I. Review the Assumptions of ANOVA, Completely Randomized Design and Randomized Complete Block Design

CRD - assumes that each sample came from an underlying population that is normally distributed and that the variances of all of these underlying distributions are equal.

RCB - assumes that each observation is a random independent sample of size 1 from the \( kn \) underlying populations; all of these underlying populations are normally distributed and all variances are equal.

RCB Model: \( X_{ij} = \mu_i + \beta_j + \tau_{ij} + \epsilon_{ij} \) for \( i = 1, 2 \ldots n \) and \( j = 1, 2 \ldots k \); if the \( \epsilon_{ij} \) are normally distributed, then the assumption of normality of the underlying populations can be accepted.

For both CRD and RCB designs, the ANOVA remains fairly robust of deviations from normality are minor - validity is only slightly affected by even moderate skewness or kurtosis. For the CRD, skewness or kurtosis can represent more of a problem if sample sizes are small than if they are large.

Homogeneity of variance can be evaluated in the single-factor CRD using Levene's test. Levene's test (as with most homogeneity of variance tests) is based on calculating a dispersion variable for each treatment group: \( z_{ij} = (y_{ij} - \bar{y}_i)^2 \) or \( z_{ij} = |y_{ij} - \bar{y}_i| \) and then comparing group means for this new variable using a one-way ANOVA. The one-way CRD is robust to deviations from the assumption of homogeneity of variance, especially if sample sizes are approximately equal.

II. The Kruskal-Wallis Test

The multi-group extension of the Wilcoxon Rank Sum Test (Mann-Whitney U Test). Even when the assumptions of the CRD ANOVA are met, the Kruskal-Wallis test is about 95% (3/\( \pi \)) as powerful as the CRD. The Kruskal-Wallis test assumes that the \( k \) groups all have equal dispersions (not necessarily normal), but the test is robust even in the face of violations of this assumption.

The Kruskal-Wallis Test is sometimes known as an "analysis of variance on ranks," and indeed, it can be performed by replacing the original observations by their ranks (rank transformation) and conducting a one-way ANOVA on the ranked data. Pursuant to obtaining a significant treatment effect, one may use any of the multiple comparison tests (BON, SIDAK, LSD, DUNNETT) available in SAS.

III. Friedman's Test

The nonparametric analog of the RCB design is known as Friedman's test, which also can be viewed as the multi-group extension of the Wilcoxon Signed Ranks Test. When the assumptions of the ANOVA are met, Friedman's test is almost as powerful as the parametric RCB: \( 3k/[\pi(k+1)] \). However, when the assumptions of ANOVA are not met, Friedman's test may be more powerful. Procedurally, Friedman's Test is conducted easily in SAS by ranking observations within blocks and then performing a one-way ANOVA CRD on the ranked data.
DATA HOGFEED;
INPUT FEEDTYPE $ MEAN SD;
COMMENT THE FOLLOWING 8 LINES GENERATE DATA
SETS GIVEN N, A MEAN, AND A STD DEV;
DO I=1 TO 50;
IF FEEDTYPE='STDMIX' THEN MASSINKG=
    MEAN + SD*RANNOR(24884);
IF FEEDTYPE='HOGGIES' THEN MASSINKG=
    MEAN + SD*RANNOR(98390);
IF FEEDTYPE='SUPERPIG' THEN MASSINKG=
    MEAN + SD*RANNOR(45034);
IF FEEDTYPE='PORKER' THEN MASSINKG=
    MEAN + SD*RANNOR(15617);
IF FEEDTYPE='SUUUEEE' THEN MASSINKG=
    MEAN + SD*RANNOR(87784);
OUTPUT;
END;
CARDS;
STDMIX 60.66 1.70
HOGGIES 69.30 2.23
SUPERPIG 100.35 12.80
PORKER 86.24 12.90
SUUUEEE 73.34 2.78;
OPTIONS LINESIZE=72 NOCENTER;
PROC PRINT DATA=HOGFEED;
PROC SORT DATA=HOGFEED;
BY FEEDTYPE;
PROC MEANS DATA=HOGFEED MEAN STD N MAX MIN;
BY FEEDTYPE;
VAR MASSINKG;
OUTPUT OUT=GPMEANS MEAN=FEEDMEAN
STD=FEEDSTD;
PROC SORT DATA=GPMEANS;
BY FEEDTYPE;
DATA HOGFEED1; MERGE HOGFEED GPMEANS;
BY FEEDTYPE;
MEANDIFF=MASSINKG-MEAN;
DISP=(MASSINKG-FEEDMEAN)**2;
PROC PRINT DATA=HOGFEED1;
VAR FEEDTYPE I MASSINKG FEEDMEAN MEAN
MEANDIFF DISP;
PROC SORT DATA=HOGFEED1;
BY FEEDTYPE;
COMMENT THE FOLLOWING PROC MEANS EXECUTES A
PAIRED T-TEST TO ASK WHETHER THE
GENERATED DATA SETS HAVE MEAN VALUES THAT
ARE STATISTICALLY EQUAL TO THE INITIALLY
SPECIFIED VALUE;
PROC MEANS DATA=HOGFEED1 MEAN N T PRT;
BY FEEDTYPE;
VAR MEANDIFF;
COMMENT THE FOLLOWING CHECKS FOR NORMALITY
WITHIN EACH TRT GROUP;
PROC UNIVARIATE NORMAL DATA=HOGFEED1;
BY FEEDTYPE;
VAR MASSINKG;
COMMENT THE FOLLOWING IS A PARAMETRIC ONE-WAY
ANOVA;
PROC GLM DATA=HOGFEED1;
CLASS FEEDTYPE;
MODEL MASSINKG=FEEDTYPE;
MEANS FEEDTYPE/BON LINES HOVTEST=LEVENE;
PROC GLM DATA=HOGFEED1;
CLASS FEEDTYPE;
MODEL DISP=FEEDTYPE;
COMMENT THE FOLLOWING REPLACES THE MASS DATA
WITH THEIR RANKS TO EXECUTE A KRUSKAL-
WALLIS TEST;
PROC RANK DATA=HOGFEED OUT=RHOGFEED;
VAR MASSINKG;
RANKS RMASS;
PROC SORT DATA=RHOGFEED;
BY FEEDTYPE;
PROC GLM DATA=RHOGFEED;
CLASS FEEDTYPE;
MODEL RMASS=FEEDTYPE;
MEANS FEEDTYPE/BON LINES;
COMMENT THE FOLLOWING REORGANIZES THE DATA AS
IF THE STUDY HAD BEEN DONE AS A
RANDOMIZED COMPLETE BLOCK DESIGN;
DATA RCB; SET HOGFEED; BLOCK=I;
PROC PRINT DATA=RCB;
VAR FEEDTYPE I BLOCK MASSINKG;
PROC SORT DATA=RCB;
BY BLOCK;
PROC GLM DATA=RCB;
CLASSES BLOCK FEEDTYPE;
MODEL MASSINKG=BLOCK FEEDTYPE;
MEANS FEEDTYPE/BON LINES;
OUTPUT OUT=RCBNORM RESIDUAL=RESMASS;
COMMENT WANT TO EVALUATE WHETHER RESIDUALS ARE
NORMALLY DISTRIBUTED AS A TEST OF THE
ASSUMPTION OF NORMALITY;
PROC UNIVARIATE NORMAL DATA=RCBNORM;
HISTOGRAM RESMASS/NORMAL;
VAR RESMASS;
PROC PLOT DATA=RCBNORM;
PLOT RESMASS*FEEDTYPE;
COMMENT THE FOLLOWING RANKS THE OBSERVATIONS
WITHIN EACH BLOCK AS A PRELUDE TO
FRIEDMANS TEST;
PROC RANK DATA=RCB OUT=RCBRANKS;
BY BLOCK;
VAR MASSINKG;
RANKS RBLOCK;
PROC PRINT DATA=RCBRANKS;
PROC SORT DATA=RCBRANKS;
BY FEEDTYPE;
PROC GLM DATA=RCBRANKS;
CLASS FEEDTYPE;
MODEL RBLOCK=FEEDTYPE;
MEANS FEEDTYPE/BON LINES;
RUN;
INPUT FEEDTYPE $ MEAN SD;
COMMENT THE FOLLOWING 8 LINES GENERATE DATA SETS GIVEN N, A MEAN, AND A STD DEV;
DO I=1 TO 50;
IF FEEDTYPE='STDMIX' THEN MASSINKG=MEAN + SD*RANNOR(24884);
IF FEEDTYPE='HOGGIES' THEN MASSINKG=MEAN + SD*RANNOR(98390);
IF FEEDTYPE='SUPERPIG' THEN MASSINKG=MEAN + SD*RANNOR(45034);
IF FEEDTYPE='PORKER' THEN MASSINKG=MEAN + SD*RANNOR(15617);
IF FEEDTYPE='SUUUEEE' THEN MASSINKG=MEAN + SD*RANNOR(87784);
OUTPUT;
END;

The SAS System                          13:46 Monday, March 26, 2001   1

Obs    FEEDTYPE     MEAN     SD      I    MASSINKG
1    STDMIX      60.66    1.70     1     60.0126
2    STDMIX      60.66    1.70     2     62.7385
3    STDMIX      60.66    1.70     3     57.3977
4    STDMIX      60.66    1.70     4     59.1605
5    STDMIX      60.66    1.70     5     57.0399
6    STDMIX      60.66    1.70     6     61.3386
7    STDMIX      60.66    1.70     7     61.0566
8    STDMIX      60.66    1.70     8     59.4117
9    STDMIX      60.66    1.70     9     61.0469
10   STDMIX      60.66    1.70    10     59.7359
11   STDMIX      60.66    1.70    11     61.4723
12   STDMIX      60.66    1.70    12     58.8979
13   STDMIX      60.66    1.70    13     59.6101
14   STDMIX      60.66    1.70    14     59.3274
15   STDMIX      60.66    1.70    15     60.2618
16   STDMIX      60.66    1.70    16     59.8439
17   STDMIX      60.66    1.70    17     61.0888
18   STDMIX      60.66    1.70    18     63.6487
19   STDMIX      60.66    1.70    19     61.9501
20   STDMIX      60.66    1.70    20     60.0289
21   STDMIX      60.66    1.70    21     59.7491
22   STDMIX      60.66    1.70    22     57.9608
23   STDMIX      60.66    1.70    23     58.6498
24   STDMIX      60.66    1.70    24     61.4567
25   STDMIX      60.66    1.70    25     61.7126
26   STDMIX      60.66    1.70    26     60.7648
27   STDMIX      60.66    1.70    27     60.3929
28   STDMIX      60.66    1.70    28     59.8895
29   STDMIX      60.66    1.70    29     61.7701
30   STDMIX      60.66    1.70    30     58.1070
31   STDMIX      60.66    1.70    31     60.4987
32   STDMIX      60.66    1.70    32     57.4778
33   STDMIX      60.66    1.70    33     61.2590
34   STDMIX      60.66    1.70    34     60.8898
35   STDMIX      60.66    1.70    35     61.6606
36   STDMIX      60.66    1.70    36     62.4679
37   STDMIX      60.66    1.70    37     61.3092
38   STDMIX      60.66    1.70    38     59.9493
39   STDMIX      60.66    1.70    39     63.5949
40   STDMIX      60.66    1.70    40     59.6169
41   STDMIX      60.66    1.70    41     58.0842

etc ...
**PROC SORT DATA=HOGFEED;**
    **BY FEEDTYPE;**
**PROC MEANS DATA=HOGFEED MEAN STD N MAX MIN;**
    **BY FEEDTYPE;**
    **VAR MASSINKG;**
    **OUTPUT OUT=GPMEANS MEAN=FEEDMEAN STD=FEEDSTD;**

The SAS System                          13:46 Monday, March 26, 2001   6

**FEEDTYPE=HOGGIES**

<table>
<thead>
<tr>
<th>Analysis Variable : MASSINKG</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mean</td>
</tr>
<tr>
<td>69.4953494</td>
</tr>
</tbody>
</table>

**FEEDTYPE=PORKER**

<table>
<thead>
<tr>
<th>Analysis Variable : MASSINKG</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mean</td>
</tr>
<tr>
<td>86.5322227</td>
</tr>
</tbody>
</table>

**FEEDTYPE=STDMIX**

<table>
<thead>
<tr>
<th>Analysis Variable : MASSINKG</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mean</td>
</tr>
<tr>
<td>60.3812626</td>
</tr>
</tbody>
</table>

**FEEDTYPE=SUPERPIG**

<table>
<thead>
<tr>
<th>Analysis Variable : MASSINKG</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mean</td>
</tr>
<tr>
<td>98.4137849</td>
</tr>
</tbody>
</table>

**FEEDTYPE=SUUUEEE**

<table>
<thead>
<tr>
<th>Analysis Variable : MASSINKG</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mean</td>
</tr>
<tr>
<td>73.0903456</td>
</tr>
</tbody>
</table>
DATA HOGFEED1; MERGE HOGFEED GPMEANS;
  BY FEEDTYPE;
  MEANDIFF=MASSINKG-MEAN;
  DISP=(MASSINKG-FEEDMEAN)**2;
PROC PRINT DATA=HOGFEED1;
  VAR FEEDTYPE I MASSINKG FEEDMEAN MEAN MEANDIFF DISP;
PROC SORT DATA=HOGFEED1;
  BY FEEDTYPE;
COMMENT THE FOLLOWING PROC MEANS EXECUTES A PAIRED T-TEST TO ASK WHETHER
THE GENERATED DATA SETS HAVE MEAN VALUES THAT ARE STATISTICALLY
EQUAL TO THE INITIALLY SPECIFIED VALUE;
PROC MEANS DATA=HOGFEED1 MEAN N T PRT;
  BY FEEDTYPE;
  VAR MEANDIFF;

Obs   FEEDTYPE    I   MASSINKG   FEEDMEAN    MEAN   MEANDIFF      DISP
  1   HOGGIES     1     66.472    69.4953   69.30    -2.8276     9.138
  2   HOGGIES     2     63.416    69.4953   69.30    -5.8835    36.952
  3   HOGGIES     3     71.998    69.4953   69.30     2.6981     6.264
  4   HOGGIES     4     67.848    69.4953   69.30    -1.4518     2.713
  5   HOGGIES     5     67.979    69.4953   69.30    -1.3213     2.300

etc.

FEEDTYPE=HOGGIES
  Analysis Variable : MEANDIFF
  Mean      N    t Value    Pr > |t|
  0.1953494     50       0.62      0.5363

FEEDTYPE=PORKER
  Analysis Variable : MEANDIFF
  Mean      N    t Value    Pr > |t|
  0.2922227     50       0.18      0.8609

FEEDTYPE=STDMIX
  Analysis Variable : MEANDIFF
  Mean      N    t Value    Pr > |t|
  -0.2787374     50      -1.27      0.2102

FEEDTYPE=SUPERPIG
  Analysis Variable : MEANDIFF
  Mean      N    t Value    Pr > |t|
  -1.9362151     50      -1.20      0.2371

FEEDTYPE=SUUUEEE
  Analysis Variable : MEANDIFF
  Mean      N    t Value    Pr > |t|
  -0.2496544     50      -0.68      0.4981
COMMENT THE FOLLOWING CHECKS FOR NORMALITY WITHIN EACH TRT GROUP;
PROC UNIVARIATE NORMAL DATA=HOGFEED1;
   BY FEEDTYPE;
   VAR MASSINKG;

FEEDTYPE=HOGGIES
Moments
Skewness           -0.3858101    Kurtosis            0.26720085

Tests for Normality
Test                  --Statistic---    -----p Value------
Shapiro-Wilk          W     0.980022    Pr < W      0.5529

FEEDTYPE=PORKER
Moments
Skewness           0.00832025    Kurtosis             -0.390737

Tests for Normality
Test                  --Statistic---    -----p Value------
Shapiro-Wilk          W     0.985557    Pr < W      0.7953

FEEDTYPE=STDMIX
Moments
Skewness           -0.0707018    Kurtosis            -0.2266925

Tests for Normality
Test                  --Statistic---    -----p Value------
Shapiro-Wilk          W     0.987579    Pr < W      0.8742

FEEDTYPE=SUPERPIG
Moments
Skewness           -0.1985784    Kurtosis            -0.3845653

Tests for Normality
Test                  --Statistic---    -----p Value------
Shapiro-Wilk          W     0.977955    Pr < W      0.4693

FEEDTYPE=SUUUEEE
Moments
Skewness           0.00619663    Kurtosis            -0.6389096

Tests for Normality
Test                  --Statistic---    -----p Value------
Shapiro-Wilk          W     0.974009    Pr < W      0.3343
**COMMENT** THE FOLLOWING IS A PARAMETRIC ONE-WAY ANOVA;

```sas
PROC GLM DATA=HOGFEED1;
   CLASS FEEDTYPE;
   MODEL MASSINKG=FEEDTYPE;
   MEANS FEEDTYPE/BON LINES HOVTEST=LEVENE;
```

The GLM Procedure

<table>
<thead>
<tr>
<th>Class Level Information</th>
</tr>
</thead>
<tbody>
<tr>
<td>Class</td>
</tr>
<tr>
<td>FEEDTYPE</td>
</tr>
</tbody>
</table>

Number of observations 250

**Dependent Variable: MASSINKG**

<table>
<thead>
<tr>
<th>Source</th>
<th>DF</th>
<th>Sum of Squares</th>
<th>Mean Square</th>
<th>F Value</th>
<th>Pr &gt; F</th>
<th>R-Square</th>
</tr>
</thead>
<tbody>
<tr>
<td>Model</td>
<td>4</td>
<td>44775.19971</td>
<td>11193.79993</td>
<td>198.16</td>
<td>&lt;.0001</td>
<td>0.763883</td>
</tr>
<tr>
<td>Error</td>
<td>245</td>
<td>13840.06138</td>
<td>56.49005</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Corrected Total</td>
<td>249</td>
<td>58615.26109</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Source</th>
<th>DF</th>
<th>Type I SS</th>
<th>Mean Square</th>
<th>F Value</th>
<th>Pr &gt; F</th>
</tr>
</thead>
<tbody>
<tr>
<td>FEEDTYPE</td>
<td>4</td>
<td>44775.19971</td>
<td>11193.79993</td>
<td>198.16</td>
<td>&lt;.0001</td>
</tr>
</tbody>
</table>

**Levene's Test for Homogeneity of MASSINKG Variance**
ANCOVA of Squared Deviations from Group Means

<table>
<thead>
<tr>
<th>Source</th>
<th>DF</th>
<th>Sum of Squares</th>
<th>Mean Square</th>
<th>F Value</th>
<th>Pr &gt; F</th>
</tr>
</thead>
<tbody>
<tr>
<td>FEEDTYPE</td>
<td>4</td>
<td>968597</td>
<td>242149</td>
<td>22.32</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>Error</td>
<td>245</td>
<td>2658377</td>
<td>10850.5</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

**Bonferroni (Dunn) t Tests for MASSINKG**

NOTE: This test controls the Type I experimentwise error rate, but it generally has a higher Type II error rate than REGWQ.

<table>
<thead>
<tr>
<th>Alpha</th>
<th>0.05</th>
</tr>
</thead>
<tbody>
<tr>
<td>Error Degrees of Freedom</td>
<td>245</td>
</tr>
<tr>
<td>Error Mean Square</td>
<td>56.49005</td>
</tr>
<tr>
<td>Critical Value of t</td>
<td>2.83268</td>
</tr>
<tr>
<td>Minimum Significant Difference</td>
<td>4.2581</td>
</tr>
</tbody>
</table>

Means with the same letter are not significantly different.

<table>
<thead>
<tr>
<th>Bon Grouping</th>
<th>Mean</th>
<th>N</th>
<th>FEEDTYPE</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>98.414</td>
<td>50</td>
<td>SUPERPIG</td>
</tr>
<tr>
<td>B</td>
<td>86.532</td>
<td>50</td>
<td>PORKER</td>
</tr>
<tr>
<td>C</td>
<td>73.090</td>
<td>50</td>
<td>SUUUEEE</td>
</tr>
<tr>
<td>C</td>
<td>69.495</td>
<td>50</td>
<td>HOGGIES</td>
</tr>
<tr>
<td>D</td>
<td>60.381</td>
<td>50</td>
<td>STDMIX</td>
</tr>
</tbody>
</table>
COMMENT THE FOLLOWING ILLUSTRATES THAT LEVENES TEST PERFORMS A ONE-WAY ANOVA ON THE DISPERSION VARIABLE CREATED ABOVE;

PROC GLM DATA=HOGFEED1;
  CLASS FEEDTYPE;
  MODEL DISP=FEEDTYPE;

The GLM Procedure

Class Level Information
Class         Levels    Values
FEEDTYPE           5    HOGGIES PORKER STDMIX SUPERPIG SUUUEEE

Number of observations 250

Dependent Variable: DISP

<table>
<thead>
<tr>
<th>Source</th>
<th>DF</th>
<th>Sum of Squares</th>
<th>Mean Square</th>
<th>F Value</th>
<th>Pr &gt; F</th>
<th>R-Square</th>
</tr>
</thead>
<tbody>
<tr>
<td>Model</td>
<td>4</td>
<td>968597.008</td>
<td>242149.252</td>
<td>22.32</td>
<td>&lt;.0001</td>
<td>0.267054</td>
</tr>
<tr>
<td>Error</td>
<td>245</td>
<td>2658377.007</td>
<td>10850.518</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Corrected Total</td>
<td>249</td>
<td>3626974.015</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Source</th>
<th>DF</th>
<th>Type I SS</th>
<th>Mean Square</th>
<th>F Value</th>
<th>Pr &gt; F</th>
</tr>
</thead>
<tbody>
<tr>
<td>FEEDTYPE</td>
<td>4</td>
<td>968597.0079</td>
<td>242149.2520</td>
<td>22.32</td>
<td>&lt;.0001</td>
</tr>
</tbody>
</table>
COMMENT THE FOLLOWING REPLACES THE MASS DATA WITH THEIR RANKS TO EXECUTE A KRUSKAL-WALLIS TEST;

PROC RANK DATA=HOGFEED OUT=RHOGFEED;
VAR MASSINKG;
RANKS RMASS;
PROC SORT DATA=RHOGFEED;
BY FEEDTYPE;
PROC GLM DATA=RHOGFEED;
CLASS FEEDTYPE;
MODEL RMASS=FEEDTYPE;
MEANS FEEDTYPE/BON LINES;

The GLM Procedure
Class Level Information

Class         Levels    Values
FEEDTYPE           5    HOGGIES PORKER STDMIX SUPERPIG SUUUEEE

Number of observations    250
Dependent Variable: RMASS  Rank for Variable MASSINKG

<table>
<thead>
<tr>
<th>Source</th>
<th>DF</th>
<th>Sum of Squares</th>
<th>Mean Square</th>
<th>F Value</th>
<th>Pr &gt; F</th>
<th>R-Square</th>
</tr>
</thead>
<tbody>
<tr>
<td>Model</td>
<td>4</td>
<td>1089219.680</td>
<td>272304.920</td>
<td>313.45</td>
<td>&lt;.0001</td>
<td>0.836534</td>
</tr>
<tr>
<td>Error</td>
<td>245</td>
<td>212842.820</td>
<td>868.746</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Corrected Total</td>
<td>249</td>
<td>1302062.500</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Source</th>
<th>DF</th>
<th>Type I SS</th>
<th>Mean Square</th>
<th>F Value</th>
<th>Pr &gt; F</th>
</tr>
</thead>
<tbody>
<tr>
<td>FEEDTYPE</td>
<td>4</td>
<td>1089219.680</td>
<td>272304.920</td>
<td>313.45</td>
<td>&lt;.0001</td>
</tr>
</tbody>
</table>

Bonferroni (Dunn) t Tests for RMASS

NOTE: This test controls the Type I experimentwise error rate, but it generally has a higher Type II error rate than REGWQ.

Alpha                              0.05
Error Degrees of Freedom            245
Error Mean Square              868.7462
Critical Value of t             2.83268
Minimum Significant Difference   16.698

Means with the same letter are not significantly different.

<table>
<thead>
<tr>
<th>Bon Grouping</th>
<th>Mean</th>
<th>N</th>
<th>FEEDTYPE</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>213.280</td>
<td>50</td>
<td>SUPERPIG</td>
</tr>
<tr>
<td>B</td>
<td>177.300</td>
<td>50</td>
<td>PORKER</td>
</tr>
<tr>
<td>C</td>
<td>124.880</td>
<td>50</td>
<td>SUUUEEE</td>
</tr>
<tr>
<td>D</td>
<td>85.520</td>
<td>50</td>
<td>HOGGIES</td>
</tr>
<tr>
<td>E</td>
<td>26.520</td>
<td>50</td>
<td>STDMIX</td>
</tr>
</tbody>
</table>
COMMENT THE FOLLOWING REORGANIZES THE DATA AS IF THE STUDY HAD BEEN DONE AS A RANDOMIZED COMPLETE BLOCK DESIGN;

DATA RCB; SET HOGFEED; BLOCK=I;
PROC PRINT DATA=RCB;
   VAR FEEDTYPE I BLOCK MASSINKG;
PROC SORT DATA=RCB;
   BY BLOCK;
PROC GLM DATA=RCB;
   CLASSES BLOCK FEEDTYPE;
   MODEL MASSINKG=BLOCK FEEDTYPE;
   MEANS FEEDTYPE/BON LINES;
   OUTPUT OUT=RCBNORM RESIDUAL=RESMASS;

Class Level Information

<table>
<thead>
<tr>
<th>Class</th>
<th>Levels</th>
<th>Values</th>
</tr>
</thead>
<tbody>
<tr>
<td>BLOCK</td>
<td>50</td>
<td>1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50</td>
</tr>
<tr>
<td>FEEDTYPE</td>
<td>5</td>
<td>HOGGIES PORKER STDMIX SUPERPIG SUUUEEE</td>
</tr>
</tbody>
</table>

Number of observations 250

Dependent Variable: MASSINKG

<table>
<thead>
<tr>
<th>Source</th>
<th>DF</th>
<th>Sum of Squares</th>
<th>Mean Square</th>
<th>F Value</th>
<th>Pr &gt; F</th>
<th>R-Square</th>
</tr>
</thead>
<tbody>
<tr>
<td>Model</td>
<td>53</td>
<td>47691.52182</td>
<td>899.84003</td>
<td>16.15</td>
<td>&lt;.0001</td>
<td>0.813637</td>
</tr>
<tr>
<td>Error</td>
<td>196</td>
<td>10923.73927</td>
<td>55.73336</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Corrected Total</td>
<td>249</td>
<td>58615.26109</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Source</th>
<th>DF</th>
<th>Type I SS</th>
<th>Mean Square</th>
<th>F Value</th>
<th>Pr &gt; F</th>
</tr>
</thead>
<tbody>
<tr>
<td>BLOCK</td>
<td>49</td>
<td>2916.32211</td>
<td>59.51678</td>
<td>1.07</td>
<td>0.3680</td>
</tr>
<tr>
<td>FEEDTYPE</td>
<td>4</td>
<td>44775.19971</td>
<td>11193.79993</td>
<td>200.85</td>
<td>&lt;.0001</td>
</tr>
</tbody>
</table>

Bonferroni (Dunn) t Tests for MASSINKG

NOTE: This test controls the Type I experimentwise error rate, ∝

Alpha 0.05
Error Degrees of Freedom 196
Error Mean Square 55.73336
Critical Value of t 2.83916
Minimum Significant Difference 4.2391

Means with the same letter are not significantly different.

<table>
<thead>
<tr>
<th>Bon Grouping</th>
<th>Mean</th>
<th>N</th>
<th>FEEDTYPE</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>98.414</td>
<td>50</td>
<td>SUPERPIG</td>
</tr>
<tr>
<td>B</td>
<td>86.532</td>
<td>50</td>
<td>PORKER</td>
</tr>
<tr>
<td>C</td>
<td>73.090</td>
<td>50</td>
<td>SUUUEEE</td>
</tr>
<tr>
<td>C</td>
<td>69.495</td>
<td>50</td>
<td>HOGGIES</td>
</tr>
<tr>
<td>D</td>
<td>60.381</td>
<td>50</td>
<td>STDMIX</td>
</tr>
</tbody>
</table>
COMMENT WANT TO EVALUATE WHETHER RESIDUALS ARE NORMALLY DISTRIBUTED AS A
TEST OF THE ASSUMPTION OF NORMALITY;
PROC UNIVARIATE NORMAL DATA=RCBNORM;
    HISTOGRAM RESMASS/NORMAL;
    VAR RESMASS;
PROC PLOT DATA=RCBNORM;
    PLOT RESMASS*FEEDTYPE;

The UNIVARIATE Procedure
Variable:  RESMASS

Moments

<table>
<thead>
<tr>
<th>Statistic</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>N</td>
<td>250</td>
</tr>
<tr>
<td>Mean</td>
<td>0</td>
</tr>
<tr>
<td>Std Deviation</td>
<td>6.62347634</td>
</tr>
<tr>
<td>Skewness</td>
<td>-0.1181504</td>
</tr>
<tr>
<td>Uncorrected SS</td>
<td>10923.7393</td>
</tr>
<tr>
<td>Coeff Variation</td>
<td>.</td>
</tr>
<tr>
<td>Variance</td>
<td>43.8704388</td>
</tr>
<tr>
<td>Kurtosis</td>
<td>1.37986628</td>
</tr>
<tr>
<td>Corrected SS</td>
<td>10923.7393</td>
</tr>
<tr>
<td>Std Error Mean</td>
<td>0.41890543</td>
</tr>
</tbody>
</table>

Tests for Normality

<table>
<thead>
<tr>
<th>Test</th>
<th>Statistic</th>
<th>p Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Shapiro-Wilk</td>
<td>W</td>
<td>0.977998</td>
</tr>
</tbody>
</table>

The histogram and probability plot show the distribution of the residuals.
PROC PLOT DATA=RCBNORM;
PLOT RESMASS*FEEDTYPE;

Plot of RESMASS*FEEDTYPE. Legend: A = 1 obs, B = 2 obs, etc.
COMMENT THE FOLLOWING RANKS THE OBSERVATIONS WITHIN EACH BLOCK AS A PRELUDE TO FRIEDMANS TEST;

PROC RANK DATA=RCB OUT=RCBRANKS;
   BY BLOCK;
   VAR MASSINKG;
   RANKS RBLOCK;
PROC PRINT DATA=RCBRANKS;
   VAR FEEDTYPE I BLOCK MASSINKG RBLOCK;

<table>
<thead>
<tr>
<th>Obs</th>
<th>FEEDTYPE</th>
<th>I</th>
<th>BLOCK</th>
<th>MASSINKG</th>
<th>RBLOCK</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>HOGGIES</td>
<td>1</td>
<td>1</td>
<td>66.472</td>
<td>2</td>
</tr>
<tr>
<td>2</td>
<td>PORKER</td>
<td>1</td>
<td>1</td>
<td>100.591</td>
<td>5</td>
</tr>
<tr>
<td>3</td>
<td>STDMIX</td>
<td>1</td>
<td>1</td>
<td>60.013</td>
<td>1</td>
</tr>
<tr>
<td>4</td>
<td>SUPERPIG</td>
<td>1</td>
<td>1</td>
<td>99.750</td>
<td>4</td>
</tr>
<tr>
<td>5</td>
<td>SUUUEEE</td>
<td>1</td>
<td>1</td>
<td>69.018</td>
<td>3</td>
</tr>
<tr>
<td>6</td>
<td>HOGGIES</td>
<td>2</td>
<td>2</td>
<td>63.416</td>
<td>2</td>
</tr>
<tr>
<td>7</td>
<td>PORKER</td>
<td>2</td>
<td>2</td>
<td>76.737</td>
<td>5</td>
</tr>
<tr>
<td>8</td>
<td>STDMIX</td>
<td>2</td>
<td>2</td>
<td>62.738</td>
<td>1</td>
</tr>
<tr>
<td>9</td>
<td>SUPERPIG</td>
<td>2</td>
<td>2</td>
<td>74.998</td>
<td>4</td>
</tr>
<tr>
<td>10</td>
<td>SUUUEEE</td>
<td>2</td>
<td>2</td>
<td>73.949</td>
<td>3</td>
</tr>
<tr>
<td>11</td>
<td>HOGGIES</td>
<td>3</td>
<td>3</td>
<td>71.998</td>
<td>2</td>
</tr>
<tr>
<td>12</td>
<td>PORKER</td>
<td>3</td>
<td>3</td>
<td>96.127</td>
<td>4</td>
</tr>
<tr>
<td>13</td>
<td>STDMIX</td>
<td>3</td>
<td>3</td>
<td>57.398</td>
<td>1</td>
</tr>
<tr>
<td>14</td>
<td>SUPERPIG</td>
<td>3</td>
<td>3</td>
<td>112.500</td>
<td>5</td>
</tr>
<tr>
<td>15</td>
<td>SUUUEEE</td>
<td>3</td>
<td>3</td>
<td>74.527</td>
<td>3</td>
</tr>
<tr>
<td>16</td>
<td>HOGGIES</td>
<td>4</td>
<td>4</td>
<td>67.848</td>
<td>2</td>
</tr>
<tr>
<td>17</td>
<td>PORKER</td>
<td>4</td>
<td>4</td>
<td>89.410</td>
<td>4</td>
</tr>
<tr>
<td>18</td>
<td>STDMIX</td>
<td>4</td>
<td>4</td>
<td>59.160</td>
<td>1</td>
</tr>
<tr>
<td>19</td>
<td>SUPERPIG</td>
<td>4</td>
<td>4</td>
<td>113.563</td>
<td>5</td>
</tr>
<tr>
<td>20</td>
<td>SUUUEEE</td>
<td>4</td>
<td>4</td>
<td>77.344</td>
<td>3</td>
</tr>
<tr>
<td>21</td>
<td>HOGGIES</td>
<td>5</td>
<td>5</td>
<td>67.979</td>
<td>2</td>
</tr>
<tr>
<td>22</td>
<td>PORKER</td>
<td>5</td>
<td>5</td>
<td>109.268</td>
<td>5</td>
</tr>
<tr>
<td>23</td>
<td>STDMIX</td>
<td>5</td>
<td>5</td>
<td>57.040</td>
<td>1</td>
</tr>
<tr>
<td>24</td>
<td>SUPERPIG</td>
<td>5</td>
<td>5</td>
<td>92.952</td>
<td>4</td>
</tr>
<tr>
<td>25</td>
<td>SUUUEEE</td>
<td>5</td>
<td>5</td>
<td>76.022</td>
<td>3</td>
</tr>
<tr>
<td>26</td>
<td>HOGGIES</td>
<td>6</td>
<td>6</td>
<td>68.249</td>
<td>2</td>
</tr>
<tr>
<td>27</td>
<td>PORKER</td>
<td>6</td>
<td>6</td>
<td>84.625</td>
<td>4</td>
</tr>
<tr>
<td>28</td>
<td>STDMIX</td>
<td>6</td>
<td>6</td>
<td>61.339</td>
<td>1</td>
</tr>
<tr>
<td>29</td>
<td>SUPERPIG</td>
<td>6</td>
<td>6</td>
<td>104.206</td>
<td>5</td>
</tr>
<tr>
<td>30</td>
<td>SUUUEEE</td>
<td>6</td>
<td>6</td>
<td>73.119</td>
<td>3</td>
</tr>
<tr>
<td>31</td>
<td>HOGGIES</td>
<td>7</td>
<td>7</td>
<td>68.741</td>
<td>2</td>
</tr>
<tr>
<td>32</td>
<td>PORKER</td>
<td>7</td>
<td>7</td>
<td>95.169</td>
<td>4</td>
</tr>
<tr>
<td>33</td>
<td>STDMIX</td>
<td>7</td>
<td>7</td>
<td>61.057</td>
<td>1</td>
</tr>
<tr>
<td>34</td>
<td>SUPERPIG</td>
<td>7</td>
<td>7</td>
<td>98.940</td>
<td>5</td>
</tr>
<tr>
<td>35</td>
<td>SUUUEEE</td>
<td>7</td>
<td>7</td>
<td>69.605</td>
<td>3</td>
</tr>
<tr>
<td>36</td>
<td>HOGGIES</td>
<td>8</td>
<td>8</td>
<td>67.917</td>
<td>2</td>
</tr>
<tr>
<td>37</td>
<td>PORKER</td>
<td>8</td>
<td>8</td>
<td>103.666</td>
<td>4</td>
</tr>
<tr>
<td>38</td>
<td>STDMIX</td>
<td>8</td>
<td>8</td>
<td>59.412</td>
<td>1</td>
</tr>
<tr>
<td>39</td>
<td>SUPERPIG</td>
<td>8</td>
<td>8</td>
<td>113.272</td>
<td>5</td>
</tr>
<tr>
<td>40</td>
<td>SUUUEEE</td>
<td>8</td>
<td>8</td>
<td>72.955</td>
<td>3</td>
</tr>
<tr>
<td>41</td>
<td>HOGGIES</td>
<td>9</td>
<td>9</td>
<td>67.415</td>
<td>2</td>
</tr>
<tr>
<td>42</td>
<td>PORKER</td>
<td>9</td>
<td>9</td>
<td>104.332</td>
<td>4</td>
</tr>
<tr>
<td>43</td>
<td>STDMIX</td>
<td>9</td>
<td>9</td>
<td>61.047</td>
<td>1</td>
</tr>
<tr>
<td>44</td>
<td>SUPERPIG</td>
<td>9</td>
<td>9</td>
<td>116.173</td>
<td>5</td>
</tr>
<tr>
<td>45</td>
<td>SUUUEEE</td>
<td>9</td>
<td>9</td>
<td>74.883</td>
<td>3</td>
</tr>
<tr>
<td>46</td>
<td>HOGGIES</td>
<td>10</td>
<td>10</td>
<td>71.837</td>
<td>2</td>
</tr>
<tr>
<td>47</td>
<td>PORKER</td>
<td>10</td>
<td>10</td>
<td>94.088</td>
<td>4</td>
</tr>
<tr>
<td>48</td>
<td>STDMIX</td>
<td>10</td>
<td>10</td>
<td>59.736</td>
<td>1</td>
</tr>
<tr>
<td>49</td>
<td>SUPERPIG</td>
<td>10</td>
<td>10</td>
<td>102.729</td>
<td>5</td>
</tr>
</tbody>
</table>
| 50  | SUUUEEE  | 10| 10    | 73.331   | 3      | etc_T.
COMMENT  CARRY OUT FRIENDMANS TEST;
PROC SORT DATA=RCBRANKS;
   BY FEEDTYPE;
PROC GLM DATA=RCBRANKS;
   CLASS FEEDTYPE;
   MODEL RBLOCK=FEEDTYPE;
   MEANS FEEDTYPE/BON LINES;

   Class Level Information

   Class         Levels    Values
   FEEDTYPE           5    HOGGIES PORKER STDMIX SUPERPIG SUUUEEE

   Number of observations  250

   Dependent Variable: RBLOCK  Rank for Variable MASSING

   Sum of
   Source                     DF        Squares    Mean Square   F Value     Pr > F     R-Square
   Model                       4    432.7200000    108.1800000    393.94     <.0001     0.865440
   Error                     245     67.2800000      0.2746122
   Corrected Total           249    500.0000000

   Source                     DF      Type I SS    Mean Square   F Value     Pr > F
   FEEDTYPE                    4    432.7200000    108.1800000    393.94     <.0001

   Bonferroni (Dunn) t Tests for RBLOCK

   NOTE: This test controls the Type I experimentwise error rate, Ï„.

   Alpha                              0.05
   Error Degrees of Freedom            245
   Error Mean Square                   0.274612
   Critical Value of t                 2.83268
   Minimum Significant Difference      0.2969

   Means with the same letter are not significantly different.

   Bon Grouping       Mean      N    FEEDTYPE
   A        4.7600     50    SUPERPIG
   B        3.9800     50    PORKER
   C        3.0600     50    SUUUEEE
   D        2.1800     50    HOGGIES
   E        1.0200     50    STDMIX