

2.2.1: SAS - Residual Diagnostics

Dr. Bean – Stat 5100

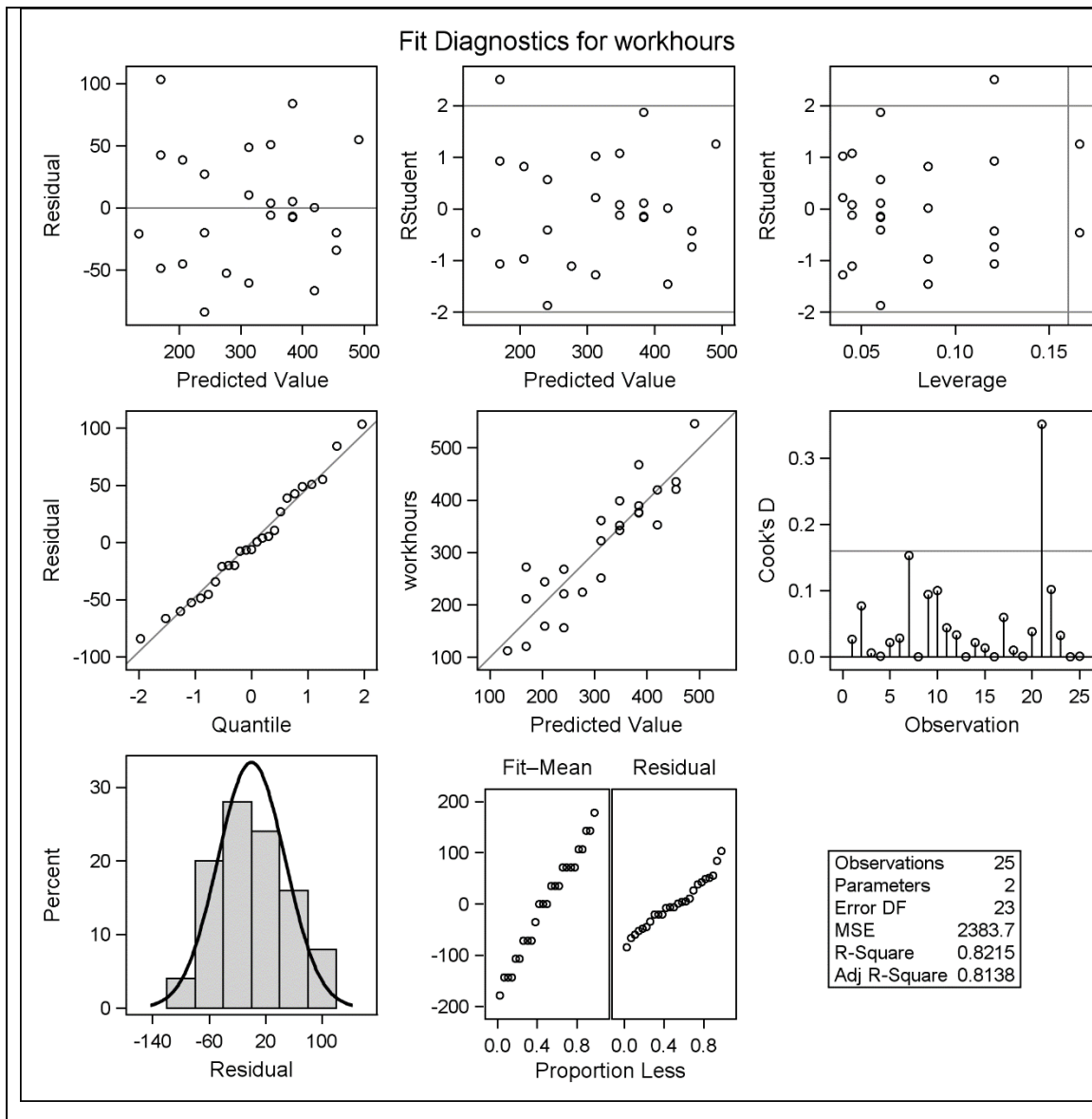
Example: (The Toluca Company data from Handout #2).

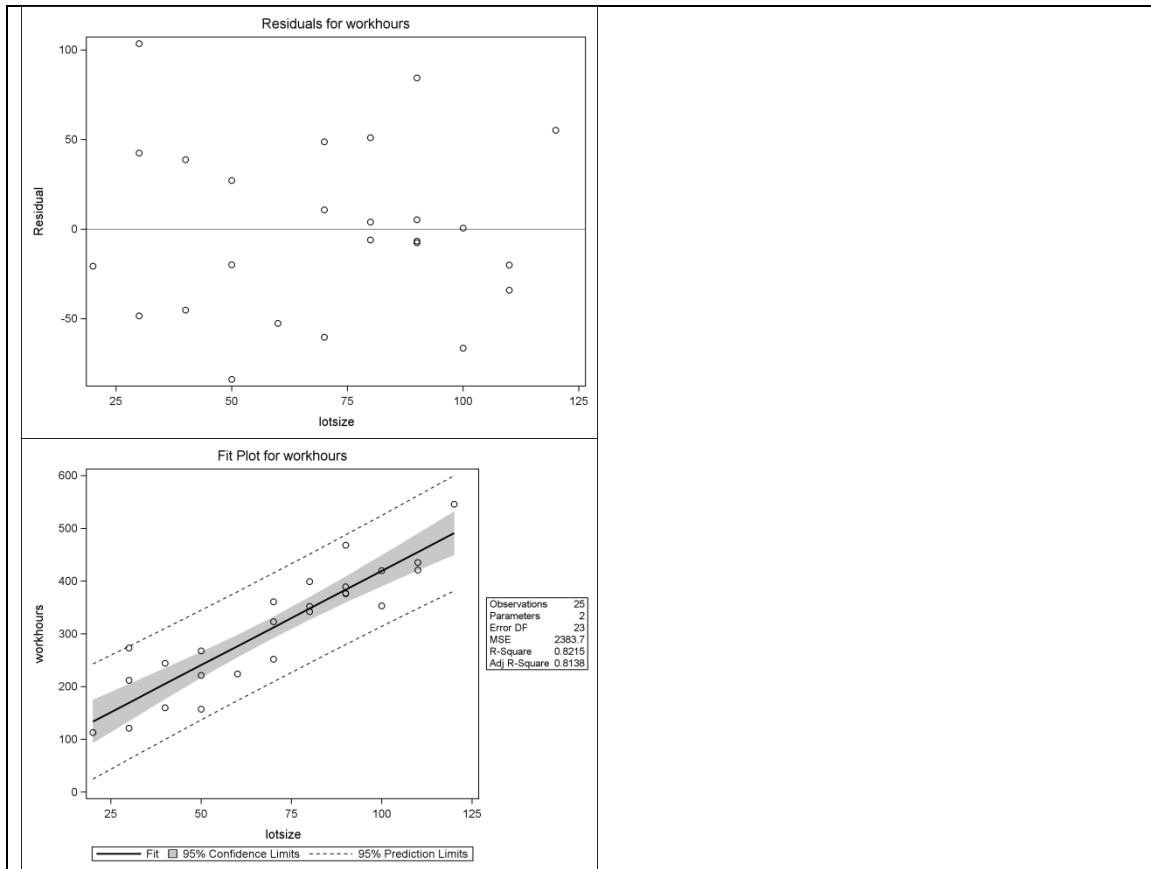
```
/* Input Toluca data (recall Ch. 1 example) */
data toluca; input lotsize workhours @@; cards;
  80 399 30 121 50 221 90 376 70 361 60 224
 120 546 80 352 100 353 50 157 40 160 70 252
 90 389 20 113 110 435 100 420 30 212 50 268
 90 377 110 421 30 273 90 468 40 244 80 342
 70 323
;
run;

/* 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;
  titlel 'Simple linear model';
run;
```

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

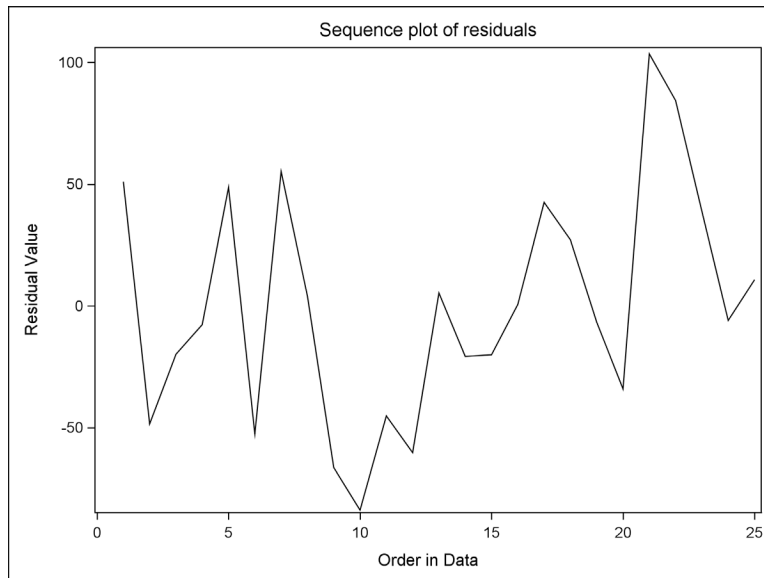




```

/* 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 | expectNorm |
| resid | 1.00000 | 0.99151 |
| residual | | <.0001 |
| expectNorm | 0.99151 | 1.00000 |
| | <.0001 | |