

```
/* Montgomery 7.5 */
proc import datafile="/home/u63048916/STAT571B/Homework/Homework 6/Q7-5.xlsx"
  dbms=xlsx
  out=mont7_5
  replace;
  getnames=yes;
run;

data inter;
  set mont7_5;
  A=A;
  B=B;
  C=C;
  D=D;
  AB=A*B;
  AC=A*C;
  AD=A*D;
  BC=B*C;
  BD=B*D;
  CD=C*D;
  ABC=AB*C;
  ABD=AB*D;
  ACD=AC*D;
  BCD=BC*D;
  block=ABC*D;
  resp=Yield;

proc glm data=inter; /* GLM Proc to Obtain Effects for unreplicated case */
  class A B C D AB AC AD BC BD CD ABC ABD ACD BCD block;
  model resp=block A B C D AB AC AD BC BD CD ABC ABD ACD BCD;
run;

proc reg outest=effects data=inter; /* REG Proc to Obtain Effects */
  model resp=A B C D AB AC AD BC BD CD ABC ABD ACD BCD block;
run;

proc print data=effects;
run;

data effect2; set effects;
  drop y intercept _RMSE_;
run;

proc transpose data=effect2 out=effect3;
run;

data effect4; set effect3; effect=col1*2;
run;

proc sort data=effect4; by effect;
run;

proc print data=effect4;
run;

proc rank data=effect4 out=effect5 normal=blom;
  var effect;
  ranks neff;
run;

proc sgplot data=effect5;
  scatter x=neff y=effect/datalabel=_NAME_;
  xaxis label='Normal Scores';
run;

/* rerun glm with specific significant effects */
proc glm data=inter; /* GLM Proc to Obtain Effects */
  class A B AB block;
  model resp= A B C D AB AC AD BC BD ABC ABD block;
  output out=two r=res p=pred;
run;

proc univariate data=two normal;
  var res;
  qqplot;
run;
/* check constant variance using graph*/
title 'residual plot: res vs predicted value';
proc sgplot data=two;
  scatter x=pred y=res;
  refline 0;
run;
```

7.5. Consider the data from the first replicate of Problem 6.7. Construct a design with two blocks of eight observations each with *ABCD* confounded. Analyze the data.

6.7. An experiment was performed to improve the yield of a chemical process. Four factors were selected, and two replicates of a completely randomized experiment were run. The results are shown in the following table:

Treatment Combination	Replicate		Treatment Combination	Replicate	
	I	II		I	II
(1)	90	93	<i>d</i>	98	95
<i>a</i>	74	78	<i>ad</i>	72	76
<i>b</i>	81	85	<i>bd</i>	87	83
<i>ab</i>	83	80	<i>abd</i>	85	86
<i>c</i>	77	78	<i>cd</i>	99	90
<i>ac</i>	81	80	<i>acd</i>	79	75
<i>bc</i>	88	82	<i>bcd</i>	87	84
<i>abc</i>	73	70	<i>abcd</i>	80	80

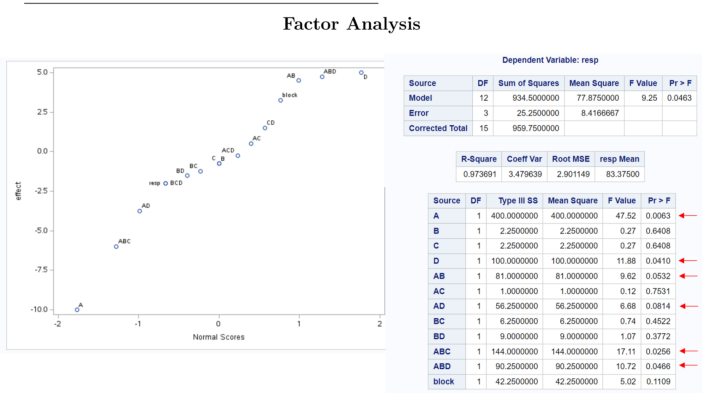
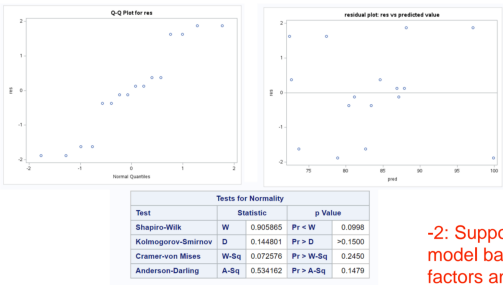


Figure 7.5.1
Residual Normality Diagnostics



-2: Supposed to make model based on selected factors and do analysis on that model