1.2 |    22 |  22.8 |    24 |
  |     2 | 0.0946 |     1 |   1.9 |    23 |  22.1 |    24 |
  |     3 | 0.1745 |     4 |   4.2 |    25 |  24.8 |    29 |
  |     4 | 0.2101 |     3 |   3.8 |    16 |  15.2 |    19 |
  |     5 | 0.2604 |     8 |   5.7 |    16 |  18.3 |    24 |
  |-------+--------+-------+-------+-------+-------+-------|
  |     6 | 0.3202 |     6 |   7.0 |    18 |  17.0 |    24 |
  |     7 | 0.3670 |     8 |   9.0 |    18 |  17.0 |    26 |
  |     8 | 0.4761 |     8 |  10.2 |    15 |  12.8 |    23 |
  |     9 | 0.5708 |    17 |  14.5 |    10 |  12.5 |    27 |
  |    10 | 0.8311 |    15 |  14.5 |     5 |   5.5 |    20 |
  +--------------------------------------------------------+

      number of observations =       240
            number of groups =        10
    Hosmer-Lemeshow chi2(8) =      4.63
                Prob > chi2 =      0.7962
```

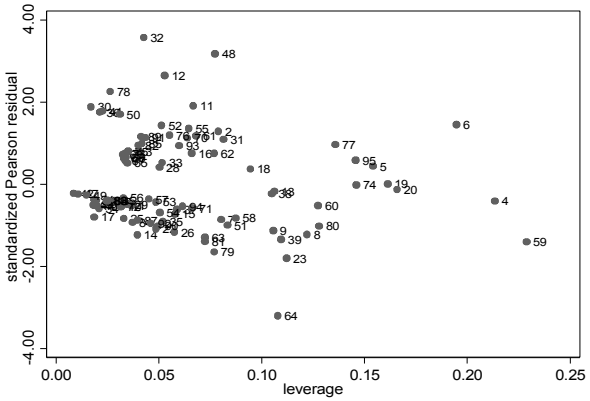
Since the observed and expected values are close, the model appears to fit well over the range of predicted probability values. Overall, there is no evidence of "lack of fit" because the value is much larger than 0.05.

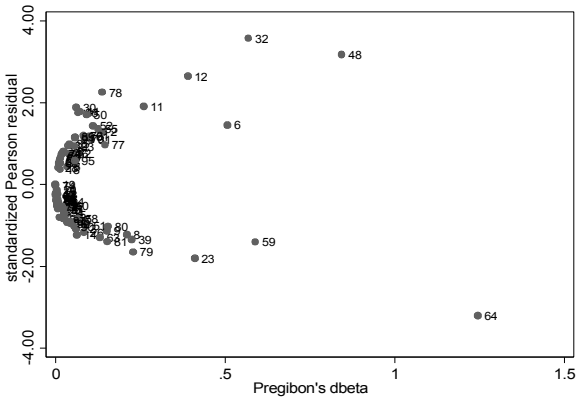
2. Outliers and influential observations

First we will compute the various diagnostic values (residuals etc.) and generate some summary statistics and a couple of graphs to identify outliers and influential observations. To do this, we will reduce the dataset to 1 record per CP.

```
. predict cov, num
. bysort cov: gen withincov=_n if e(sample)
. sum num_obs pv rst lev db if withincov==1

    Variable |       Obs        Mean    Std. Dev.       Min        Max
-------------+--------------------------------------------------------
     num_obs |        95    2.526316    2.082562          1         10
          pv |        95    .3374078    .2166876    .049139   .8311161
         rst |        95      .04099    1.143371  -3.208725   3.571799
         lev |        95    .0631579    .0459353   .0086876   .2290239
          db |        95    .0951538    .1839791   1.22e-06   1.245695
```

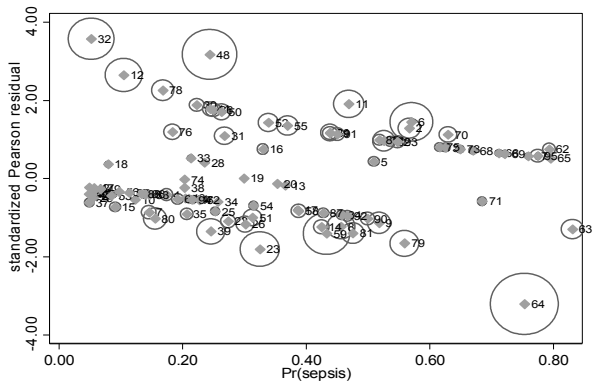
There were 95 CPs with and average of 2.5 calves per pattern (range was 1 to 10). There were some standardised Pearson residuals outside of the range of -3 to +3, and we should investigate these for errors or other explanations for their poor fit. Note that not all the graphs presented in the solution do-file will be discussed here.

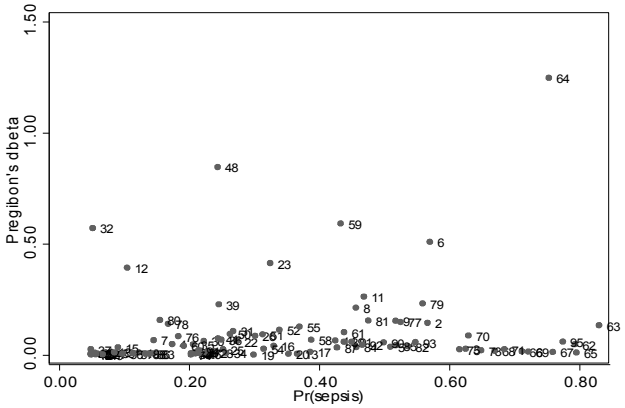




The graph of standardised Pearson residuals vs leverage identifies two CPs (32 and 48) with large positive residuals and one (64) with a large negative residual. However, none of these had particularly high leverage values. Three CPs (4, 6 and 59) stand out as having the largest leverage values.

The graph of standardised Pearson residuals vs delta-betas identifies two CPs (48 and 64) as being quite influential, and they also had large residuals (despite their influence, the model still did not fit those points very well).





The graphs above show the CPs 12, 32, 48 and 64 with high standardized Pearson residuals and high delta beta (size of the bubble). Remember that we are expecting to see large delta beta values at predicted probabilities (Pr(sepsis)) in the range of 0.1-0.3 and 0.7-0.9 even if they are not influential. CP #48 is the most influential, but all these CPs are worth exploring.

Lets look at what types of calves were in each of those CPs.

cov	num_obs	age	post	umb	avg_se~s	pv	rst	lev	dx2	db
78	1	9	standing	yes	1.00	0.17	2.25	0.03	5.08	0.14
12	4	5	standing	no	0.50	0.11	2.64	0.05	6.98	0.39
32	5	12	standing	no	0.40	0.05	3.57	0.04	12.76	0.57
48	3	20	sternal	no	1.00	0.24	3.17	0.08	10.05	0.84
64	3	2	sternal	yes	0.00	0.75	-3.21	0.11	10.30	1.25

CPs 32, 48 and 64 stand out as having had a large influence on the model. Neither of these patterns contained a very large number of calves (ranged from 2 to 5), so their influence has derived from the fact that they have high residuals, not because they represented a large number of cases. Neither group had particularly high leverage, or their influence would have been greater.

We will now refit the model, leaving each of these CPs out (sequentially), to see what effect they have on the parameter estimates.

```
. estimates table final no48 no32 no64, se stats(N)
```

Variable	final	no48	no32	no64
post				
sternal	1.5943382	1.4733121	1.838132	1.773588
	.4175655	.42444626	.45133212	.4280993
lateral	1.8389785	1.841746	2.0903666	1.8818255
	.43451415	.43797718	.46810051	.44381281
umb	1.0784534	1.1658411	1.1709217	1.3449707
	.35773568	.36228683	.36938763	.37739276
age_ct	-.08231092	-.09908383	-.09132431	-.10183239
	.02890848	.03008591	.02981698	.03036576
c.age_ct#c.age_ct	.0086873	.00842812	.00986948	.01039121
	.00336432	.0034537	.00348273	.00350951
_cons	-2.7683427	-2.8140512	-3.0959294	-2.9619031
	.4018875	.40678358	.44786843	.42228093
N	240	237	235	237

legend: b/se

The biggest effect of leaving CP #48 out is that the linear effect of -age- is increased. This is not surprising since this group of calves were old and and hence expected to have a low probability of sepsis, but in fact all 3 were septicemic. This has reduced the effect of age in the full model.

Leaving out CP #32 results in a larger estimated effect for -umb- and -post- also a small larger linear effect of -age- was observed. These were calves just above average age (average 9 days) which were standing and did not have swollen umbilicus so were expected to be septicemic free, but two of them were.

Leaving out CP #64 results in the largest effect on the coefficients as suggested by the delta beta value. It reduces the estimated effect for -post-, -umb- and -age-. This CP is composed by two very young calves with the presence of risk factors (sternal posture and swollen umbilicus) but were septicemic free.

For these CPs, removal of that individual group of calves resulted in more extreme estimates for one or more parameters. Consequently, the full model may be underestimating these effects, but there is no valid reason for not using the full model.

You can also compute the predicted probabilities without these CPs:

```
. list age1 umb1 post1 final no48 no64  no32 if age1~=. , sep(6) noobs

   +-------------------------------------------------------+
   |   age1   umb1   post1   final   no48   no64   no32   |
   |-------------------------------------------------------|
   |    5      0       0    0.059   0.057   0.049   0.043 |
   |    5      0       1    0.236   0.207   0.234   0.221 |
   |    5      0       2    0.283   0.274   0.253   0.268 |
   |    5      1       0    0.156   0.161   0.166   0.127 |
   |    5      1       1    0.476   0.456   0.539   0.478 |
   |    5      1       2    0.537   0.548   0.566   0.541 |
   |-------------------------------------------------------|
   |   18      0       0    0.192   0.134   0.193   0.176 |
   |   18      0       1    0.540   0.403   0.586   0.573 |
   |   18      0       2    0.600   0.494   0.612   0.634 |
   |   18      1       0    0.412   0.332   0.479   0.408 |
   |   18      1       1    0.775   0.684   0.844   0.813 |
   |   18      1       2    0.815   0.758   0.858   0.848 |
   +-------------------------------------------------------+
```

Although these CPs influence the model coefficients, they don't seem to have a large influence on the predicted probabilities. CP #48 seems to have the largest influence.

3. Predicting sepsis

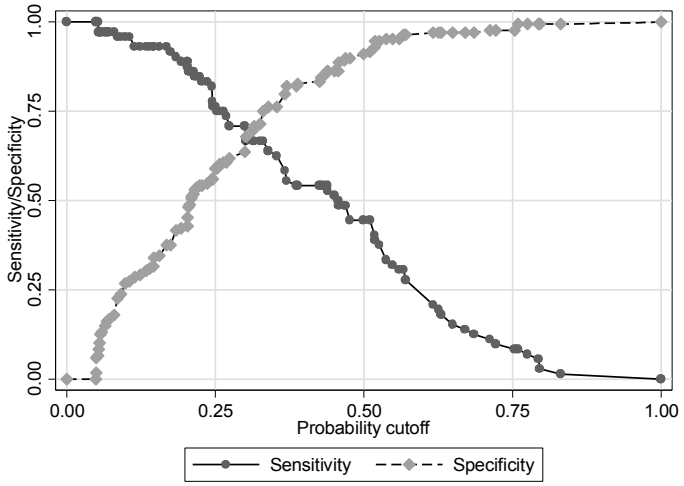
```
. logit sepsis i.post umb c.age_ct##c.age_ct
...output omitted

. estat class
Logistic model for sepsis
              -------- True --------
Classified |         D            ~D  |      Total
-----------+--------------------------+-----------
     +     |        32            14  |         46
     -     |        40           154  |        194
-----------+--------------------------+-----------
   Total   |        72           168  |        240
```

```
Classified + if predicted Pr(D) >= .5
True D defined as sepsis != 0
--------------------------------------------------
Sensitivity                     Pr( +| D)   44.44%
Specificity                     Pr( -|~D)   91.67%
Positive predictive value       Pr( D| +)   69.57%
Negative predictive value       Pr(~D| -)   79.38%
--------------------------------------------------
False + rate for true ~D        Pr( +|~D)    8.33%
False - rate for true D         Pr( -| D)   55.56%
False + rate for classified +   Pr(~D| +)   30.43%
False - rate for classified -   Pr( D| -)   20.62%
--------------------------------------------------
Correctly classified                        77.50%
```

The sensitivity of the model is quite low (44%) while the specificity is quite high (92%). However, both of these values depend on the cutpoint chosen to classify calves as septicemic or not. The values shown are based on the default value of 0.5, but it can be manipulated depending on the prevalence of the outcome in the study group and the seriousness of making a false prediction.

Next we will generate a graph of the sensitivity and specificity against possible cutpoints using a two-graph ROC curve.

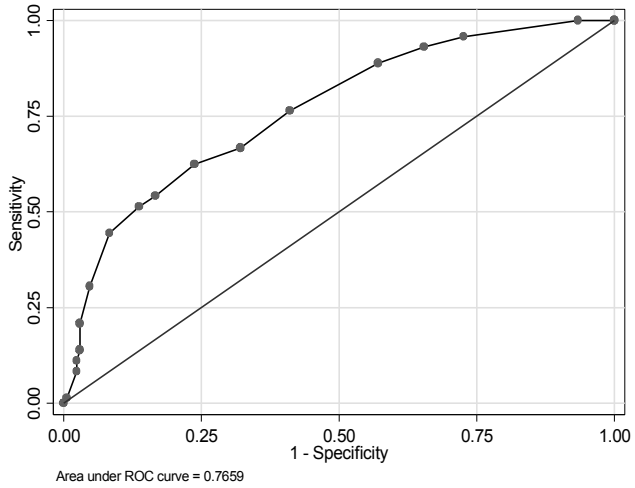
```
.lsens, scheme(s1mono)
```



The sensitivity and specificity are equal (both approximately 70%) at a cutpoint of about 0.3. This suggests that the model has moderate predictive ability. Since a cutpoint of 0.3 is approximately the prevalence of sepsis in the study population you might use that as a cutpoint.

Also, you can evaluate the overall predictive ability of the model by generating an ROC curve using various cutpoints of predicted values. To do this, we will first categorize the predicted values (obtained in Q2) at increments of 0.05 units.

```
. egen pv_cat=cut(pv), at(0(.05)1)
(14 missing values generated)

. roctab sepsis pv_cat, graph sum detail scheme(s1mono)

Detailed report of sensitivity and specificity

Correctly
Cutpoint      Sensitivity   Specificity   Classified          LR+ LR-

( >= 0 )          100.00%         0.00%       30.00%       1.0000
( >= .05 )        100.00%         6.55%       34.58%       1.0701 0.0000
( >= .1 )          95.83%        27.38%       47.92%       1.3197 0.1522
( >= .15 )         93.06%        34.52%       52.08%       1.4212 0.2011
( >= .2 )          88.89%        42.86%       56.67%       1.5556 0.2593
( >= .25 )         76.39%        58.93%       64.17%       1.8599 0.4007
( >= .3 )          66.67%        67.86%       67.50%       2.0741 0.4912
( >= .35 )         62.50%        76.19%       72.08%       2.6250 0.4922
( >= .4 )          54.17%        83.33%       74.58%       3.2500 0.5500
( >= .45 )         51.39%        86.31%       75.83%       3.7536 0.5632
( >= .5 )          44.44%        91.67%       77.50%       5.3333 0.6061
( >= .55 )         30.56%        95.24%       75.83%       6.4167 0.7292
( >= .6 )          20.83%        97.02%       74.17%       7.0000 0.8160
( >= .65 )         13.89%        97.02%       72.08%       4.6667 0.8875
( >= .7 )          11.11%        97.62%       71.67%       4.6667 0.9106
( >= .75 )          8.33%        97.62%       70.83%       3.5000 0.9390
( >= .8 )           1.39%        99.40%       70.00%       2.3333 0.9920
( >  .8 )           0.00%       100.00%       70.00%       1.0000


ROC                    -Asymptotic Normal--
Obs       Area     Std. Err.      [95% Conf. Interval]
-------------------------------------------------------
240     0.7659       0.0330        0.70119     0.83064
```



The area under the curve being less than 0.8 suggests only a very good level of predictability by the model. The estimates of sensitivity and specificity at various cutpoints show how the sensitivity decreases as the cutpoint is raised, while the specificity goes up. From the table above, you can see that a calf with a model-based probability of sepsis of at least 0.35 is 2.6 times more likely to be septic than a calf with a model based probability below this value.

4. Choosing an appropriate cutpoint

Generally speaking, where you set the cutpoint will depend on whether it is more important to maximize sensitivity or specificity and this will depend on what decisions you are going to make as a result of your predictions. For instance, if you were using this model in a clinical setting, your choice of cutpoint would also depend on how serious you considered false positive results to be compared to false negative ones.

If you wanted to be certain of detecting a high proportion of septicemic calves in order to ensure that they received aggressive therapy for the condition, then you would choose a low cutpoint (eg. 0.2).

```
. estat class, cut(0.2)

Logistic model for sepsis

              -------- True --------
Classified |         D            ~D  |      Total
-----------+--------------------------+-----------
     +     |        64            96  |        160
     -     |         8            72  |         80
-----------+--------------------------+-----------
   Total   |        72           168  |        240

Classified + if predicted Pr(D) >= .2
True D defined as sepsis != 0
-------------------------------------------------
Sensitivity                     Pr( +| D)   88.89%
Specificity                     Pr( -|~D)   42.86%
Positive predictive value       Pr( D| +)   40.00%
Negative predictive value       Pr(~D| -)   90.00%
-------------------------------------------------
False + rate for true ~D        Pr( +|~D)   57.14%
False - rate for true D         Pr( -| D)   11.11%
False + rate for classified +   Pr(~D| +)   60.00%
False - rate for classified -   Pr( D| -)   10.00%
-------------------------------------------------
Correctly classified                        56.67%
-------------------------------------------------
```

This gets the sensitivity up to 89%, but the positive predictive value (assuming the prevalence in the study population is similar to the prevalence in your clinical population) is only 40%. This means that 60% of the calves that are treated much more aggressively, would, in fact, not have needed the more extensive treatment.

On the other hand, if you were going to euthanise all calves that were classified as septicemic (on the grounds that the prognosis was very poor), you might want to maximise specificity (ie minimise false positives). A cutpoint of 0.6 provides a specificity of 97%.

```
. estat class , cut(0.6)
Logistic model for sepsis

              -------- True --------
Classified |         D            ~D  |      Total
-----------+--------------------------+-----------
     +     |        15             5  |         20
     -     |        57           163  |        220
-----------+--------------------------+-----------
   Total   |        72           168  |        240

Classified + if predicted Pr(D) >= .6
True D defined as sepsis != 0
-------------------------------------------------
Sensitivity                     Pr( +| D)   20.83%
Specificity                     Pr( -|~D)   97.02%
Positive predictive value       Pr( D| +)   75.00%
Negative predictive value       Pr(~D| -)   74.09%
-------------------------------------------------
False + rate for true ~D        Pr( +|~D)    2.98%
False - rate for true D         Pr( -| D)   79.17%
False + rate for classified +   Pr(~D| +)   25.00%
False - rate for classified -   Pr( D| -)   25.91%
-------------------------------------------------
Correctly classified                        74.17%
-------------------------------------------------
```

The positive predictive value is now 75% so you are reasonably sure that calves that are euthanised were, in fact, septicemic. However, the negative predictive value is down to 74%, which means that 26% of calves that were assumed to be non-septicemic are, in fact, septicemic. If they only receive conventional therapy for diarrhea, their prognosis is very poor.