Displays for Statistics 5303

Lecture 18

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Class Web Page

http://www.stat.umn.edu/~kb/classes/5303

I entered coefficients for the terms in a 5 by 4 factorial model with interaction.

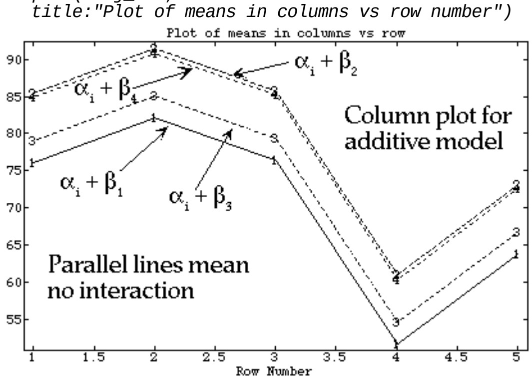
```
Cmd> print(mu,alpha,beta,alphabeta) # print coefficients
mu:
(1)         75.3
alpha:     A main effects
(1)         6.1        12.1         6.4       -18.4        -6.2
beta:      B main effects
(1)        -5.3         4.1        -2.3         3.5
alphabeta: AB interaation effects
(1,1)        7.2        -1.8         1.4        -6.8
(2,1)        1.9        -0.9         0.4        -1.4
(3,1)       -2.6           1           3        -1.4
(4,1)       -2.7        -4.6        -6.8        14.1
(5,1)       -3.8         6.3           2        -4.5

Cmd> muij_add <- mu + alpha + beta'; muij_add
(1,1)       76.1        85.5        79.1        84.9
(2,1)       82.1        91.5        85.1        90.9
(3,1)       76.4        85.8        79.4        85.2
(4,1)       51.6          61        54.6        60.4
(5,1)       63.8        73.2        66.8        72.6
```

These are the means for the model $\mu_{ij} = \mu + \alpha_i + \beta_j$, without interaction. It is said to be *additive* since the effects for A and B operate additively.

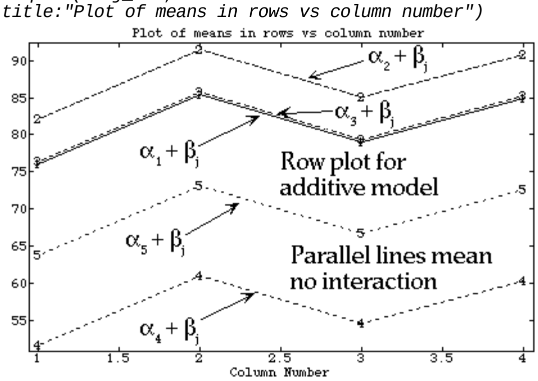
```
Cmd> muij_full <- muij + alphabeta; muij_full# full model
(1,1)       83.3        83.7        80.5        78.1
(2,1)         84        90.6        85.5        89.5
(3,1)       73.8        86.8        82.4        83.8
(4,1)       48.9        56.4        47.8        74.5
(5,1)         60        79.5        68.8        68.1
```

These are the means for the **full** model $\mu_{ij} = \mu + \alpha_i + \beta_j + \alpha\beta_{ij}$, *with* interaction.

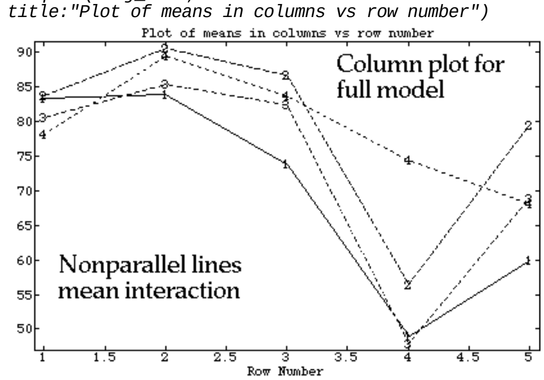

```
Cmd> colplot(muij_add,\
      title:"Plot of means in columns vs row number")
```



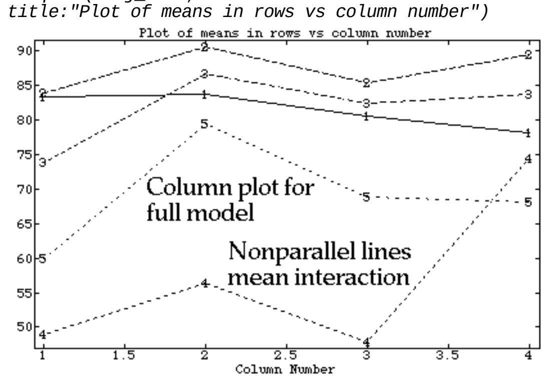

```
Cmd> rowplot(muij_add,\
      title:"Plot of means in rows vs column number")
```




```
Cmd> colplot(muij_full,\
      title:"Plot of means in columns vs row number")
```




```
Cmd> rowplot(muij_full,\
      title:"Plot of means in rows vs column number")
```



What would it mean for factor B to have *no* effect? The no B effect model is

$y_{ijk} = \mu + \alpha_i + \varepsilon_{ijk}$ (no β_j, no $\alpha\beta_{ij}$)

That is, in general, the null hypothesis that factor B has no effect means *both*

$\beta_j = 0$, $j = 1,\ldots,b$

and

$\alpha\beta_{ij} = 0$, $i = 1, \ldots a$, $j = 1,\ldots,b$

There is no B main effect or AB interaction.

Similarly, A has no effect only when

$\alpha_i = 0$, $i = 1,\ldots,a$ *and* $\alpha\beta_{ij} = 0$, all i, j

Conclusion:

When you cannot reject H_0: $\alpha\beta_{ij} = 0$, you can conclude that *both* A and B have *some* effect, regardless of whether you can reject either H_0: $\alpha_i = 0$, all i, or H_0: $\beta_j = 0$, all j.

Q. When does $\alpha_1 = \ldots = \alpha_a = 0$ imply that A has no effect?

A. When there is no interaction.

One of the advantages of having no interaction is easier interpretation of the ANOVA. You can base inference about the effects of A or B solely on the main effect lines and main effect contrasts.

No interaction means that any A-contrast has the same value for all levels of B and any B contrast has the same value for all levels of A.

```
Cmd> w_a <- vector(1/3,1/3,1/3,-1/2,-1/2) # Contrast in A
Cmd> w_b <- vector(-3,-1,1,3)            # Contrast in B
```

Contrast is the same for every level of B

```
Cmd> sum(w_a*muij_add) # values for each level of B
(1,1)      20.5      20.5      20.5      20.5
```

Contrast is the same for every level of A

```
Cmd> sum(w_b*muij_add') # note the transpose
(1,1)        20        20        20        20        20
```


But for the full, non-additive model with interaction, the A-contrast has a different value for each level of B:

```
Cmd> sum(w_a*muij_full)
(1,1)    25.917    19.083      24.5      12.5
```

and the B-contrast has a different value for each level of A:

```
Cmd> sum(w_b*muij_full')
(1,1)     -18.8      11.4      25.6      68.2      13.6
```

In particular, when there is no interaction, a pairwise contrast in A (comparison of two levels) is the same for all levels of B. That means you can think of *the* difference between, say, A_1 and A_2. When there is interaction, this may vary depending on the level of B.

When there is interaction, the effect of level i of A at level j of B is $\alpha_i + \alpha\beta_{ij}$. This depends on the particular level of B.

```
Cmd> alpha + alphabeta # effects of A
(1,1)      13.3       4.3       7.5      -0.7
(2,1)        14      11.2      12.5      10.7
(3,1)       3.8       7.4       9.4         5
(4,1)     -21.1       -23     -25.2      -4.3
(5,1)       -10       0.1      -4.2     -10.7
```

Each column sums to 0 over the levels of B.

Similarly there is interaction, the effect of level j of B at level i of A is $\beta_j + \alpha\beta_{ij}$. This depends on the particular level of B.

```
Cmd> beta' + alphabeta # effects of B
(1,1)       1.9       2.3      -0.9      -3.3
(2,1)      -3.4       3.2      -1.9       2.1
(3,1)      -7.9       5.1       0.7       2.1
(4,1)        -8      -0.5      -9.1      17.6
(5,1)      -9.1      10.4      -0.3        -1
```

But when there is no interaction, you can speak of *the* effects $\{\alpha_i\}$ of A because the effects of A are the same at every level of B.

```
Cmd> alpha + 0*alphabeta # effects of B when no interaction
(1,1)          6.1          6.1          6.1          6.1
(2,1)         12.1         12.1         12.1         12.1
(3,1)          6.4          6.4          6.4          6.4
(4,1)        -18.4        -18.4        -18.4        -18.4
(5,1)         -6.2         -6.2         -6.2         -6.2
```

(Multiplying **alphabeta** by 0 sets all interactions to 0).

Similarly, with no interaction, $\{\beta_j\}$ are *the* effects of B which are the same at every level of A

```
Cmd> beta' + 0*alphabeta # effects of B when no interaction
(1,1)         -5.3          4.1         -2.3          3.5
(2,1)         -5.3          4.1         -2.3          3.5
(3,1)         -5.3          4.1         -2.3          3.5
(4,1)         -5.3          4.1         -2.3          3.5
(5,1)         -5.3          4.1         -2.3          3.5
```


Example from Snedecor and Cochran.

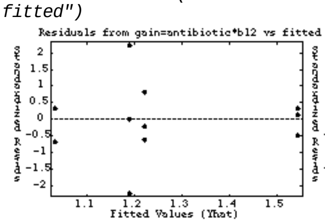
2×2 factorial CRD. Factors were vitamin B_{12} fed to swine at 0 and 5 mg and antibiotics fed at 0 and 40 mg.

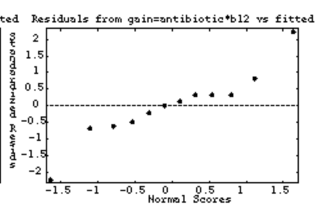
Antibiotics	0		40 mg	
B_{12}	0	5 mg	0	5 mg
Average daily gain of swine	1.30 1.19 1.08	1.26 1.21 1.19	1.05 1.00 1.05	1.52 1.56 1.55

```
Cmd> gain <- vector(1.30, 1.19, 1.08,  1.26, 1.21, 1.19,\
      1.05, 1.00, 1.05,  1.52, 1.56, 1.55)

Cmd> antibiotic <- factor(rep(rep(run(2),rep(3,2)),2))

Cmd> b12 <- factor(rep(run(2), rep(6,2)))

Cmd> anova("gain = antibiotic + b12 + antibiotic.b12",fstat:T)
Model used is gain = antibiotic + b12 + antibiotic.b12
                DF         SS          MS          F      P-value
CONSTANT         1      18.65       18.65  5086.40000  1.6639e-12
antibiotic       1     0.2187      0.2187    59.64545  5.6224e-05
b12              1   0.020833    0.020833     5.68182    0.044292
antibiotic.b12   1     0.1728      0.1728    47.12727  0.00012902
ERROR1           8   0.029333   0.0036667
```



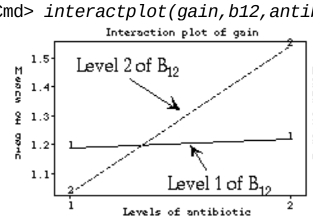
```
Cmd> resvsyhat(title:"Residuals from gain=antibiotic*b12 vs
fitted")

Cmd> resvsrankits(title:"Residuals from gain=antibiotic*b12 vs
fitted")
```

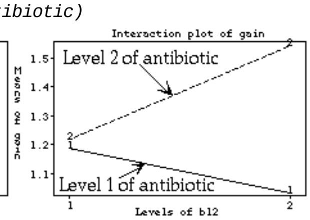




There are no obvious violation of assumptions. You can discount the apparently larger variance for **yhat** near 1.2 because the samples sizes are so small.


```
Cmd> tabs(gain,b12,antibiotic,mean:T) # two way table of means
(1,1)        1.19        1.22
(2,1)      1.0333      1.5433

Cmd> interactplot(gain,antibiotic,b12)

Cmd> interactplot(gain,b12,antibiotic)
```





Interpretation

At **b12** level 1, **antibiotic** has virtually *no* effect.
At **b12** level 2, **antibiotic** has a substantial *positive* effect.

At **antibiotic** level 1, **b12** decreases gain
At **antibiotic** level 2, **b12** increases gain

```
Cmd> coefs()[-1] # all coefficients except muhat
antibiotic
(1)     -0.135       0.135
b12
(1)   -0.041667    0.041667
antibiotic.b12
(1,1)        0.12       -0.12
(2,1)       -0.12        0.12
```

Averaged over both levels of **b12**, **antibiotic** has a positive effect.

```
Cmd> alpha <- coefs(antibiotic) # estimated effects

Cmd> beta <- coefs(b12) # estimated effects

Cmd> alphabeta <- coefs("antibiotic.b12") # estimated effects

Cmd> alpha + alphabeta
(1,1)      -0.015      -0.255
(2,1)       0.015       0.255
```

These are $\hat{\alpha}_i + \widehat{\alpha\beta}_{ij}$, the estimated effects of **antibiotic** at both levels of **b12**.

```
Cmd> beta' + alphabeta
(1,1)    0.078333   -0.078333
(2,1)    -0.16167     0.16167
```

These are $\hat{\beta}_j + \widehat{\alpha\beta}_{ij}$, the estimated effects of **b12** at both levels of **antibiotic**.

```
Cmd> alpha + beta' + alphabeta
(1,1)   -0.056667    -0.21333
(2,1)   -0.026667     0.29667
```

These are $\hat{\alpha}_i + \hat{\beta}_j + \widehat{\alpha\beta}_{ij}$, the overall estimated treatment effects.

Analyze as single factor experiment with 4 treatments.

```
Cmd> treat <- makefactor(antibiotic + 10*b12)

Cmd> print(treat,format:"2.0f")
treat:
(1)  1  1  1  2  2  2  3  3  3  4  4  4

Cmd> anova("gain=treat",silent:T)

Cmd> coefs(treat) # same treatment effects
(1)   -0.056667   -0.026667    -0.21333     0.29667
```


Now look at contrasts. With only two levels, there is really only one main effect contrast with $w_2 = -w_1$

```
Cmd> c_a <- vector(-1,1); c_b <- vector(-1,1)

Cmd> contrast(antibiotic, c_a)
component: estimate
(1)        0.27
component: ss
(1)      0.2187       Same as ANOVA SS for antibiotic
component: se
(1)     0.03496

Cmd> contrast(b12, c_b)
component: estimate
(1)    0.083333
component: ss
(1)    0.020833       Same as ANOVA SS for b2
component: se
(1)     0.03496
```

This computes the values of the contrast in a white box way.

```
Cmd> vector(alpha[2]-alpha[1],beta[2]-beta[1])
(1)        0.27    0.083333 Same as contrast() estimates
```

There is only one interaction contrast.

```
Cmd> c_ab <- matrix(vector(1,-1, -1, 1),2); c_ab
(1,1)          1          -1
(2,1)         -1           1

Cmd> contrast("antibiotic.b12", c_ab)
component: estimate
(1)        0.48   ybar_11 - ybar_12 - ybar_21 + ybar_22
component: ss
(1)      0.1728
component: se
(1)    0.069921
```


You can calculate **c_ab** using **outer()**

```
Cmd> outer(c_a,c_b) # another way
(1,1)           1          -1
(2,1)          -1           1
```

In general, if **c_a** and **c_b** are main effect contrasts, **outer(c_a,c_b)** is interaction contrast. Each element of **outer(c_a,c_b)** is a product of one element of **c_a** and one element of **c_b**

```
Cmd> c_lin <- vector(-1,0,1) # linear polynomial contrast

Cmd> c_quad <- vector(1,-2,1) # quadratic polynomial contrast

Cmd> outer(c_lin,c_lin) # linear by linear
(1,1)           1           0          -1
(2,1)           0           0           0
(3,1)          -1           0           1

Cmd> outer(c_lin,c_quad) # linear by quadratic
(1,1)          -1           2          -1
(2,1)           0           0           0
(3,1)           1          -2           1

Cmd> outer(c_quad,c_lin) # quadratic by linear
(1,1)          -1           0           1
(2,1)           2           0          -2
(3,1)          -1           0           1

Cmd> outer(c_quad,c_quad) # quadratic by quadratic
(1,1)           1          -2           1
(2,1)          -2           4          -2
(3,1)           1          -2           1
```


More than two factors

Suppose you have 4 factors A, B, C and D with a, b, c and d levels.

You have many more possibilities for interactions

$$y_{ijk\ell m} = \mu + \alpha_i + \beta_j + \gamma_k + \delta_\ell + \alpha\beta_{ij} + \alpha\gamma_{ik} + \alpha\delta_{i\ell} + \beta\gamma_{jk} + \beta\delta_{j\ell} + \gamma\delta_{k\ell} + \alpha\beta\gamma_{ijk} + \alpha\beta\delta_{ij\ell} + \alpha\gamma\delta_{ik\ell} + \beta\gamma\delta_{jk\ell} + \alpha\beta\gamma\delta_{ijk\ell} + \varepsilon_{ijk\ell m}$$

The ANOVA table has a line for each term. There are 4, 6, 4 and 1 main effect, 2 way, 3 way and 4 way terms.

The main and interaction effects are defined so that sums over any subscript are 0.

For example, if the number of levels of A, B, C and D are a, b, c and d respectively,

$$\sum_{1\le i\le a}\alpha\beta\delta_{ij\ell} = \sum_{1\le j\le b}\alpha\beta\delta_{ij\ell} = \sum_{1\le \ell\le d}\alpha\beta\delta_{ij\ell} = 0$$