## 2.2.1: SAS - Residual Diagnostics

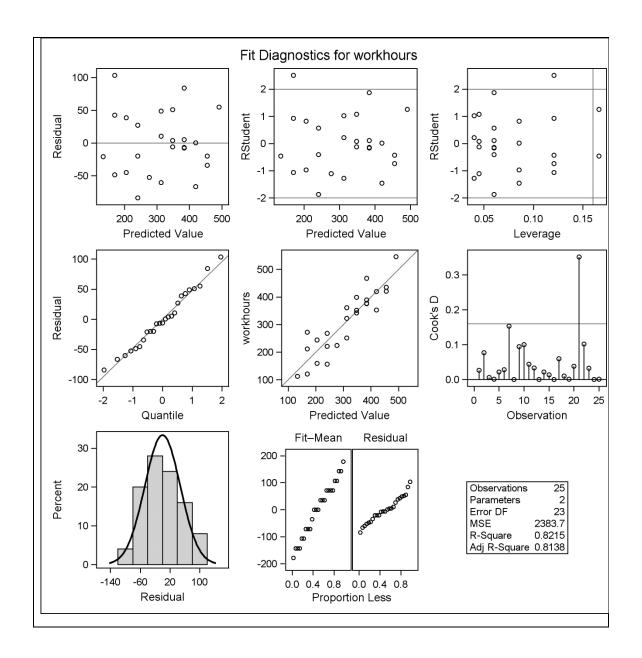
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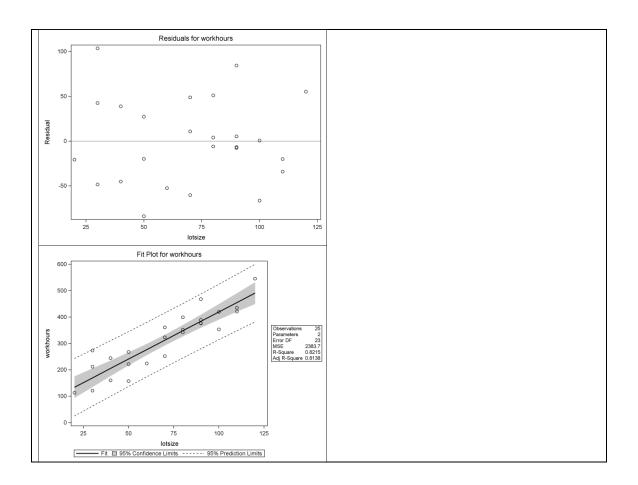
Example: (The Toluca Company data from Handout #2).

```
/* Input Toluca data (recall Ch. 1 example) */
data toluca; input lotsize workhours @@; cards;
      399
             30
                 121
                       50
                           221
                                 90
                                     376
                                           70 361
                                                     60
                                                         224
   80
  120
       546
             80
                 352
                      100
                           353
                                 50
                                     157
                                           40 160
                                                     70 252
                                                     50 268
   90
      389
                113
                     110
                          435
                                100
                                    420
                                           30 212
            20
                421
   90
      377 110
                       30 273
                                 90
                                    468
                                           40 244
                                                     80 342
   70
      323
run;
/* Now fit simple linear model with Y=workhours and X=lotsize,
  with residuals and predicted values saved in data set
   tolucaout */
proc reg data=toluca;
  model workhours = lotsize;
  output out=tolucaout r=resid p=pred;
  title1 'Simple linear model';
run;
```

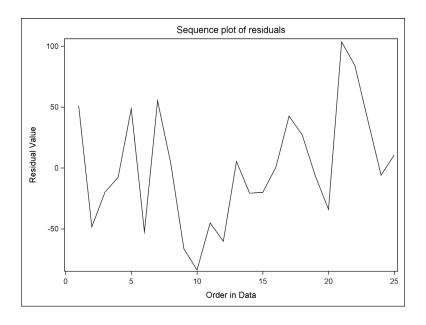
Analysis of Variance					
Source	DF	Sum of Squares	Mean Square	F Value	<b>Pr</b> > <b>F</b>
Model	1	252378	252378	105.88	<.0001
Error	23	54825	2383.71562		
<b>Corrected Total</b>	24	307203			

Parameter Estimates					
Variable	DF	Parameter Estimate	Standard Error	t Value	Pr >  t
Intercept	1	62.36586	26.17743	2.38	0.0259
lotsize	1	3.57020	0.34697	10.29	<.0001





```
/* Look at sequence plot */
data temp; set tolucaout;
  order = _n_;
proc sgplot data=temp;
  series x=order y=resid / lineattrs=(pattern=solid);
  xaxis label='Order in Data';
  yaxis label='Residual Value';
  title1 'Sequence plot of residuals';
run;
```



```
/*********** Numerical Diagnostics *********/
/* F-test for lack of fit */
proc rsreg data=toluca;
  model workhours = lotsize / lackfit covar=1 noopt;
  title1 'F-test for lack of fit';
run;
```

Residual	DF	Sum of Squares	Mean Square	F Value	Pr > F
Lack of Fit	9	17245	1916.069540	0.71	0.6893
Pure Error	14	37581	2684.345238		
Total Error	23	54825	2383.715617		

```
/** Brown-Forsythe and Correlation Test of Normality (shortcut)
**/
/* Two [unused] ways to access shortcut:
    filename macrourl "C:\[filepath]\resid num diag.sas";
     %include macrourl;
 */
%macro resid num diag(dataset,datavar,label= ...
/*
  This resid num diag.sas file provides a convenient shortcut
   to obtaining numerical checks of residuals from
   a fitted linear regression model.
   The macro takes five arguments:
    dataset is the name of the data set
    datavar is the name of the variable in the data set
             for which numerical diagnostics are desired
             (usually a residual)
    label is a character string for detail in output
    predvar is the name of the variable (usually predicted
          value) on which to sort for the Brown-Forsythe test
          (t-statistic and p-value reported)
    predlabel is the character string for detail in output
          related to the predvar variable
*/
```

```
/* Call the shortcut: */
%resid_num_diag(dataset=tolucaout, datavar=resid,
    label='residual', predvar=pred, predlabel='predicted');
```

## P-value for Brown-Forsythe test of constant variance in residual vs. predicted

Obs	t_BF	BF_pvalue
1	1.31648	0.20098

## Output for correlation test of normality of residual (Check text Table B.6 for threshold)

Pearson Correlation Coefficients, N = 25 Prob >  r  under H0: Rho=0				
	resid expectNorr			
resid residual	1.00000	0.99151 <.0001		
expectNorm	0.99151 <.0001	1.00000		