5.1.1 – SAS: Logistic Regression

Example: (Text Table 14.3) Individuals were randomly sampled within two sectors of a city, and checked for presence of disease (here, spread by mosquitoes). Subjects' age (in years), socioeconomic status (low, medium, high), and city sector are to be used to predict the probability of contracting the disease.

```
/* Input data -- see Table 14.3 in text
     Case = subject ID
     Age  = years
     SES_mid = indicator of middle socioeconomic status
     SES_low = indicator of low socioeconomic status
       (upper is reference level for socioeconomic status)
     Sector = indicator of sector 2 in city
       (sector 1 is reference level)
     Disease = indicator of disease presence
  */
filename myurl url
"http://users.stat.ufl.edu/~rrandles/sta4210/Rclassnotes/data/tex
tdatasets/KutnerData/Chapter%2014%20Data%20Sets/CH14TA03.txt";
data outbreak;
  infile myurl delimiter = '09'x;
  input Case Age SES_mid SES_low Sector Disease;
  Observation = _n_;
run;

/* Run logistic regression, checking for lack of fit */
proc logistic data=outbreak  plots=(roc effect);
  model Disease(event = '1') = Age SES_mid SES_low Sector /
                               clparm=wald alpha=.05 lackfit;
  SES: test SES_mid=SES_low=0;
  output out=a1out prob=phat;
  title1 'Logistic Regression';
run;
```

Logistic Regression

Probability modeled is Disease=1.

Model Convergence Status
Convergence criterion (GCONV=1E-8) satisfied.

Model Fit Statistics		
Criterion	**Intercept Only**	**Intercept and Covariates**
AIC	124.318	111.054
SC	126.903	123.979
-2 Log L	122.318	101.054

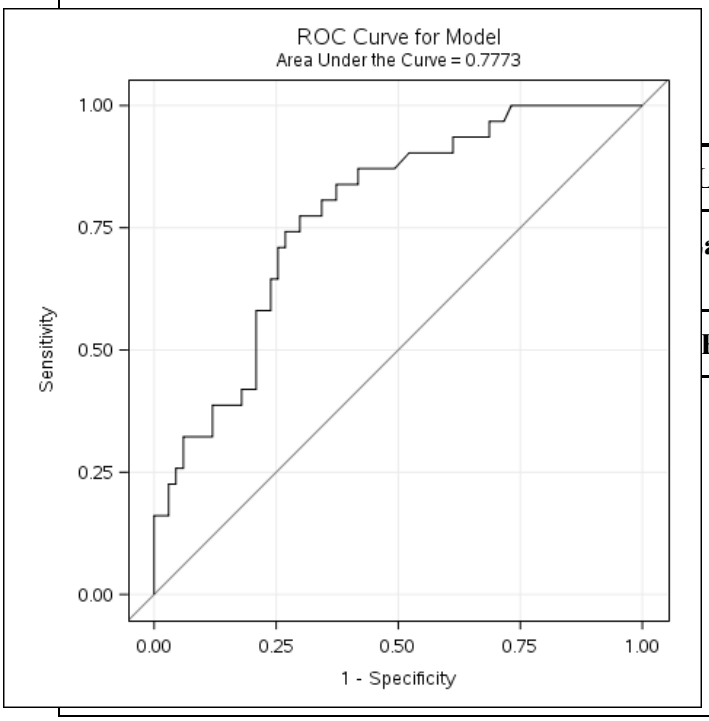
Testing Global Null Hypothesis: BETA=0			
Test	**Chi-Square**	**DF**	**Pr > ChiSq**
Likelihood Ratio	21.2635	4	0.0003
Score	20.4067	4	0.0004
Wald	16.6437	4	0.0023

Analysis of Maximum Likelihood Estimates					
Parameter	**DF**	**Estimate**	**Standard Error**	**Wald Chi-Square**	**Pr > ChiSq**
Intercept	1	-2.3127	0.6426	12.9545	0.0003
Age	1	0.0297	0.0135	4.8535	0.0276
SES_mid	1	0.4088	0.5990	0.4657	0.4950
SES_low	1	-0.3051	0.6041	0.2551	0.6135
Sector	1	1.5746	0.5016	9.8543	0.0017

Odds Ratio Estimates			
Effect	**Point Estimate**	**95% Wald Confidence Limits**	
Age	1.030	1.003	1.058
SES_mid	1.505	0.465	4.868
SES_low	0.737	0.226	2.408
Sector	4.829	1.807	12.907

Association of Predicted Probabilities and Observed Responses			
Percent Concordant	77.5	**Somers' D**	0.554
Percent Discordant	22.1	**Gamma**	0.556
Percent Tied	0.3	**Tau-a**	0.242
Pairs	2077	**c**	0.777

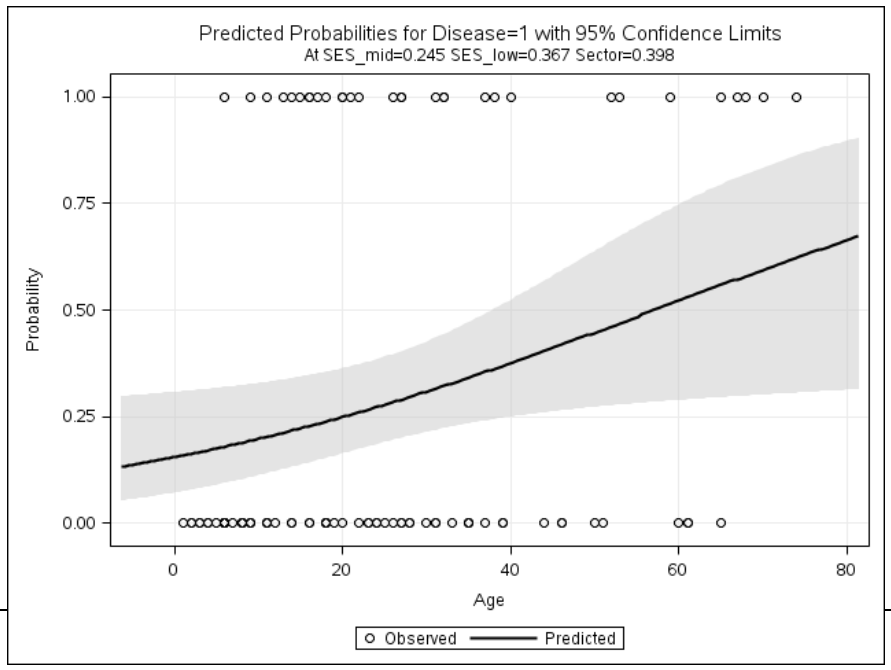
Parameter Estimates and Wald Confidence Intervals			
Parameter	**Estimate**	**95% Confidence Limits**	
Intercept	-2.3127	-3.5721	-1.0533
Age	0.0297	0.00328	0.0562
SES_mid	0.4088	-0.7653	1.5828
SES_low	-0.3051	-1.4891	0.8789
Sector	1.5746	0.5915	2.5578



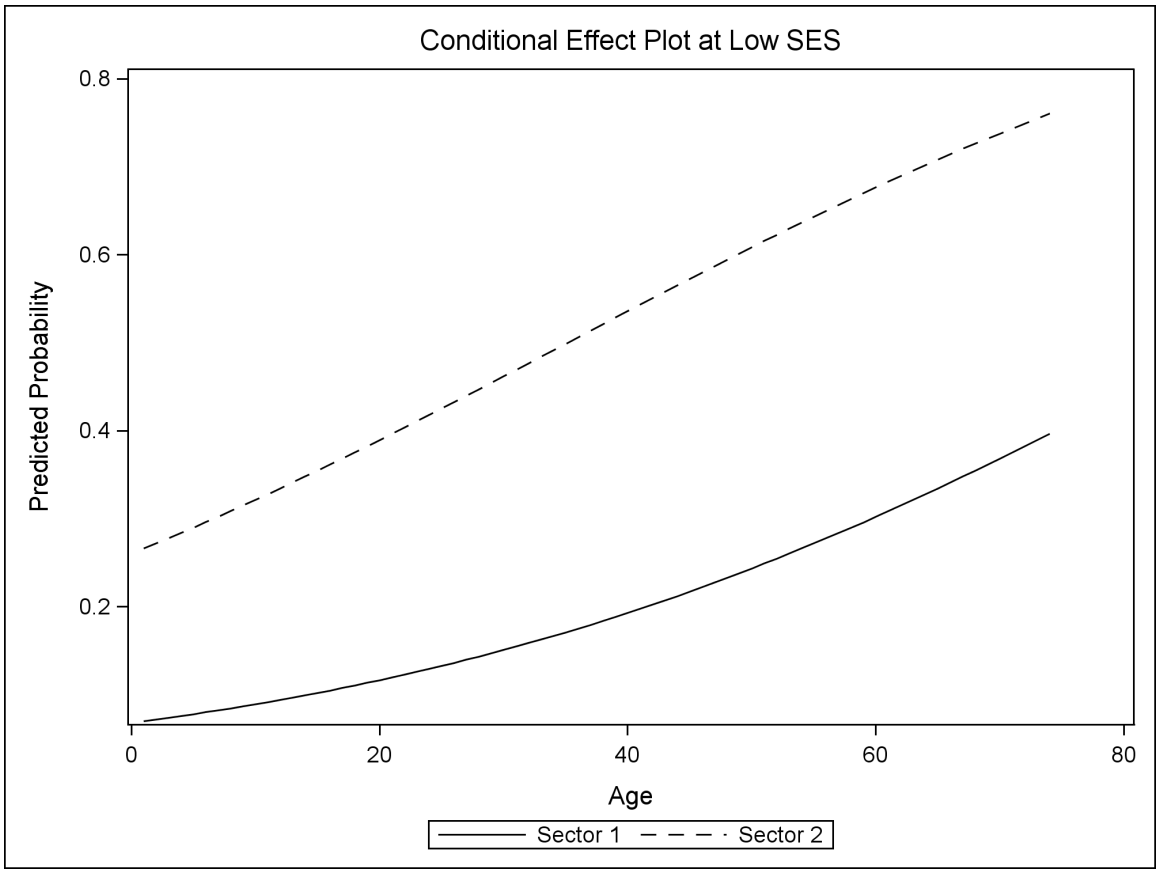
Linear Hypotheses Testing Results			
abel	**Wald Chi-Square**	**DF**	**Pr > ChiSq**
ES	1.2053	2	0.5474

Partition for the Hosmer and Lemeshow Test					
Group	Total	Disease = 1		Disease = 0	
		Observed	Expected	Observed	Expected
1	10	0	0.79	10	9.21
2	10	1	1.02	9	8.98
3	11	2	1.51	9	9.49
4	10	1	1.78	9	8.22
5	10	3	2.34	7	7.66
6	10	4	3.09	6	6.91
7	10	7	3.91	3	6.09
8	11	3	5.51	8	5.49
9	10	5	6.32	5	3.68
10	6	5	4.75	1	1.25

Hosmer and Lemeshow Goodness-of-Fit Test		
Chi-Square	**DF**	**Pr > ChiSq**
9.1871	8	0.3268



```
/* Make better 'Conditional Effect' plot, compare predicted
   disease probabilities for sector 1 (Sector=0) vs
   sector 2 (Sector=1) at low socioeconomic status
   (SES_mid=0, SES_low=1), as a function of Age */
data new; set outbreak;
  p1 = 1/(1+exp(-(-2.3127+0.0297*Age+0.4088*0
                  -0.3051*1+1.5746*0)));
  p2 = 1/(1+exp(-(-2.3127+0.0297*Age+0.4088*0
                  -0.3051*1+1.5746*1)));
  label p1 = 'Sector 1'
        p2 = 'Sector 2';
proc sort data=new; by Age;
proc sgplot data=new;
  series y=p1 x=Age / lineattrs=(pattern=solid);
  series y=p2 x=Age / lineattrs=(pattern=dash);
  xaxis label='Age';
  yaxis label='Predicted Probability';
  title1 'Conditional Effect Plot at Low SES';
run;
```



```
/* Check for multicollinearity */
proc reg data=outbreak;
  model Disease = Age SES_mid SES_low Sector / vif collin;
  title1 'Collinearity Check';
run;
```

Collinearity Check

Parameter Estimates

Variable	DF	Parameter Estimate	Standard Error	t Value	Pr > |t|	Variance Inflation
Intercept	1	0.04699	0.10470	0.45	0.6546	0
Age	1	0.00555	0.00238	2.33	0.0218	1.05242
SES_mid	1	0.07595	0.11139	0.68	0.4970	1.24616
SES_low	1	-0.04150	0.10323	-0.40	0.6886	1.34514
Sector	1	0.31702	0.09180	3.45	0.0008	1.09668

Collinearity Diagnostics

Number	Eigenvalue	Condition Index	Proportion of Variation				
			Intercept	Age	SES_mid	SES_low	Sector
1	2.91249	1.00000	0.01791	0.02993	0.02390	0.01836	0.03753
2	1.03987	1.67357	0.00177	0.00043477	0.23886	0.23672	0.02873
3	0.56543	2.26957	0.00369	0.01213	0.41619	0.08529	0.46221
4	0.36812	2.81280	0.00172	0.50905	0.06301	0.18584	0.37255
5	0.11410	5.05233	0.97491	0.44845	0.25805	0.47378	0.09897

```
/* Variable selection */
/*  - here, backward elimination;
      may also consider selection=stepwise */
proc logistic data=outbreak;
  model Disease(event = '1') = Age SES_mid SES_low Sector /
                          selection=backward slstay=0.10;
  title1 'Backward Elimination';
run;
```

Backward Elimination

Probability modeled is Disease=1.

Backward Elimination Procedure

Step 0. The following effects were entered:

Intercept Age SES_mid SES_low Sector

Step 1. Effect SES_low is removed:

Step 2. Effect SES_mid is removed:

Note: No (additional) effects met the 0.1 significance level for removal from the model.

Summary of Backward Elimination

Step	Effect Removed	DF	Number In	Wald Chi-Square	Pr > ChiSq
1	**SES_low**	1	3	0.2551	0.6135
2	**SES_mid**	1	2	0.9590	0.3274

Analysis of Maximum Likelihood Estimates

Parameter	DF	Estimate	Standard Error	Wald Chi-Square	Pr > ChiSq
Intercept	1	-2.3350	0.5111	20.8713	<.0001
Age	1	0.0293	0.0132	4.9455	0.0262
Sector	1	1.6734	0.4873	11.7906	0.0006

```
/* Variable selection */
/* - here, display the 'best' two models containing
     between 1 and 2 predictors */
proc logistic data=outbreak;
  model Disease(event = '1') = Age SES_mid SES_low Sector /
                    selection=score best=2 start=1 stop=2;
  title1 'Variable Selection: best by score';
run;
```

Variable Selection: best by score

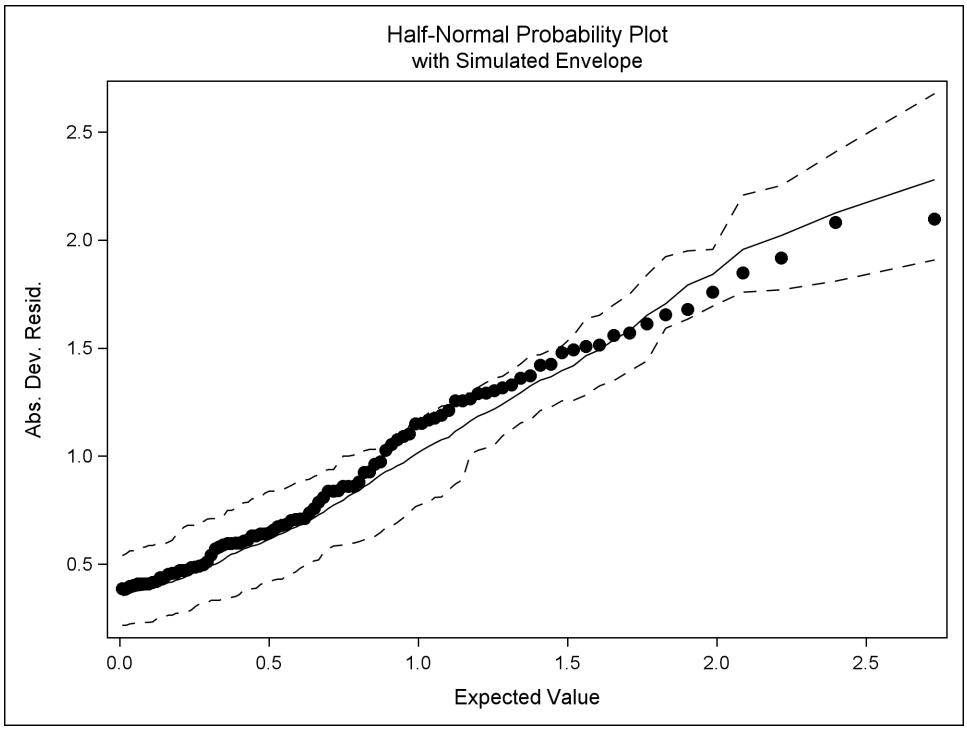
Probability modeled is Disease=1.

Regression Models Selected by Score Criterion

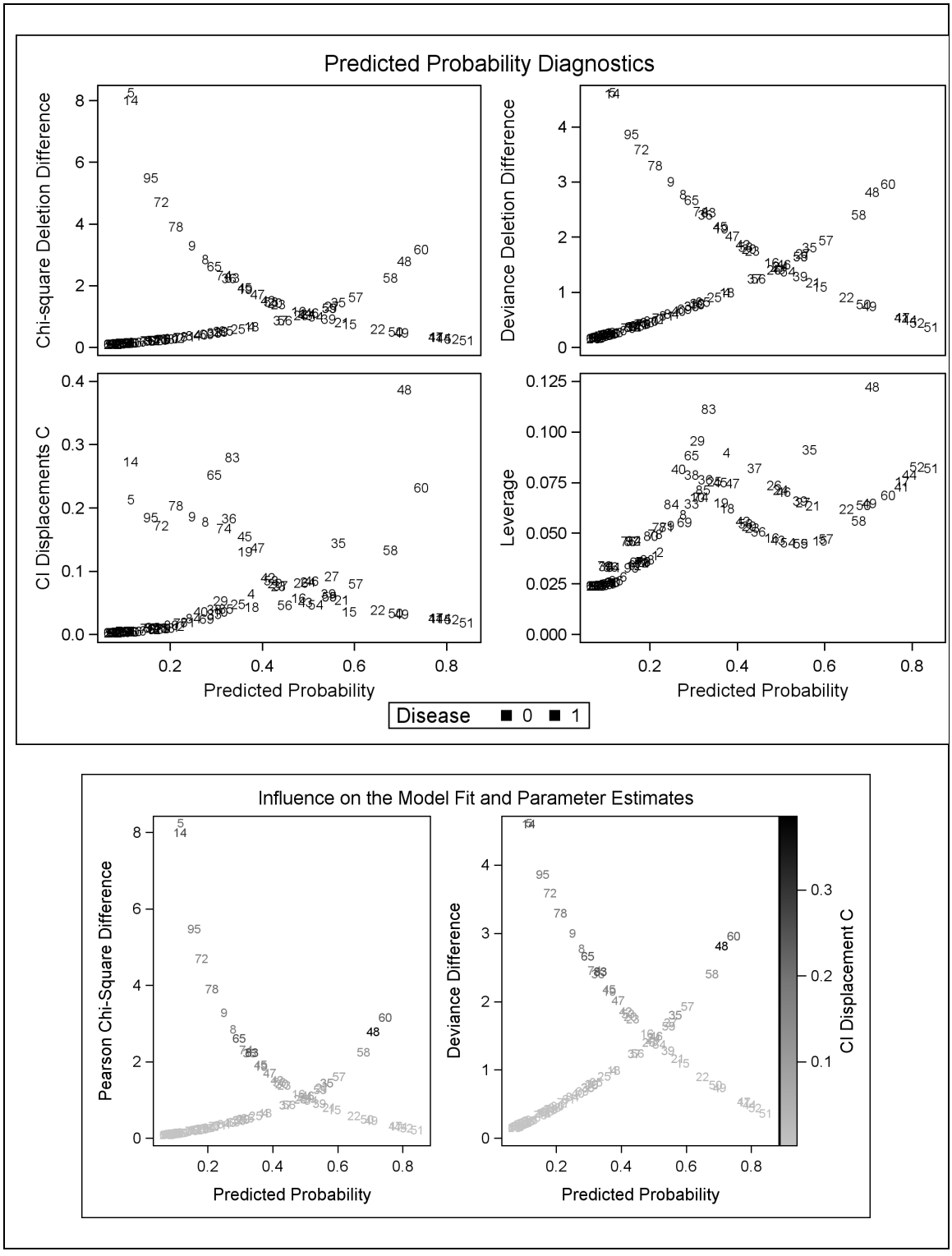
Number of Variables	Score Chi-Square	Variables Included in Model
1	14.7805	Sector
1	7.5802	Age
2	19.5250	Age Sector
2	15.7058	SES_low Sector

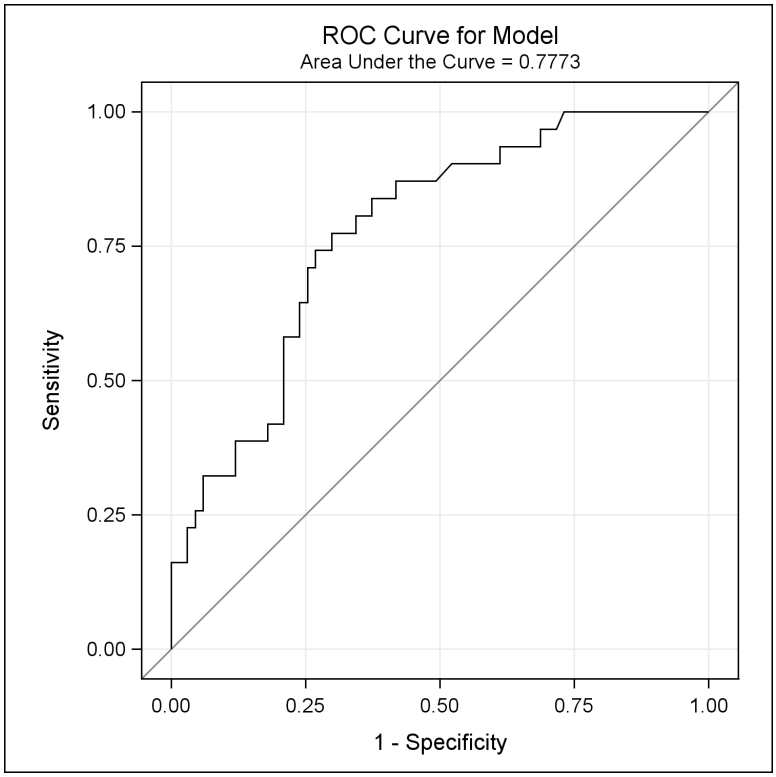
```
/* Check for outliers using the half-normal probability
   plot with simulated envelope
   -- note that this macro can be slow for large
      sample sizes
 */


/* Alternative way to access simulated envelope macro:

  filename macrourl "<add SAS studio file path here>";
  %include macrourl;

OR Just load the one line version of the macro provided on
canvas into your SAS session
  */
%macro simEnv(dataset, response, predictors, N);  proc  ...


/* Call simEnv macro; arguments:
```

```
        dataset = name of dataset containing data
        response = name of response variable in dataset,
                   coded 0/1
        predictors = name(s) of predictor variable(s)
                          (if multiple, separated by spaces)
        N = number of observations (sample size)
 */


%simEnv(dataset = outbreak, response = disease,
    predictors = Age SES_mid SES_low Sector, N=98);
run;
```



```
/* Check for influential observations */
proc logistic data=outbreak
              plots(only label)=(phat influence dpc roc);
  ID Case;
  model Disease(event = '1') = Age SES_mid SES_low Sector;
run;
```






```
/* Look at suspect observation */
proc print data=outbreak;
  where Case = 48;
  var Case Age SES_mid SES_low Sector Disease;
  title1 'Suspect point';
run;
```

Suspect point

Obs	Case	Age	SES_mid	SES_low	Sector	Disease
48	48	65	0	1	1	0