Basic Statistical and Modeling Procedures Using SAS

One-Sample Tests

The statistical procedures illustrated in this handout use two datasets. The first, Pulse, has information collected in a classroom setting, where students were asked to take their pulse two times. Half the class was asked to run in place between the two readings and the other group was asked to stay seated between the two readings. The raw data for this study are contained in a file called pulse.csv. The other dataset we use is a dataset called Employee.sas7bdat. It is a SAS dataset that contains information about salaries in a mythical company.

Read in the pulse data and create a temporary SAS dataset for the examples:

```
data pulse;
   infile "pulse.csv" firstobs=2 delimiter="," missover;
   input pulse1 pulse2 ran smokes sex height weight activity;
   label pulse1 = "Resting pulse, rate per minute"
         pulse2 = "Second pulse, rate per minute";
run;
```

Create and assign formats to variables:

```
proc format;
     value sexfmt 1="Male" 2="Female";
     value yesnofmt  1="Yes" 2="No";
     value actfmt 1="Low" 2="Medium" 3="High";
run;

proc print data=pulse (obs=25) label;
format sex sexfmt. ran smokes yesnofmt. activity actfmt.;
run;
```

Descriptive Statistics:

```
proc means data=pulse;
run;
```

The MEANS Procedure

Variable	Label	N	Mean	Std Dev	Minimum	Maximum
pulse1	Resting pulse, rate per minute	92	72.8695652	11.0087052	48.0000000	100.0000000
pulse2	Second pulse, rate per minute	92	80.0000000	17.0937943	50.0000000	140.0000000
ran		92	1.6195652	0.4881540	1.0000000	2.0000000
smokes		92	1.6956522	0.4626519	1.0000000	2.0000000
sex		92	1.3804348	0.4881540	1.0000000	2.0000000
height		92	68.7391304	3.6520943	61.0000000	75.0000000
weight		92	145.1521739	23.7393978	95.0000000	215.0000000
activity		92	2.1195652	0.5711448	1.0000000	3.0000000

Binomial Confidence Intervals and Tests for Binary Variables:

If you have a categorical variable with only two levels, you can use the **binomial** option to request a 95% confidence interval for the proportion in the first level of the variable. In the PULSE data set, SMOKES=1 indicates those who were smokers, and SMOKES=2 indicates non-smokers. Use the **(p=)** option to specify the null hypothesis proportion that you wish to test for the first level of the variable. In the commands below, we test hypotheses for the proportion of SMOKES=1 (i.e., proportion of smokers) in the population. By default SAS produces an asymptotic test of the null hypothesis:

H_0: proportion of smokers = 0.25
H_A: proportion of smokers $\neq$ 0.25

```
proc freq data = pulse;
   tables  smokes / binomial(p=.25);
run;
```

smokes

smokes	Frequency	Percent	Cumulative Frequency	Cumulative Percent
1	28	30.43	28	30.43
2	64	69.57	92	100.00

```
       Binomial Proportion
          for smokes = 1
--------------------------------
Proportion                0.3043
ASE                       0.0480
95% Lower Conf Limit      0.2103
95% Upper Conf Limit      0.3984

Exact Conf Limits
95% Lower Conf Limit      0.2127
95% Upper Conf Limit      0.4090

 Test of H0: Proportion = 0.25

ASE under H0              0.0451
Z                         1.2039
One-sided Pr >  Z         0.1143
Two-sided Pr > |Z|        0.2286

         Sample Size = 92
```

If you wish to obtain an exact binomial test of the null hypothesis, use the exact statement. If you include the mc option for large datasets, you will get a Monte Carlo p-value.

```
proc freq data = pulse;
   tables  smokes / binomial(p=.25);
   exact binomial / mc;
run;
```

This results in an exact test of the null hypothesis, in addition to the default asymptotic test, the exact test results for both a one-sided and two-sided alternative hypothesis are shown.

```
Binomial Proportion for smokes = 1
-----------------------------------
Proportion (P)               0.3043
ASE                          0.0480
95% Lower Conf Limit         0.2103
95% Upper Conf Limit         0.3984

Exact Conf Limits
95% Lower Conf Limit         0.2127
95% Upper Conf Limit         0.4090

   Test of H0: Proportion = 0.25

ASE under H0                 0.0451
Z                            1.2039
One-sided Pr >  Z            0.1143
Two-sided Pr > |Z|           0.2286

Exact Test
One-sided Pr >=  P           0.1399
Two-sided = 2 * One-sided    0.2797
          Sample Size = 92
```

Chi-square Goodness of Fit Tests for Categorical Variables:

Use the chisq option in the tables statement to get a chi-square goodness of fit test, which can be used for categorical variables with two or more levels. By default SAS assumes that you wish to test the null hypothesis that the proportion of cases is equal in all categories. In the variable ACTIVITY, a value of 1 indicates a low level of activity, a value of 2 is a medium level of activity, and a value of 3 indicates a high level of activity.

```
proc freq data = pulse;
   tables activity / chisq;
run;
```

```
                        activity
                                        Cumulative    Cumulative
activity    Frequency     Percent     Frequency      Percent
-------------------------------------------------------------
       1           10       10.87            10        10.87
       2           61       66.30            71        77.17
       3           21       22.83            92       100.00

                    Chi-Square Test
                 for Equal Proportions
                 ---------------------
                 Chi-Square    46.9783
                 DF                  2
                 Pr > ChiSq     <.0001

                   Sample Size = 92
```

If you wish to specify your own proportions, use the testp = option in the tables statement. This option allows you to specify any proportions that you wish to test for each level of the variable in the tables statement, as long as the sum of the proportions equals 1.0. In the example below we test the null hypothesis:

H_0: $P_1 = 0.20$, $P_2=.50$, $P_3=.30$

```
proc freq data = pulse;
   tables activity  /chisq testp = ( .20 , .50, .30 );
run;
```

```
                          The FREQ Procedure
                               activity

                                                Test     Cumulative    Cumulative
        activity    Frequency     Percent     Percent     Frequency      Percent
        --------------------------------------------------------------------------
               1          10       10.87       20.00            10        10.87
               2          61       66.30       50.00            71        77.17
               3          21       22.83       30.00            92       100.00


                            Chi-Square Test
                          for Specified Proportions
                          -------------------------
                          Chi-Square       10.3043
                          DF                     2
                          Pr > ChiSq        0.0058

                              Sample Size = 92
```

You may also specify percentages to test, rather than proportions, as long as they add up to 100 percent:

```
proc freq data = pulse;
   tables activity  /chisq testp = ( 20 , 50, 30 );
run;
```

One-Sample test for a continuous variable:

You can use Proc Univariate to carry out a one-sample t-test to test the population mean against any null hypothesis value you specify by using mu0= option. The default, if no value of mu0 is specified is that mu0 = 0. In the commands below, we test:

H_0: $\mu_0=72$
H_A: $\mu_0\neq72$

Note that SAS also provides the non-parametric Sign test and Wilcoxon signed rank test.

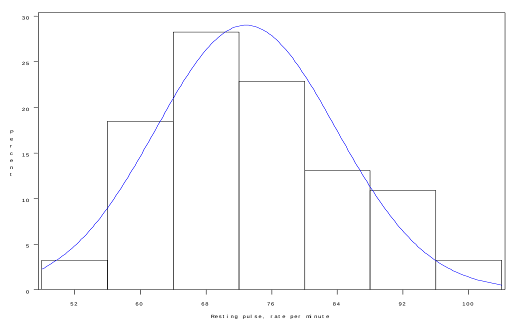
```
proc univariate data=pulse mu0=72;
      var pulse1;
      histogram / normal (mu=est sigma=est);
      qqplot /normal (mu=est sigma=est);
run;
```

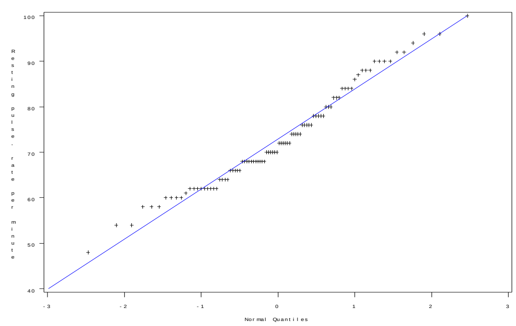
Selected output from Proc Univariate:

Proc Univariate

Tests for Location: Mu0=72

Test	-Statistic-		-----p Value------	
Student's t	t	0.757635	Pr > |t|	0.4506
Sign	M	-3	Pr >= |M|	0.5900
Signed Rank	S	96.5	Pr >= |S|	0.6797





Equivalently, we can carry out a one-sample t-test in Proc Ttest by specifying the H0= option.:

```
proc ttest data=pulse H0=72 ;
  var pulse1;
run;
```

Variable: pulse1 (Resting pulse, rate per minute

N	Mean	Std Dev	Std Err	Minimum	Maximum
92	72.8696	11.0087	1.1477	48.0000	100.0

Mean	95% CL Mean		Std Dev	95% CL Std Dev	
72.8696	70.5897	75.1494	11.0087	9.6155	12.8779

DF	t Value	Pr > |t|
91	0.76	0.4506

Paired Samples t-test:

If you wish to compare the means of two variables that are paired (i.e. correlated), you can use a paired sample t-test for continuous variables. To do this use Proc ttest with a **paired** statement, to get a paired samples t-test:

```
proc ttest data=pulse;
  paired pulse2*pulse1;
run;
```

The TTEST Procedure

Statistics

Difference	N	Lower CL Mean	Mean	Upper CL Mean	Lower CL Std Dev	Std Dev	Upper CL Std Dev	Std Err
pulse2 - pulse1	92	4.3406	7.1304	9.9203	11.766	13.471	15.759	1.4045

T-Tests

Difference	DF	t Value	Pr > |t|
pulse2 - pulse1	91	5.08	<.0001

The paired t-test can be carried out for each level of RAN. The commands and results of these commands are shown below:

```
proc sort data=pulse;
  by ran;
run;
proc ttest data=pulse;
  paired pulse2*pulse1;
  by ran;
run;
```

--------------------------------------- ran=1 --

The TTEST Procedure

Statistics

Difference	N	Lower CL Mean	Mean	Upper CL Mean	Lower CL Std Dev	Std Dev	Upper CL Std Dev	Std Err
pulse2 - pulse1	35	13.745	18.914	24.084	12.173	15.05	19.718	2.5439

T-Tests

Difference	DF	t Value	Pr > |t|
pulse2 - pulse1	34	7.44	<.0001

-- ran=2 --

The TTEST Procedure

Statistics

Difference	N	Lower CL Mean	Mean	Upper CL Mean	Lower CL Std Dev	Std Dev	Upper CL Std Dev	Std Err
pulse2 - pulse1	57	-1.209	-0.105	0.9987	3.5126	4.1605	5.1039	0.5511

T-Tests

Difference	DF	t Value	Pr > |t|
pulse2 - pulse1	56	-0.19	0.8492

Independent samples t-tests

An independent samples t-test can be used to compare the means in two independent groups of observations.:

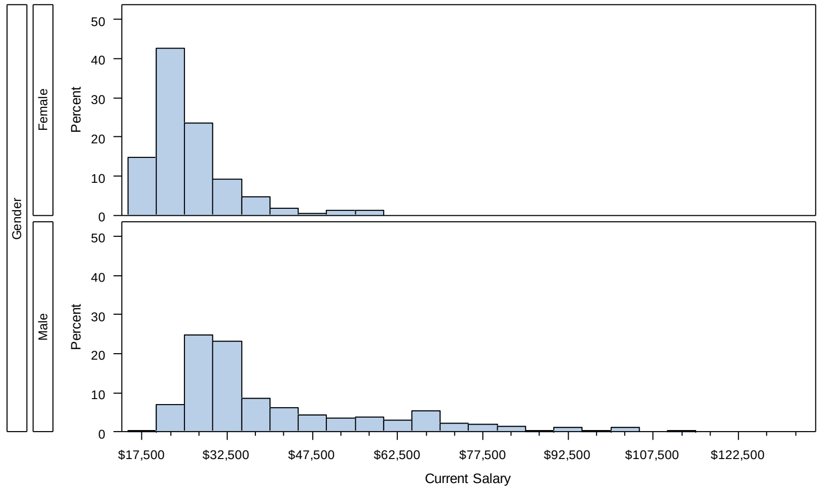
```
proc ttest data=sasdata2.employee2;
  class gender;
  var salary;
run;
```

The output from this procedure is shown below:

```
                                   The TTEST Procedure

                           Variable:  salary  (Current Salary)

      gender            N        Mean     Std Dev     Std Err     Minimum     Maximum
      f               216     26031.9      7558.0       514.3     15750.0     58125.0
      m               258     41441.8     19499.2      1214.0     19650.0      135000
      Diff (1-2)             -15409.9     15265.9      1407.9


gender       Method             Mean      95% CL Mean       Std Dev     95% CL Std Dev
 f                           26031.9    25018.3  27045.6     7558.0     6906.2   8346.8
 m                           41441.8    39051.2  43832.4    19499.2    17949.3  21344.3
 Diff (1-2)   Pooled        -15409.9   -18176.4 -12643.3    15265.9    14351.1  16306.1
 Diff (1-2)   Satterthwaite -15409.9   -18003.0 -12816.7


               Method           Variances        DF    t Value    Pr > |t|
               Pooled           Equal           472     -10.95      <.0001
               Satterthwaite    Unequal      344.26     -11.69      <.0001

                                  Equality of Variances

                    Method      Num DF    Den DF    F Value    Pr > F
                    Folded F       257       215       6.66    <.0001
```

If you want to check on the distribution of Salary for males and females, you can use Proc Univariate.

```
proc univariate data=sasdata2.employee2;
  var salary;
  class gender;
  histogram;
run;
```



Because it looks like salary is highly skewed, you might want to use a log transformation of salary to compare the two genders. Proc ttest has the **dist=lognormal** option to accompllish this:

```
proc ttest data=sasdata2.employee2 dist=lognormal;
  class gender;
  var salary ;
run;
```

The output from this procedure shows that the geometric mean and coefficient of variation are reported, rather than the arithmetic mean and standard deviation.

Variable: salary (Current Salary)

gender	N	Geometric Mean	Coefficient of Variation	Minimum	Maximum
Female	216	25146.1	0.2582	15750.0	58125.0
Male	258	37972.2	0.4149	19650.0	135000
Ratio (1/2)		0.6622	0.3505		

gender	Method	Geometric Mean	95% CL Mean		Coefficient of Variation	95% CL CV	
Female		25146.1	24303.8	26017.5	0.2582	0.2353	0.2862
Male		37972.2	36161.3	39873.8	0.4149	0.3796	0.4579
Ratio (1/2)	Pooled	0.6622	0.6226	0.7044	0.3505	0.3284	0.3760
Ratio (1/2)	Satterthwaite	0.6622	0.6240	0.7028			

Method	Coefficients of Variation	DF	t Value	Pr > |t|
Pooled	Equal	472	-13.13	<.0001
Satterthwaite	Unequal	442.4	-13.63	<.0001

```
                         Equality of Variances

       Method      Num DF    Den DF    F Value    Pr > F
       Folded F       257       215       2.46    <.0001
```

To get an independent samples t-test within each job category, use a BY statement, after sorting by jobcat.

```
proc sort data=sasdata2.employee;
  by jobcat;
run;
proc ttest data=sasdata2.employee;
  by jobcat;
  class gender;
  var salary;
run;
```

Wilcoxon rank sum test:

If you are unwilling to assume normality for your continuous test variable or the sample size is too small for you to appeal to the central-limit-theorem, you may want to use non-parametric tests. The Wilcoxon rank sum test (also known as the Mann-Whitney test) is the non-parametric analog of the independent sample t test.

```
/*NON-PARAMETRIC TEST: WILCOXON/MANN-WHITNEY TEST*/
proc npar1way data=sasdata2.employee wilcoxon;
      class gender;
      var salary;
run;
```

A Monte-Carlo approximation of the exact p-value can be obtained for the Wilcoxon test by using an exact statement, as shown below:

```
proc npar1way data=sasdata2.employee wilcoxon;
      class gender;
      var salary;
      exact wilcoxon / mc;
run;
```

Correlation

Proc corr can be used to calculate correlations for several variables:

```
proc corr data=sasdata2.employee;
  var salary salbegin educ;
run;
```

```
                          The CORR Procedure
                    3  Variables:    salary   salbegin educ
                              Simple Statistics
Variable          N          Mean       Std Dev           Sum       Minimum       Maximum
salary          474         34420         17076      16314875         15750        135000
salbegin        474         17016          7871       8065625          9000         79980
educ            474      13.49156       2.88485          6395       8.00000      21.00000
```

```
                    Prob > |r| under H0: Rho=0

                               salary      salbegin          educ
salary                        1.00000       0.88012       0.66056
Current Salary                               <.0001        <.0001

salbegin                      0.88012       1.00000       0.63320
Beginning Salary               <.0001                      <.0001

educ                          0.66056       0.63320       1.00000
Educational Level (years)      <.0001        <.0001
```

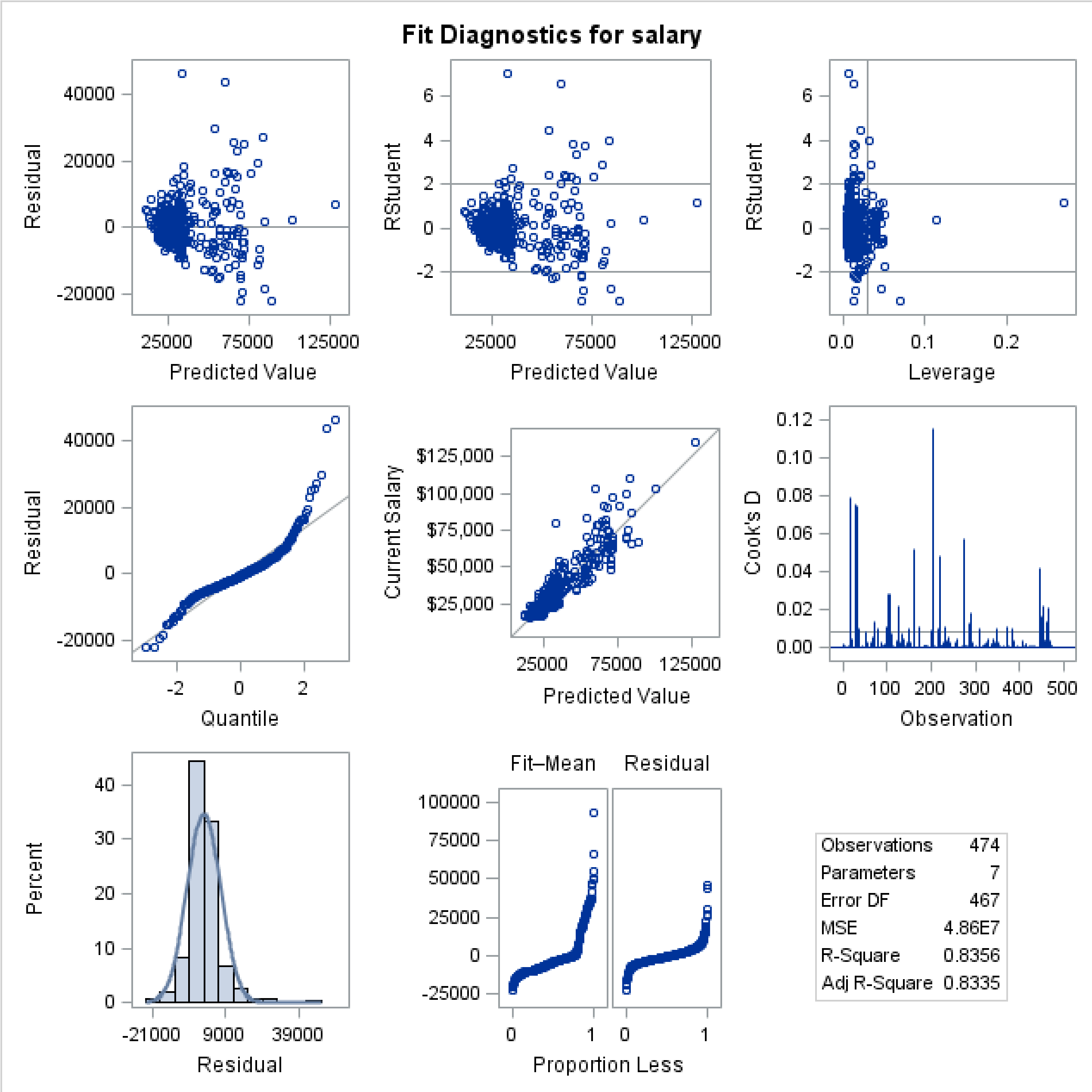
Linear regression

You can fit a linear regression model using Proc Reg:

```
ods graphics on;
proc reg data=sasdata2.employee2;
  model salary = salbegin educ jobdum2 jobdum3 prevexp female;
run; quit;
ods graphics off;
```

Note that the output dataset that we created, REGDAT, has all the original observations and variables in it, plus the new variables Predict, Resid, and Rstudent.
Output from the linear regression model is shown below:

```
                          The REG Procedure
                            Model: MODEL1
                Dependent Variable: salary Current Salary

                Number of Observations Read         474
                Number of Observations Used         474

                          Analysis of Variance
                                 Sum of           Mean
Source                    DF        Squares         Square    F Value    Pr > F
Model                      6     1.15239E11    19206503793     395.52    <.0001
Error                    467    22677472676       48559899
Corrected Total          473    1.379165E11

             Root MSE           6968.49328    R-Square     0.8356
             Dependent Mean          34420    Adj R-Sq     0.8335
             Coeff Var            20.24573

                          Parameter Estimates

                                             Parameter     Standard
Variable   Label                        DF    Estimate        Error  t Value  Pr > |t|
Intercept  Intercept                     1  5333.10875   2337.45787     2.28    0.0230
salbegin   Beginning Salary              1     1.31359      0.07433    17.67    <.0001
educ       Educational Level (years)     1   548.90277    163.27562     3.36    0.0008
jobdum2                                  1  6764.00748   1666.58592     4.06    <.0001
jobdum3                                  1       11389   1394.92854     8.16    <.0001
prevexp    Previous Experience (months)  1   -21.98825      3.64720    -6.03    <.0001
female                                   1 -2122.17197    775.86768    -2.74    0.0065
```



We note that the distribution of the residuals is highly skewed. This is an indication that we may want to use a transformation of the dependent variable.

The variance of the residuals is highly heteroskedastic; we note that there is much more variability of residuals for large predicted values, making a megaphone-like appearance in the graph.

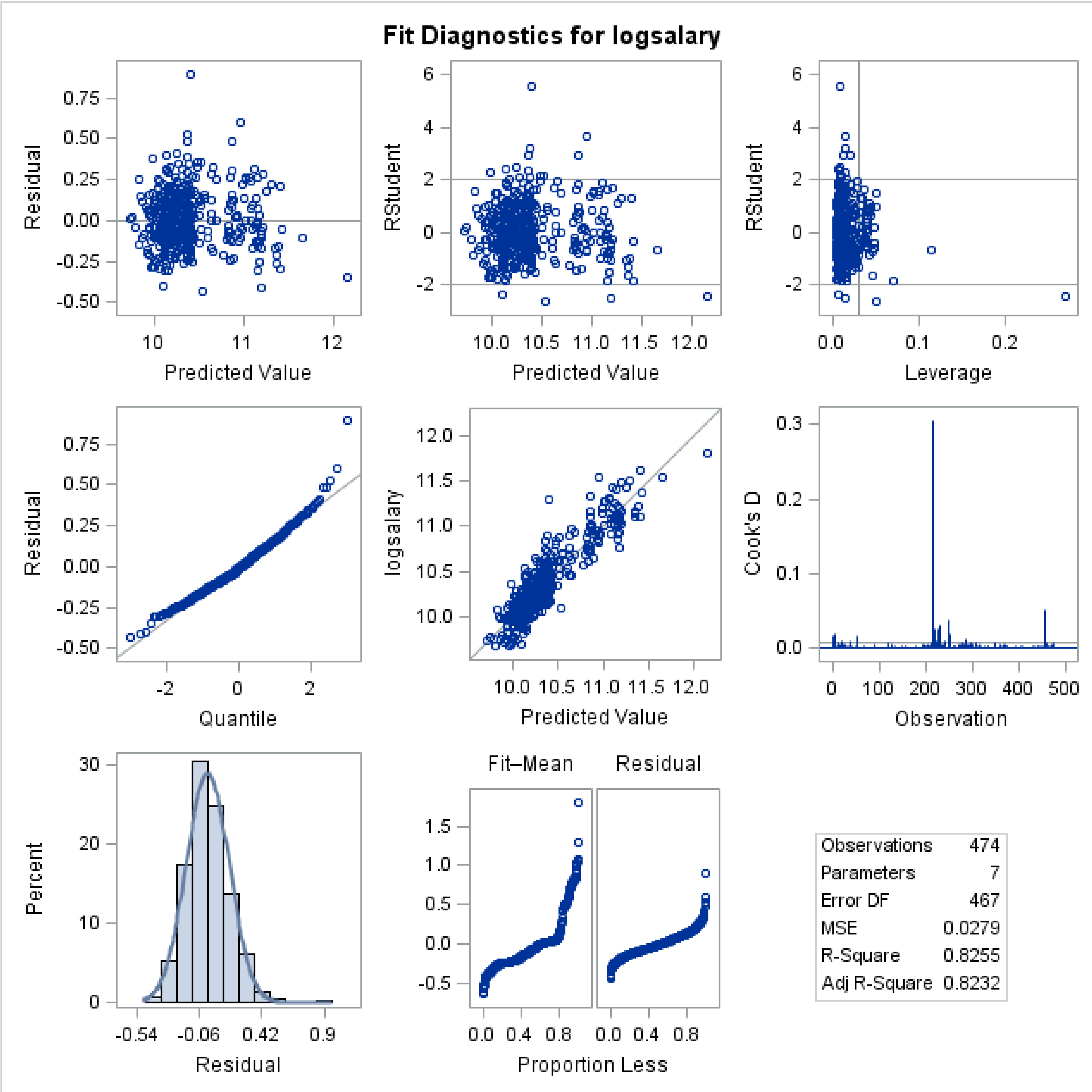
We may want to transform salary using the natural log. The commands below show how Logsalary can be created to be used in the regression. Note that to create a new variable, we need to use a data step. Submit these commands and check the residuals from this new regression model.

```
data temp;
  set sasdata2.employee2;
  logsalary = log(salary);
run;

ods graphics on;
proc reg data=temp;
  model logsalary = salbegin educ jobdum2 jobdum3 prevexp female;
  output out=regdat2 p=predict r=resid rstudent=rstudent;
run; quit;
ods graphics off;
```

```
                              The REG Procedure
                                Model: MODEL1
                        Dependent Variable: logsalary

                   Number of Observations Read         474
                   Number of Observations Used         474


                             Analysis of Variance

                                    Sum of           Mean
        Source                DF       Squares         Square    F Value    Pr > F

        Model                  6      61.64142       10.27357     368.12    <.0001
        Error                467      13.03320        0.02791
        Corrected Total      473      74.67462


                     Root MSE              0.16706    R-Square     0.8255
                     Dependent Mean       10.35679    Adj R-Sq     0.8232
                     Coeff Var             1.61303


                             Parameter Estimates

                                                Parameter      Standard
Variable     Label                         DF     Estimate         Error   t Value   Pr > |t|

Intercept    Intercept                      1      9.66675       0.05604    172.51     <.0001
salbegin     Beginning Salary               1   0.00002304    0.00000178     12.93     <.0001
educ         Educational Level (years)      1      0.02592       0.00391      6.62     <.0001
jobdum2                                     1      0.24880       0.03995      6.23     <.0001
jobdum3                                     1      0.28225       0.03344      8.44     <.0001
prevexp      Previous Experience (months)   1  -0.00063575    0.00008744     -7.27     <.0001
female                                      1     -0.12070       0.01860     -6.49     <.0001
```

The distribution of the residuals appears to be much more normal after the log transformation was applied.

The variance of the residuals appears to be much more constant across all predicted values after applying the log transformation to the dependent variable. We no longer appear to have heteroskedasticity of the residuals.



Cross-tabulations

You can carry out a Pearson Chi-square test of independence using Proc Freq. This procedure is extremely versatile and flexible, and has many options available.

```
proc freq data=sasdata2.employee2;
   tables gender*jobcat / chisq;
run
```

```
                The FREQ Procedure

              Table of gender by jobcat
    gender(Gender)
                jobcat(Employment Category)

    Frequency|
    Percent  |
    Row Pct  |
    Col Pct  |       1|       2|       3|  Total
    ---------+--------+--------+--------+
    f        |    206 |      0 |     10 |    216
             |  43.46 |   0.00 |   2.11 |  45.57
             |  95.37 |   0.00 |   4.63 |
             |  56.75 |   0.00 |  11.90 |
    ---------+--------+--------+--------+
    m        |    157 |     27 |     74 |    258
             |  33.12 |   5.70 |  15.61 |  54.43
             |  60.85 |  10.47 |  28.68 |
             |  43.25 | 100.00 |  88.10 |
    ---------+--------+--------+--------+
    Total         363       27       84      474
                76.58     5.70    17.72   100.00


         Statistics for Table of gender by jobcat

    Statistic                     DF       Value      Prob
    ------------------------------------------------------
    Chi-Square                     2     79.2771    <.0001
    Likelihood Ratio Chi-Square    2     95.4629    <.0001
    Mantel-Haenszel Chi-Square     1     67.4626    <.0001
    Phi Coefficient                       0.4090
    Contingency Coefficient               0.3785
    Cramer's V                            0.4090

                     Sample Size = 474
```

You can get an exact test for this by using an Exact statement. In this case, we requested Fisher's exact test, but exact p-values for other statistics can be requested:

```
proc freq data=sasdata2.employee;
   tables gender*jobcat / chisq;
   exact fisher;
run;
```

In the output below, be sure to read the last p-value at the bottom of the output for Fisher's exact test.

```
        Fisher's Exact Test
 ----------------------------------
 Table Probability (P)    2.854E-22
 Pr <= P                  5.756E-21

          Sample Size = 474
```

If your problem is large, you may wish to get a Monte Carlo simulation for the p-value, based on 10, 000 tables. To do this use the following syntax. Seed=0 will use a random seed for the process based on the clock time when you run the procedure.

```
proc freq data=sasdata2.employee;
 tables gender*jobcat / chisq;
 exact fisher / mc seed=0;
run;
```

Partial output from this procedure is shown below:

```
                  The FREQ Procedure

       Statistics for Table of gender by jobcat

                 Fisher's Exact Test
          ----------------------------------
          Table Probability (P)    2.854E-22

        Monte Carlo Estimate for the Exact Test

          Pr <= P                     0.0000
          99% Lower Conf Limit        0.0000
          99% Upper Conf Limit     4.604E-04

          Number of Samples            10000
          Initial Seed             445615001

                  Sample Size = 474
```

Each time the procedure is run using this syntax, you will get different answers. If you wish to get the same result, simply use the Initial Seed value reported by SAS in the output in your Exact statement.

```
proc freq data=sasdata2.employee;
   tables gender*jobcat / chisq;
   exact fisher / mc seed=445615001;
run;
```

McNemar’s test for paired categorical data:

If you wish to compare the proportions in a 2 by 2 table for paired data, you can use McNemar’s test, by specifying the **agree** option in Proc Freq. Before running the McNemar’s test, we recode PULSE1 and PULSE2 into two categorical variables HIPULSE1 and HIPULSE2, as shown below:

```
data newpulse;
  set pulse;
  if pulse1 > 80 then hipulse1 = 1;
  if pulse1 > 0 and pulse1 <=89 then hipulse1=0;

  if pulse2 > 80 then hipulse2 = 1;
  if pulse2 > 0 and pulse2 <=89 then hipulse2=0;
run;
```

```
proc freq data=newpulse;
  tables hipulse1 hipulse2;
run;
```

```
                           The FREQ Procedure
                                                Cumulative    Cumulative
hipulse1    Frequency     Percent     Frequency      Percent
-------------------------------------------------------------
       0          82       89.13            82        89.13
       1          10       10.87            92       100.00

                                                Cumulative    Cumulative
hipulse2    Frequency     Percent     Frequency      Percent
-------------------------------------------------------------
       0          71       77.17            71        77.17
       1          21       22.83            92       100.00
```

We can now carry out McNemar's test of symmetry to see if the proportion of participants with a high value of PULSE1 is different than the proportion of participants with a high value of PULSE2.

```
proc freq data=newpulse;
  tables hipulse1*hipulse2/ agree;
run;
```

```
   Table of hipulse1 by hipulse2
hipulse1     hipulse2
Frequency|
Percent  |
Row Pct  |
Col Pct  |       0|       1|  Total
---------+--------+--------+
       0 |     69 |     13 |     82
         |  75.00 |  14.13 |  89.13
         |  84.15 |  15.85 |
         |  97.18 |  61.90 |
---------+--------+--------+
       1 |      2 |      8 |     10
         |   2.17 |   8.70 |  10.87
         |  20.00 |  80.00 |
         |   2.82 |  38.10 |
---------+--------+--------+
Total          71       21       92
            77.17    22.83   100.00
```

```
          Statistics for Table of hipulse1 by hipulse2

                    McNemar's Test
               -----------------------
               Statistic (S)    8.0667
               DF                    1
               Pr > S           0.0045

                  Sample Size = 92
```

Logistic regression

If the outcome is coded as 0,1 and you wish to predict the probability of a 1, use the descending option for Proc Logistic.

```
data afifi;
  set sasdata2.afifi;
  if survive=3 then died=1;
  if survive=1 then died=0;
run;

proc logistic data=afifi descending;
  model died = map1 shockdum sex / risklimits;
  units map1 = 1 10  shockdum = 1 sex=1;
run;
```

```
                         Data Set                      WORK.AFIFI
                         Response Variable             died
                         Number of Response Levels     2
                         Model                         binary logit
                         Optimization Technique        Fisher's scoring

                            Number of Observations Read         113
                            Number of Observations Used         113

                                        Response Profile

                               Ordered                      Total
                                 Value          died     Frequency
                                     1             1            43
                                     2             0            70

                                 Probability modeled is died=1.

                                    Model Convergence Status

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

                                      Model Fit Statistics
                                                              Intercept
                                              Intercept             and
                             Criterion             Only      Covariates
                             AIC                152.137         127.874
                             SC                 154.864         138.784
                             -2 Log L           150.137         119.874


                            Testing Global Null Hypothesis: BETA=0

                    Test                 Chi-Square       DF     Pr > ChiSq
                    Likelihood Ratio        30.2628        3         <.0001
                    Score                   26.1922        3         <.0001
                    Wald                    20.3328        3         0.0001
```

Analysis of Maximum Likelihood Estimates

Parameter	DF	Estimate	Standard Error	Wald Chi-Square	Pr > ChiSq
Intercept	1	-0.9571	1.2827	0.5568	0.4556
MAP1	1	-0.0285	0.0114	6.2204	0.0126
SHOCKDUM	1	1.8999	0.6694	8.0540	0.0045
SEX	1	0.6760	0.4450	2.3082	0.1287

Association of Predicted Probabilities and Observed Responses

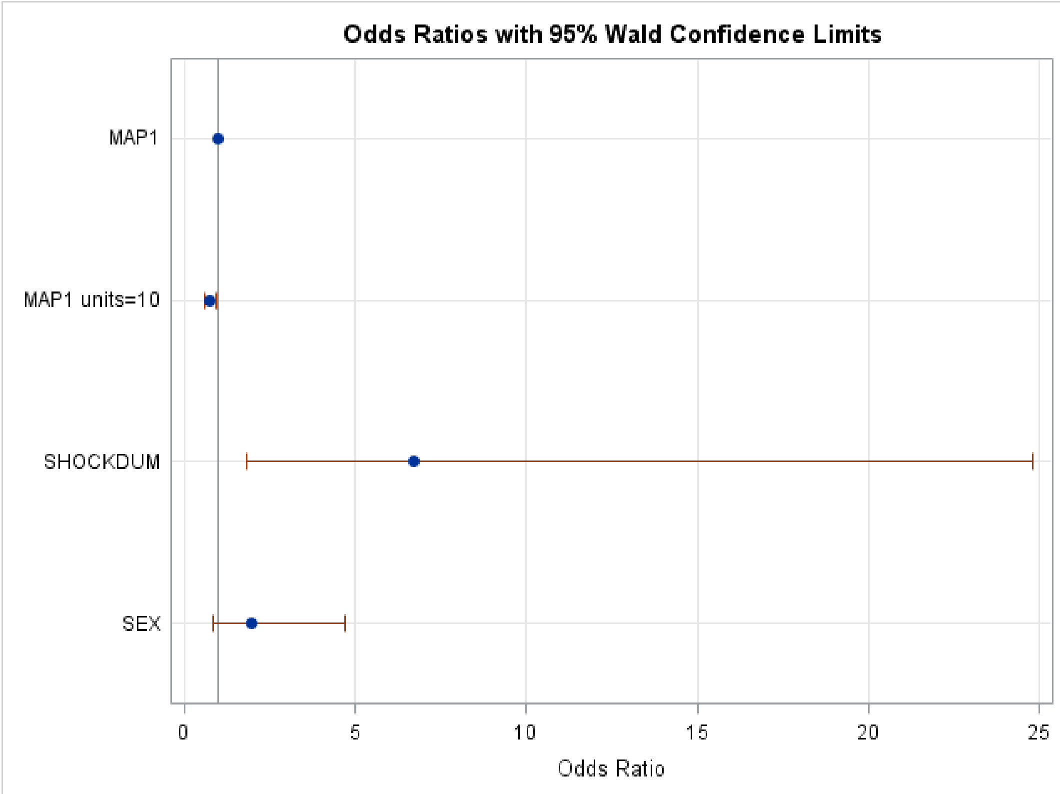
Percent Concordant	79.1	Somers' D	0.586
Percent Discordant	20.5	Gamma	0.588
Percent Tied	0.4	Tau-a	0.279
Pairs	3010	c	0.793

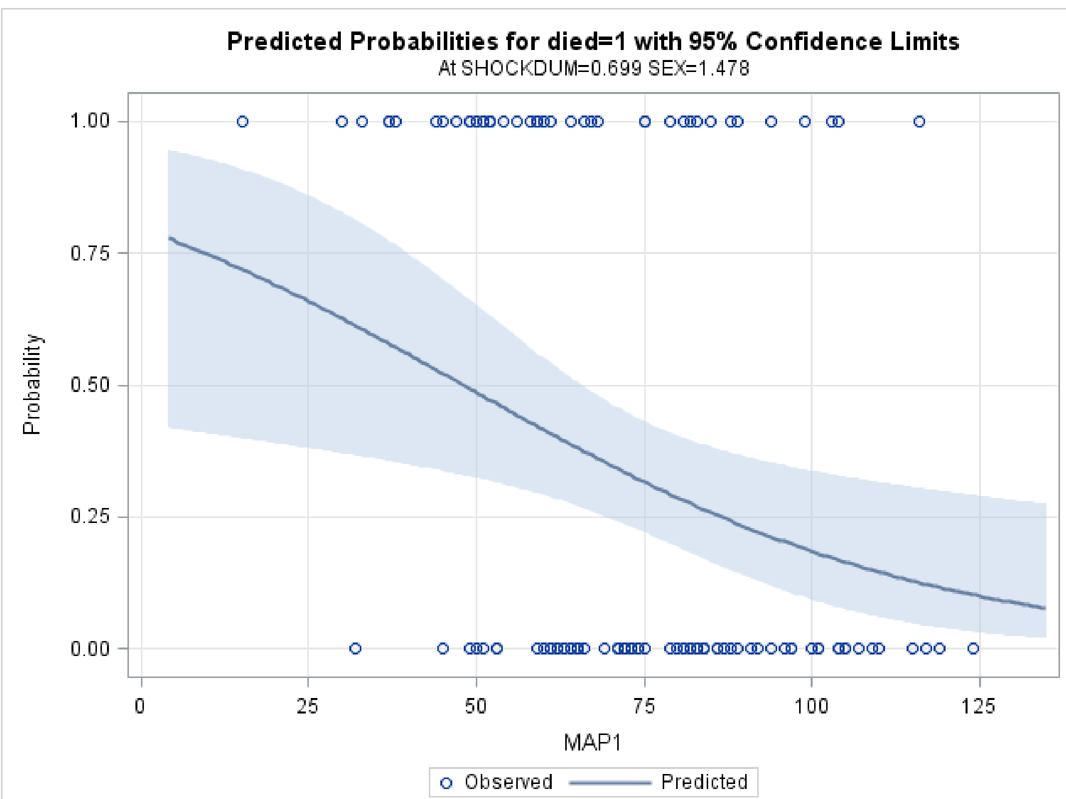
Odds Ratio Estimates and Wald Confidence Intervals

Effect	Unit	Estimate	95% Confidence Limits	
MAP1	1.0000	0.972	0.950	0.994
SHOCKDUM	1.0000	6.685	1.800	24.827
SEX	1.0000	1.966	0.822	4.703

To get graphical output, include the plots = option in the SAS code. We also request odds ratios for a 1-unit and for 10 units increase in MAP1. The oddsratio plot will not be produced unless the risklimits option is specified at the end of the model statement.

```
ods graphics on;
proc logistic data=afifi descending PLOTS(ONLY) = (effect oddsratio);
  model died = map1 shockdum sex / risklimits;
  units map1 = 1 10  shockdum = 1 sex=1;
run;
ods graphics off;
```


Odds Ratios with 95% Wald Confidence Limits
MAP1
MAP1 units=10
SHOCKDUM
SEX
0
5
10
15
20
25
Odds Ratio


Predicted Probabilities for died=1 with 95% Confidence Limits
At SHOCKDUM=0.699 SEX=1.478
1.00
0.75
0.50
0.25
0.00
Probability
0
25
50
75
100
125
MAP1
Observed
Predicted

Generalized Linear Model for Count Data

If the outcome is a count variable, you may want to fit a generalized linear model using Proc Genmod. To use this procedure, you must include an option in the model statement specifying the distribution to use. In this example we are modeling the number of home runs that a major league baseball player will get in a season as a function of his salary. We first use a Poisson regression, in which we specify the log of the number of times at bat as the offset (so that we are really modeling the Poisson rate). In the Poisson distribution, the variance is equal to the mean. If we have an appropriate model, we expect the scaled deviance divided by the degrees of freedom to equal approximately 1.0, which is not the case in this example.

```
proc genmod data=baseball ;
  class league division;
  model no_home = salary /  dist=poisson offset=log_atbat;
  estimate "Effect of 100k salary increase" salary 100 / est;
  output out=Pfitdata p=predict resraw=resraw reschi=reschi;
run;
```

```
                                    The GENMOD Procedure

                                       Model Information
                              Data Set                WORK.BASEBALL
                              Distribution                  Poisson
                              Link Function                     Log
                              Dependent Variable            no_home
                              Offset Variable             log_atbat

                            Number of Observations Read         322
                            Number of Observations Used         263
                            Missing Values                       59

                                    Class Level Information
                           Class         Levels    Values
                           league             2    American National
                           division           2    East West


                             Criteria For Assessing Goodness Of Fit

                Criterion                     DF           Value        Value/DF
                Deviance                     261       1187.5050          4.5498
                Scaled Deviance              261       1187.5050          4.5498
                Pearson Chi-Square           261       1074.2680          4.1160
                Scaled Pearson X2            261       1074.2680          4.1160
                Log Likelihood                         4853.9066
                Full Log Likelihood                   -1110.3858
                AIC (smaller is better)                2224.7716
                AICC (smaller is better)               2224.8178
                BIC (smaller is better)                2231.9159

          Algorithm converged.
```

Analysis Of Maximum Likelihood Parameter Estimates

Parameter	DF	Estimate	Standard Error	Wald 95% Confidence Limits		Wald Chi-Square	Pr > ChiSq
Intercept	1	-3.6957	0.0291	-3.7527	-3.6387	16152.5	<.0001
salary	1	0.0002	0.0000	0.0002	0.0003	49.78	<.0001
Scale	0	1.0000	0.0000	1.0000	1.0000		

NOTE: The scale parameter was held fixed.

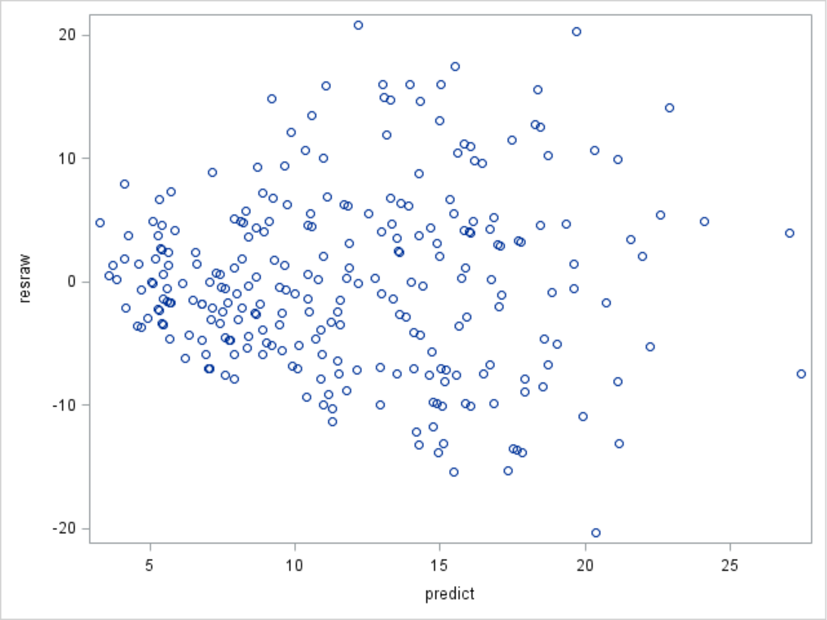
Contrast Estimate Results

Label	Mean Estimate	Mean Confidence Limits		L'Beta Estimate	Standard Error	Alpha
Effect of 100k salary increase	1.0244	1.0176	1.0313	0.0241	0.0034	0.05

The effect of a 100k increase in salary is estimated to be about a 2.4% increase in home run production (95% CI = 1.8% to 3.1% increase).

We look at the distribution of the raw residuals vs. the predicted value. If the Poisson distribution is appropriate, we expect the spread of the residuals to be a function of the mean (which is approximated by the predicted value). This in fact seems to be true, as seen the the graph below:

```
proc sgplot data=fitdata;
  scatter y=resraw x=predict;
run;
```



Here, we use some SAS code to create groups based on the predicted value (i.e., an approximation to the mean of the conditional distribution). We then look at the distribution of the mean of the predicted value in each interval, and the variance of the raw residuals. We see that the mean of the distribution is in all cases less than the variance of the raw residuals. This is another indication that the Poisson distribution is not the best choice for this problem.

```
data Pfitdata2;
  set Pfitdata;
  if 0<= predict <5 then group=1;
  if 5<= predict <10 then group=2;
  if 10<= predict < 15 then group=3;
  if 15<= predict < 20 then group=4;
  if 20<= predict then group=5;
run;
proc format;
  value grpfmt 1="0 to 4.9" 2="5 to 9.9" 3="10 to 14.9"
               4="15 to 19.9" 5="20 to Max";
run;
proc means data=Pfitdata2 n min max mean std var;
 class group;
 var predict resraw;
 format group grpfmt.;
run;
```

group	N Obs	Variable	N	Minimum	Maximum	Mean	Std Dev	Variance
0 to 4.9	**13**	**predict**	13	3.2578916	4.9212568	4.1868213	0.4976284	0.2476340
		resraw	13	-3.6719335	7.9021423	0.6593325	3.4251530	11.7316732
5 to 9.9	**95**	**predict**	95	5.0315488	9.9696055	7.4209071	1.4917644	2.2253609
		resraw	95	-7.9171285	14.8172419	-0.2209071	4.6511984	21.6336467
10 to 14.9	**81**	**predict**	81	10.1005542	14.9827472	12.5494485	1.5378169	2.3648810
		resraw	81	-13.9169213	20.8129702	0.1912922	8.1655403	66.6760486
15 to 19.9	**60**	**predict**	60	15.0114917	19.9416355	16.9885310	1.4100640	1.9882804
		resraw	60	-15.4846933	20.2883934	-0.0218643	9.1883062	84.4249700
20 to Max	**14**	**predict**	14	20.3345690	27.4575979	22.4834298	2.2746223	5.1739064
		resraw	14	-20.3773828	14.1047560	-0.1262870	9.7491252	95.0454412

We now change the distribution to a negative binomial.

```
ods graphics on;
proc genmod data=baseball plots = (predicted(clm));
  class league division;
  model no_home = salary / dist=negbin  offset=log_atbat;
  output out=nbfitdata p=predict resraw=resraw reschi=reschi;
  estimate "Effect of 100k salary increase" salary 100 / est;
run;
ods graphics off;
```

```
                    Model Information

Data Set                      WORK.BASEBALL
Distribution              Negative Binomial
Link Function                           Log
Dependent Variable                  no_home
Offset Variable                   log_atbat
```

Number of Observations Read	322
Number of Observations Used	263
Missing Values	59

Class Level Information

Class	Levels	Values
league	2	American National
division	2	East West

Parameter Information

Parameter	Effect
Prm1	Intercept
Prm2	salary

Criteria For Assessing Goodness Of Fit

Criterion	DF	Value	Value/DF
Deviance	261	296.8518	1.1374
Scaled Deviance	261	296.8518	1.1374
Pearson Chi-Square	261	217.5268	0.8334
Scaled Pearson X2	261	217.5268	0.8334
Log Likelihood		5104.3910	
Full Log Likelihood		-859.9014	
AIC (smaller is better)		1725.8028	
AICC (smaller is better)		1725.8954	
BIC (smaller is better)		1736.5192	

Algorithm converged.

Analysis Of Maximum Likelihood Parameter Estimates

Parameter	DF	Estimate	Standard Error	Wald 95% Confidence Limits		Wald Chi-Square	Pr > ChiSq
Intercept	1	-3.7020	0.0650	-3.8294	-3.5745	3241.64	<.0001
salary	1	0.0003	0.0001	0.0001	0.0004	7.82	0.0052
Dispersion	1	0.3480	0.0407	0.2768	0.4375		

NOTE: The negative binomial dispersion parameter was estimated by maximum likelihood.

Contrast Estimate Results

Label	Mean Estimate	Mean Confidence Limits		L'Beta Estimate	Standard Error	Alpha
Effect of 100k salary increase	1.0253	1.0075	1.0434	0.0250	0.0089	0.05

We now see that the scaled deviance divided by df is approximately 1.0, which is an improvement over the previous model.

In this model, the predicted effect of a 100k increase in salary is predicted to be about a 2.5% increase in home run production, with a wider Confidence Interval (CI = 0.75% to 4.3%).

We also look at the predicted values and their respective 95% Confidence intervals. Notice that the smaller residuals have smaller estimated CI, as we expect when fitting this type of model.