# Week 7.2--IES 612-STA 4-573-STA 4-576.doc

**IES 612/STA 4-573/STA 4-576 Winter 2009**

## Multiple Comparisons

Suppose you reject the overall hypothesis $H_0$: $\mu_1 = \mu_2 = \mu_3 = \ldots = \mu_t$

What next? Which means differ?

Linear combination: $\ell = \sum_{i=1}^{t} a_i\mu_i$ which is estimated by $\hat{\ell} = \sum_{i=1}^{t} a_i\bar{y}_i$. This linear combination is called a CONTRAST if $\sum_{i=1}^{t} a_i = 0$

Suppose t=4 populations

Example 1: The contrast for comparing two means, $\mu_1 = \mu_2$, is the contrast of the difference of the two means, $\mu_1 - \mu_2$, $\ell = \sum_{i=1}^{t} a_i\mu_i = (1)\mu_1 + (-1)\mu_2 + (0)\mu_3 + (0)\mu_4$

Example 2: Contrast for comparing the mean of one population with the average of two other population means $\frac{\mu_1 + \mu_2}{2} = \mu_3$. This can be written as a the contrast

$$\ell = \sum_{i=1}^{t} a_i\mu_i = (-1)\mu_1 + (-1)\mu_2 + (2)\mu_3 + (0)\mu_4 = (-\frac{1}{2})\mu_1 + (-\frac{1}{2})\mu_2 + (1)\mu_3 + (0)\mu_4$$

You can test hypotheses about contrasts.

$H_0$: $\ell = \sum_{i=1}^{t} a_i\mu_i = 0$

$H_a$: $\ell = \sum_{i=1}^{t} a_i\mu_i \neq 0$

TS: $F_{obs} = \frac{SSC}{MSE}$ where $SSC = \frac{\hat{\ell}^2}{\sum_{i=1}^{t} a_i^2 / n_i}$ with p-value = $Pr(F_{1,n_T-t} > F_{obs})$

Two contrasts: $\ell_1 = \sum_{i=1}^{t} a_i\mu_i$ and $\ell_2 = \sum_{i=1}^{t} b_i\mu_i$ are ORTHOGONAL if $\sum_{i=1}^{t} \frac{a_i b_i}{n_i} = 0$

Treatment SS can be partitioned into t-1 mutually orthogonal contrasts

## Example: The Meat study with using logCounts

## Using R

Consider the following contrasts:

1. Compare the mean log Bacteria count for $CO_2$ to the mean log Bacteria count for the plastic condition.

   What would this contrast look like?

2. Compare the mean log Bacteria count for $CO_2$ to the mean log Bacteria count for the mixed condition.

   What would this contrast look like?

3. Compare the mean log Bacteria count for $CO_2$ to the mean log Bacteria count for the vacuum condition.

   What would this contrast look like?

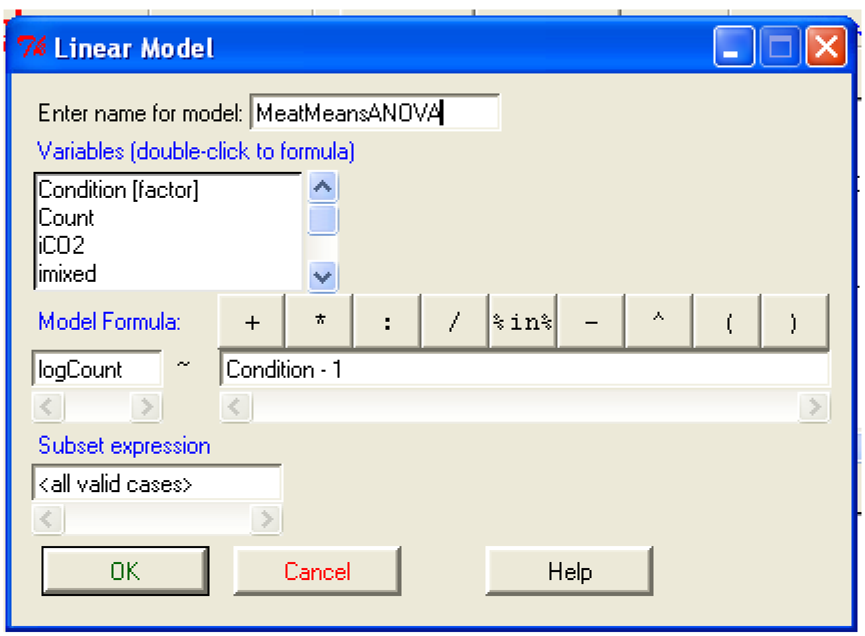
4. Compare the mean log Bacteria count for plastic to the average mean log Bacteria count for the other three conditions.

What would this contrast look like?

OK, so how do we do this on R? We first need to fit the Means Model, so:

With ***MeatBacteria*** the active data set, using RCommander:

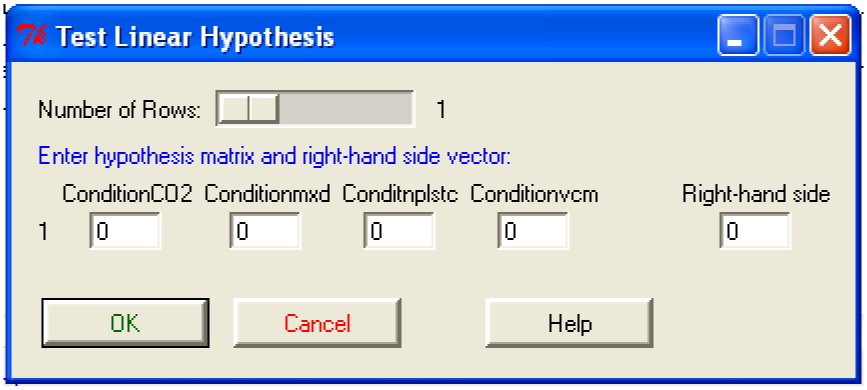
**Statistics > Fit Models > Linear model ...**




Now we can obtain contrasts of the means using this Means model.

With ***MeatMeansANOVA*** the active model, using RCommander:

**Models > Hypothesis tests > Linear hypothesis ...**

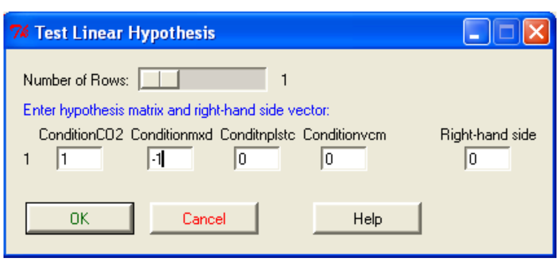



For each of the four contrasts we just plug in the constants as follows.

The four contrasts of interest were:

1. Compare the mean log Bacteria count for CO2 to the mean log Bacteria count for the plastic condition.

   this contrast was: $\ell_1 = +1^*\mu_{CO2} + -1^*\mu_{plas} + 0^*\mu_{mixed} + 0^*\mu_{vac} = 0$.

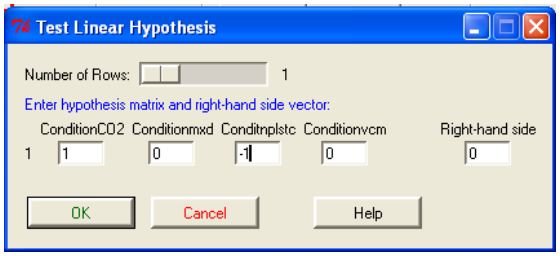



```
> linear.hypothesis(MeatMeansANOVA, .Hypothesis,
rhs=.RHS)
Linear hypothesis test

Hypothesis:
ConditionCO2 - Conditionmixed = 0

Model 1: logCount ~ Condition - 1
Model 2: restricted model

  Res.Df     RSS Df Sum of Sq      F    Pr(>F)
1      8  0.9268
2      9 23.7418 -1  -22.8150 196.94 6.451e-07 ***
---
```

Conclusion?

2. Compare the mean log Bacteria count for CO2 to the mean log Bacteria count for the mixed condition.

   this contrast was: $\ell_2 = +1^*\mu_{CO2} + 0^*\mu_{plas} + -1^*\mu_{mixed} + 0^*\mu_{vac} = 0$.

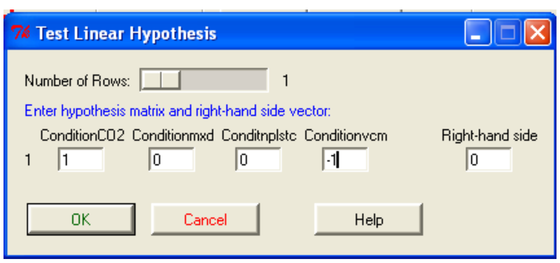



```
> linear.hypothesis(MeatMeansANOVA, .Hypothesis,
rhs=.RHS)
Linear hypothesis test

Hypothesis:
ConditionCO2 - Conditionplastic = 0

Model 1: logCount ~ Condition - 1
Model 2: restricted model

  Res.Df     RSS Df Sum of Sq      F    Pr(>F)
1      8  0.9268
2      9 26.3884 -1  -25.4616 219.78 4.22e-07 ***
```

Conclusion?

3. Compare the mean log Bacteria count for CO2 to the mean log Bacteria count for the vacuum condition.

   this contrast was: $\ell_3 = +1^*\mu_{CO2} + 0^*\mu_{plas} + 0^*\mu_{mixed} + -1^*\mu_{vac} = 0$.

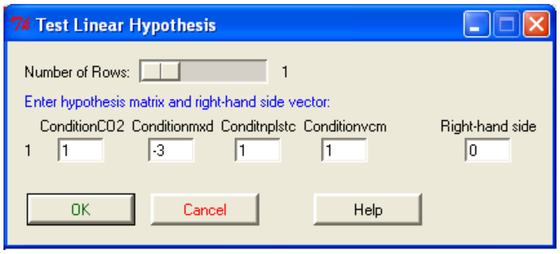



```
> linear.hypothesis(MeatMeansANOVA, .Hypothesis,
rhs=.RHS)
Linear hypothesis test

Hypothesis:
ConditionCO2 - Conditionvacuum = 0

Model 1: logCount ~ Condition - 1
Model 2: restricted model

  Res.Df    RSS Df Sum of Sq      F    Pr(>F)
1      8 0.9268
2      9 7.7962 -1   -6.8694 59.296 5.742e-05 ***
---
```

Conclusion?

4. Compare the mean log Bacteria count for plastic to the average mean log Bacteria count for the other three conditions.

this contrast was: $\ell_4 = +1^*\mu_{CO2} + -3^*\mu_{plas} + 1^*\mu_{mixed} + 1^*\mu_{vac} = 0$.




```
> linear.hypothesis(MeatMeansANOVA, .Hypothesis,
rhs=.RHS)
Linear hypothesis test

Hypothesis:
ConditionCO2 - 3 Conditionmixed + Conditionplastic +
Conditionvacuum = 0

Model 1: logCount ~ Condition - 1
Model 2: restricted model

  Res.Df     RSS Df Sum of Sq      F    Pr(>F)
1      8  0.9268
2      9  8.3252 -1   -7.3984 63.862 4.401e-05 ***
```

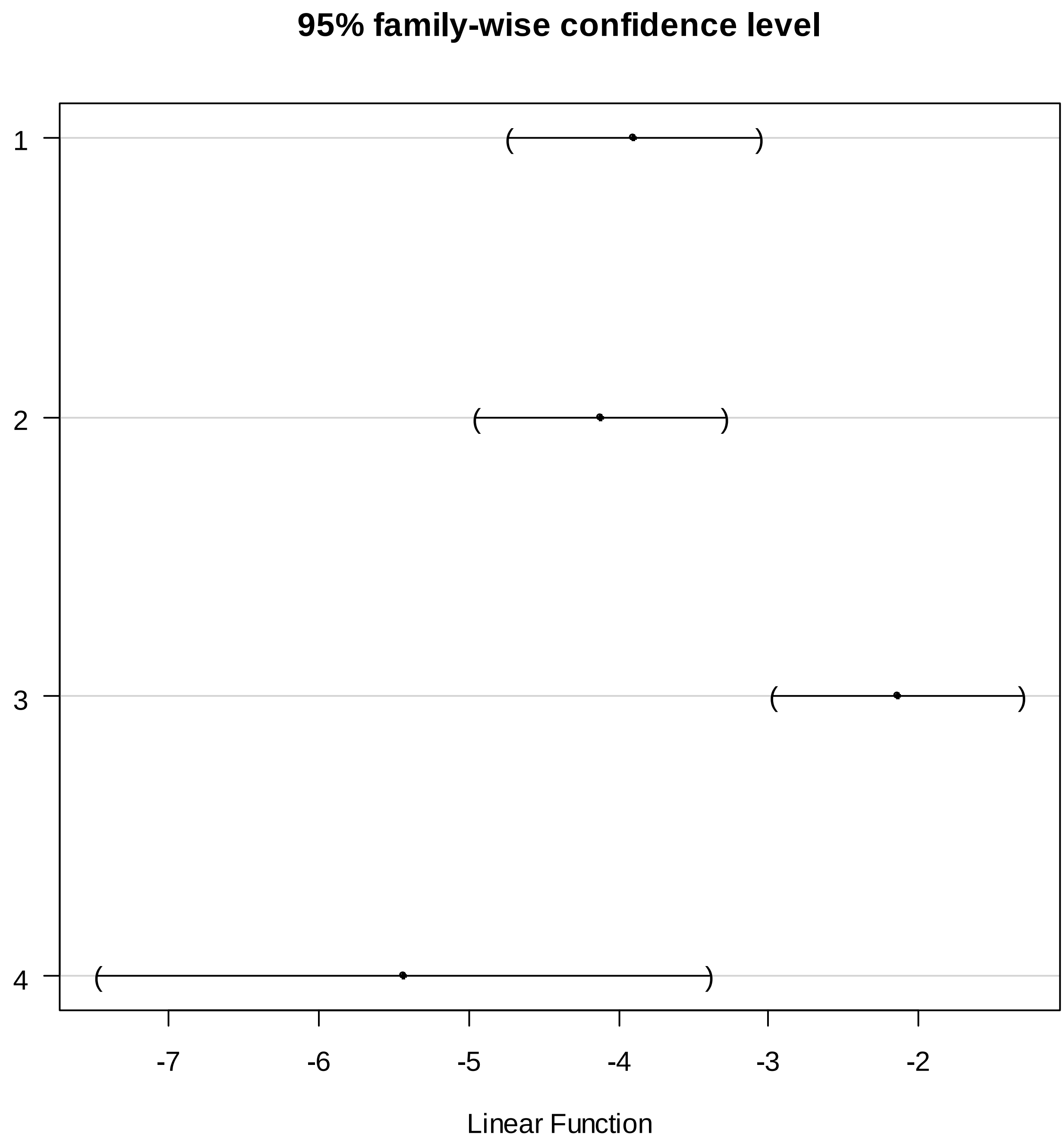
Conclusion?

Can we obtain estimates and CI's for these contrasts using R?

```
> library(multcomp)
Loading required package: mvtnorm
> glht(MeatMeansANOVA, linfct=matrix(c(1, -1, 0 , 0,
+                                       1, 0, -1, 0,
+                                       1, 0, 0, -1,
+                                       1, -3, 1, 1), byrow=TRUE, ncol=4))

         General Linear Hypotheses

Linear Hypotheses:
       Estimate
1 == 0    -3.90
2 == 0    -4.12
3 == 0    -2.14
4 == 0    -5.44
> summary(glht(MeatMeansANOVA, linfct=matrix(c(1, -1, 0 , 0,
+                                             1, 0, -1, 0,
+                                             1, 0, 0, -1,
+                                             1, -3, 1, 1), byrow=TRUE, ncol=4)))

         Simultaneous Tests for General Linear Hypotheses

Fit: lm(formula = logCount ~ Condition - 1, data = MeatBacteria)

Linear Hypotheses:
       Estimate Std. Error t value p value
1 == 0  -3.9000     0.2779 -14.033  <0.001 ***
2 == 0  -4.1200     0.2779 -14.825  <0.001 ***
3 == 0  -2.1400     0.2779  -7.700  <0.001 ***
4 == 0  -5.4400     0.6807  -7.991  <0.001 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
(Adjusted p values reported)
```

And a plot of these contrast estimates and CI's is

```
> plot(glht(MeatMeansANOVA, linfct=matrix(c(1, -1, 0 , 0,
+                                           1, 0, -1, 0,
+                                           1, 0, 0, -1,
+                                           1, -3, 1, 1), byrow=TRUE, ncol=4)))
```



## Using SAS

```
title “One-way ANOVA/ CRD example + contrasts”;
title2 “Bacteria in meat data”;
data meat;
  input condition $ logcount @@;
  datalines;
plastic 7.66 plastic 6.98 plastic 7.80
 vacuum 5.26  vacuum 5.44  vacuum 5.80
  mixed 7.41   mixed 7.33   mixed 7.04
    CO2 3.51     CO2 2.91     CO2 3.66
;
*  ORDER=DATA says plastic < vacuum < mixed < CO2 in Labels otherwise sorts
proc glm data=meat order=data;
  class condition;
  model logcount=condition;
  output out=new p=yhat r=resid;
  contrast 'plastic vs. rest' condition 3 -1 -1 -1;
  estimate 'plastic vs. rest' condition 3 -1 -1 -1;
  contrast 'CO2 vs. plastic'  condition -1  0  0 1;
  estimate 'CO2 vs. plastic'  condition -1  0  0 1;
  contrast 'CO2 vs. vacuum'   condition  0 -1  0 1;
  estimate 'CO2 vs. vacuum'   condition  0 -1  0 1;
  contrast 'CO2 vs. mixed'    condition  0  0 -1 1;
  estimate 'CO2 vs. mixed'    condition  0  0 -1 1;
  run;
```

```
* output (edited)
The GLM Procedure
Dependent Variable: logcount
                                          Sum of
Source                      DF           Squares     Mean Square    F Value    Pr > F
Model                        3       32.87280000     10.95760000      94.58    <.0001
Error                        8        0.92680000      0.11585000
Corrected Total             11       33.79960000

R-Square      Coeff Var      Root MSE     logcount Mean
0.972580       5.768940      0.340367          5.900000

Source                      DF       Type I SS     Mean Square    F Value    Pr > F
condition                      3      32.87280000     10.95760000      94.58    <.0001

Source                      DF     Type III SS     Mean Square    F Value    Pr > F
condition                      3      32.87280000     10.95760000      94.58    <.0001

Contrast                    DF     Contrast SS     Mean Square    F Value    Pr > F
plastic vs. rest             1      9.98560000      9.98560000      86.19    <.0001
CO2 vs. plastic              1     25.46160000     25.46160000     219.78    <.0001
CO2 vs. vacuum               1      6.86940000      6.86940000      59.30    <.0001
CO2 vs. mixed                1     22.81500000     22.81500000     196.94    <.0001


Dependent Variable: logcount

                                                Standard
Parameter                   Estimate               Error     t Value     Pr > |t|
plastic vs. rest          6.32000000          0.68073490        9.28       <.0001
CO2 vs. plastic          -4.12000000          0.27790886      -14.83       <.0001
CO2 vs. vacuum           -2.14000000          0.27790886       -7.70       <.0001
CO2 vs. mixed            -3.90000000          0.27790886      -14.03       <.0001
```

## Individual versus Experimentwise Error Rates

$\alpha_I$ = **Individual** Type I error rate

= Pr(Type I Error on a PARTICULAR comparison)

$\alpha_E$ =**Experimentwise** Type I error rate

= Pr(at least one Type I error when conducting a collection of comparisons)

If you have "m" independent comparisons, $\alpha_E = 1 - (1 - \alpha_I)^m$

So, $\alpha_E$ increases with the number of comparisons.

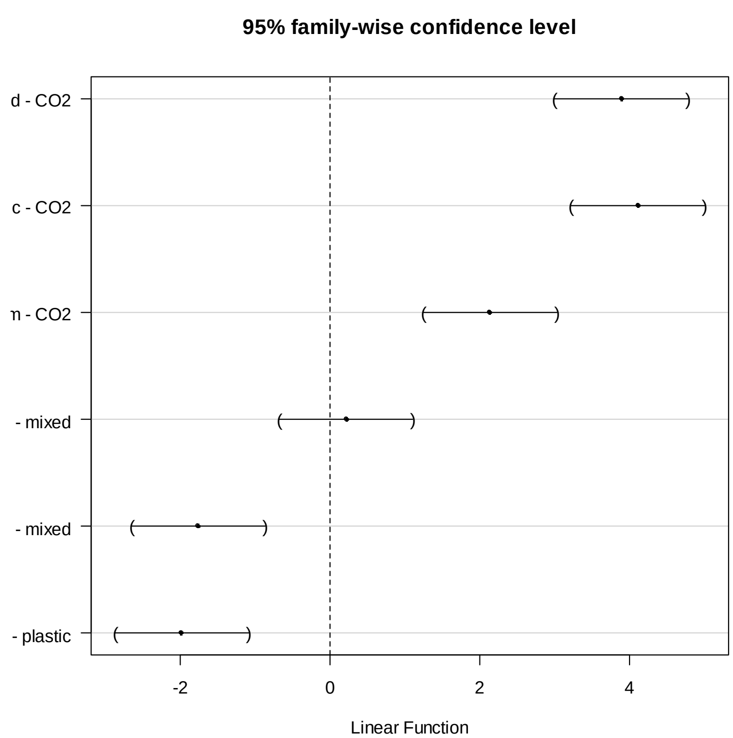
Bonferroni inequality: $\alpha_E \le m\, \alpha_I$ so …
set $\alpha_I = \alpha_E / m$ for individual tests to protect overall at fixed $\alpha_E$

| Procedure | | |
|---|---|---|
| Bonferroni | t-based with Bonferroni adjustment for $\alpha_I$ | |
| Fisher's LSD | t-based ("protected" if require overall F to reject first) | -MCA |
| Tukey's HSD | Based on Studentized Range distribution - | -MCA<br>-Can also form simultaneous CIs<br>- harmonic mean often substituted if $n_i$ not same |
| Dunnett's Procedure | Comparing all groups to control (i.e. "t-1" comparisons) | -MCC |
| Scheffe' S | General procedure for comparing all possible contrasts | |

## Example: The Meat study with using logCounts

## Using R

```
> library(multcomp)
Loading required package: mvtnorm
> confint(MeatANOVA)
                          2.5 %   97.5 %
(Intercept)          2.906844 3.813156
Condition[T.mixed]   3.259141 4.540859
Condition[T.plastic] 3.479141 4.760859
Condition[T.vacuum]  1.499141 2.780859
> print(confint(glht(MeatANOVA, linfct=mcp(Condition="Tukey"))))

         Simultaneous Confidence Intervals for General Linear Hypotheses

Multiple Comparisons of Means: Tukey Contrasts


Fit: lm(formula = logCount ~ Condition, data = MeatData)

Estimated Quantile = 3.2024

Linear Hypotheses:
                      Estimate lwr     upr
mixed - CO2 == 0       3.9000   3.0100  4.7900
plastic - CO2 == 0     4.1200   3.2300  5.0100
vacuum - CO2 == 0      2.1400   1.2500  3.0300
plastic - mixed == 0   0.2200  -0.6700  1.1100
vacuum - mixed == 0   -1.7600  -2.6500 -0.8700
vacuum - plastic == 0 -1.9800  -2.8700 -1.0900

95% family-wise confidence level

> plot(print(confint(glht(MeatANOVA, linfct=mcp(Condition="Tukey")))))
```



## Using SAS

```
title “One-way ANOVA/ CRD example + contrasts”;
title2 “Bacteria in meat data”;
data meat;
  input condition $ logcount @@;
  datalines;
plastic 7.66 plastic 6.98 plastic 7.80
 vacuum 5.26  vacuum 5.44  vacuum 5.80
  mixed 7.41   mixed 7.33   mixed 7.04
    CO2 3.51     CO2 2.91     CO2 3.66
;
/*
  ORDER=DATA says plastic < vacuum < mixed < CO2 in
             Labels otherwise sorts
*/
proc glm data=meat order=data;
  class condition;
  model logcount=condition;
  lsmeans condition / stderr pdiff;
  means condition / lsd clm;                      * Fisher LSD;
  means condition / bon scheffe tukey;  * Bonferroni, Scheffe, Tukey;
    means condition / bon tukey cldiff;      * pairwise CIs generated;
  run;
```

```
The GLM Procedure
Least Squares Means

               logcount        Standard                        LSMEAN
condition         LSMEAN          Error     Pr > |t|       Number
plastic      7.48000000     0.19651124     <.0001            1
vacuum       5.50000000     0.19651124     <.0001            2
mixed        7.26000000     0.19651124     <.0001            3
CO2          3.36000000     0.19651124     <.0001            4

           Least Squares Means for effect condition
            Pr > |t| for H0: LSMean(i)=LSMean(j)
                Dependent Variable: logcount
i/j              1             2             3             4
   1                       <.0001        0.4514        <.0001
   2        <.0001                       0.0002        <.0001
   3        0.4514        0.0002                       <.0001
   4        <.0001        <.0001        <.0001

NOTE: To ensure overall protection level, only probabilities associated with pre-planned comparisons should be
used

t Confidence Intervals for logcount

Alpha                                  0.05
Error Degrees of Freedom                  8
Error Mean Square                   0.11585
Critical Value of t                 2.30600
Half Width of Confidence Interval 0.453156

                                      95% Confidence
condition          N          Mean            Limits
plastic          3        7.4800       7.0268       7.9332
mixed            3        7.2600       6.8068       7.7132
vacuum           3        5.5000       5.0468       5.9532
CO2              3        3.3600       2.9068       3.8132
```

```
means condition / bon scheffe tukey;
```

## Tukey's Studentized Range (HSD) Test for logcount

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 | 8 |
| Error Mean Square | 0.11585 |
| Critical Value of Studentized Range | 4.52880 |
| Minimum Significant Difference | 0.89 |

Means with the same letter are not significantly different.

| | Mean | N | condition |
|---|---|---|---|
| A | 7.4800 | 3 | plastic |
| A | | | |
| A | 7.2600 | 3 | mixed |
| B | 5.5000 | 3 | vacuum |
| C | 3.3600 | 3 | CO2 |

## Bonferroni (Dunn) t Tests for logcount

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 | 8 |
| Error Mean Square | 0.11585 |
| Critical Value of t | 3.47888 |
| Minimum Significant Difference | 0.9668 |

Means with the same letter are not significantly different.

| | Mean | N | condition |
|---|---|---|---|
| A | 7.4800 | 3 | plastic |
| A | | | |
| A | 7.2600 | 3 | mixed |
| B | 5.5000 | 3 | vacuum |
| C | 3.3600 | 3 | CO2 |

## Scheffe's Test for logcount

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

| | |
|---|---|
| Alpha | 0.05 |
| Error Degrees of Freedom | 8 |
| Error Mean Square | 0.11585 |
| Critical Value of F | 4.06618 |
| Minimum Significant Difference | 0.9706 |

Means with the same letter are not significantly different.

| | Mean | N | condition |
|---|---|---|---|
| A | 7.4800 | 3 | plastic |
| A | | | |
| A | 7.2600 | 3 | mixed |

| | | | |
|---|---|---|---|
| B | 5.5000 | 3 | vacuum |
| C | 3.3600 | 3 | CO |

```
means condition / bon tukey cldiff;
```

## Tukey's Studentized Range (HSD) Test for logcount

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

| | |
|---|---|
| Alpha | 0.05 |
| Error Degrees of Freedom | 8 |
| Error Mean Square | 0.11585 |
| Critical Value of Studentized Range | 4.52880 |
| Minimum Significant Difference | 0.89 |

Comparisons significant at the 0.05 level are indicated by ***.

| condition Comparison | Difference Between Means | Simultaneous 95% Confidence Limits | | |
|---|---|---|---|---|
| plastic - mixed | 0.2200 | -0.6700 | 1.1100 | |
| plastic - vacuum | 1.9800 | 1.0900 | 2.8700 | *** |
| plastic - CO2 | 4.1200 | 3.2300 | 5.0100 | *** |
| mixed - plastic | -0.2200 | -1.1100 | 0.6700 | |
| mixed - vacuum | 1.7600 | 0.8700 | 2.6500 | *** |
| mixed - CO2 | 3.9000 | 3.0100 | 4.7900 | *** |
| vacuum - plastic | -1.9800 | -2.8700 | -1.0900 | *** |
| vacuum - mixed | -1.7600 | -2.6500 | -0.8700 | *** |
| vacuum - CO2 | 2.1400 | 1.2500 | 3.0300 | *** |
| CO2 - plastic | -4.1200 | -5.0100 | -3.2300 | *** |
| CO2 - mixed | -3.9000 | -4.7900 | -3.0100 | *** |
| CO2 - vacuum | -2.1400 | -3.0300 | -1.2500 | ** |

## Bonferroni (Dunn) t Tests for logcount

NOTE: This test controls the Type I experimentwise error rate, but it generally has a higher Type II error rate than Tukey's for all pairwise comparisons.

| | |
|---|---|
| Alpha | 0.05 |
| Error Degrees of Freedom | 8 |
| Error Mean Square | 0.11585 |
| Critical Value of t | 3.47888 |
| Minimum Significant Difference | 0.9668 |

Comparisons significant at the 0.05 level are indicated by ***.

| condition Comparison | Difference Between Means | Simultaneous 95% Confidence Limits | | |
|---|---|---|---|---|
| plastic - mixed | 0.2200 | -0.7468 | 1.1868 | |
| plastic - vacuum | 1.9800 | 1.0132 | 2.9468 | *** |
| plastic - CO2 | 4.1200 | 3.1532 | 5.0868 | *** |
| mixed - plastic | -0.2200 | -1.1868 | 0.7468 | |
| mixed - vacuum | 1.7600 | 0.7932 | 2.7268 | *** |
| mixed - CO2 | 3.9000 | 2.9332 | 4.8668 | *** |
| vacuum - plastic | -1.9800 | -2.9468 | -1.0132 | *** |
| vacuum - mixed | -1.7600 | -2.7268 | -0.7932 | *** |
| vacuum - CO2 | 2.1400 | 1.1732 | 3.1068 | *** |
| CO2 - plastic | -4.1200 | -5.0868 | -3.1532 | *** |
| CO2 - mixed | -3.9000 | -4.8668 | -2.9332 | *** |
| CO2 - vacuum | -2.1400 | -3.1068 | -1.1732 | *** |