Displays for Statistics 5303

Lecture 33

November 22, 2002

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

Use of Hasse diagrams in Expected mean squares

This uses the same definition of *eligibility* as for selecting F denominators

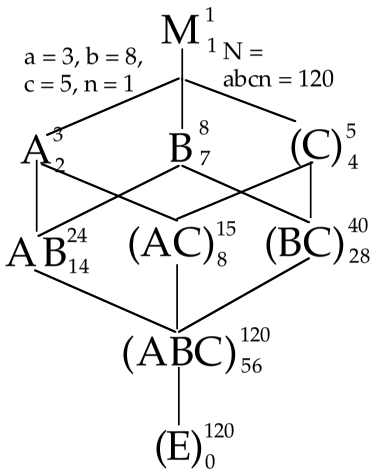
- **Unrestricted**: *All* random terms below term X are **eligible**
  Restricted: All random terms below X are **eligible** except those containing a fixed factor not in X

The concept of **leading eligible** terms does *not* apply

Representative elements for term

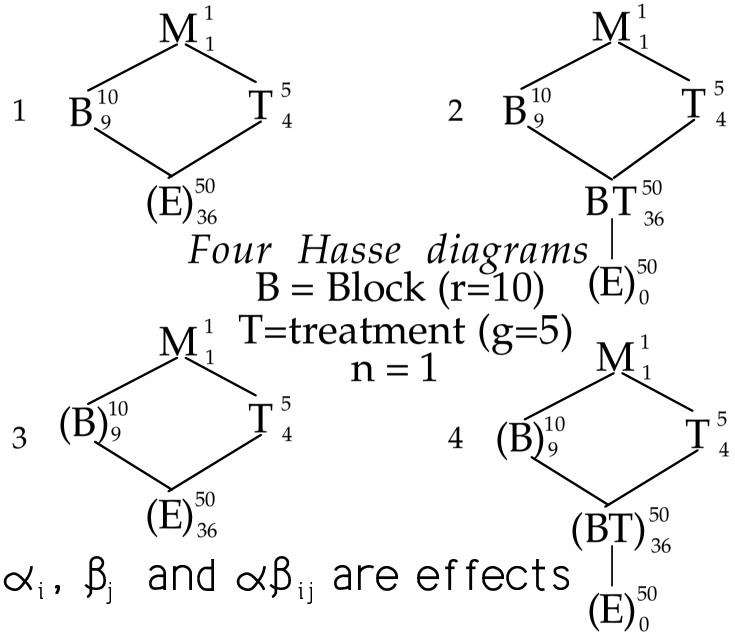
- *Fixed*: Q = $\sum$(all effects)^2/DF
  Example $\sum_i \sum_j \alpha\beta_{ij}^2/(a-1)(b-1)$
- *Random*: V = variance component (σ_X^2 for pure random, $r_x\sigma_x^2$ for mixed)
- The **contribution** of a term is N/(number of effects) (e.g.. N/(bc))
- EMS_X = sum of contributions of *all eligible random* terms *below* X

U = unrestricted, R = unrestricted



R $EMS_A = 40Q_A + 8\sigma_{\alpha\gamma}^2 + \sigma^2$
U $EMS_A = 40Q_A + 8\sigma_{\alpha\gamma}^2 + \sigma_{\alpha\beta\gamma}^2 + \sigma^2$
R $EMS_B = 15Q_B + 3\sigma_{\beta\gamma}^2 + \sigma^2$
U $EMS_B = 15Q_B + 3\sigma_{\beta\gamma}^2 + \sigma_{\alpha\beta\gamma}^2 + \sigma^2$

R $EMS_C = 24\sigma_\gamma^2 + \sigma^2$	
U $EMS_C = 24\sigma_\gamma^2 + 8\sigma_{\alpha\gamma}^2 + 3\sigma_{\beta\gamma}^2 + \sigma_{\alpha\beta\gamma}^2 + \sigma^2$	
RU $EMS_{AB} = 5Q_{AB} + \sigma_{\alpha\beta\gamma}^2 + \sigma^2$	
R $EMS_{AC} = 8\sigma_{\alpha\gamma}^2 + \sigma^2$	U $= 8\sigma_{\alpha\gamma}^2 + \sigma_{\alpha\beta\gamma}^2 + \sigma^2$
R $EMS_{BC} = 3\sigma_{\beta\gamma}^2 + \sigma^2$	U $= 3\sigma_{\beta\gamma}^2 + \sigma_{\alpha\beta\gamma}^2 + \sigma^2$
RU $EMS_{ABC} = \sigma_{\alpha\beta\gamma}^2 + \sigma^2$	



Four Hasse diagrams
B = Block (r=10)
T=treatment (g=5)
n = 1

α_i, β_j and $\alpha\beta_{ij}$ are effects

1 $y_{ij} = \mu + \alpha_i + \beta_j + \varepsilon_{ij}$, T and B fixed, *no interaction*,

2 $y_{ij} = \mu + \alpha_i + \beta_j + (\alpha\beta)_{ij} + \varepsilon_{ij}$, T and B fixed, *BT interaction*

3 $y_{ij} = \mu + \alpha_i + \beta_j + \varepsilon_{ij}$, T fixed, B random, *no interaction*

4 $y_{ij} = \mu + \alpha_i + \beta_j + (\alpha\beta)_{ij} + \varepsilon_{ij}$, T fixed, B random, *BT interaction*

Each is a possible model for a **randomized complete block** (**RCB**) design with g = 5 treatments and r = 10 blocks.

T is the *treatment* factor, **fixed**.
B is the blocking factor, fixed or random.

B and T are crossed, so every treatment appears in each block. For this reason, a block is often called a *replicate*.

The purpose of a randomized block design is to segregate a known source of variation so that it does not influence comparison of treatment effects.

For example, since no β_j's appear in

$$\bar{y}_{1\bullet} - \bar{y}_{2\bullet} = \alpha_1 - \alpha_2 + \bar{\varepsilon}_{1\bullet} - \bar{\varepsilon}_{2\bullet}$$

only $\sigma^2 = \sigma_\varepsilon^2$ affects accuracy.

In a successful RCB design, much of the variability should be among blocks, not between treatments within a block. The result is that treatment effects and contrasts are estimated more accurately.

There are two essential elements of a CRB to compare g treatments:

- Division of N = rg experimental units into homogeneous groups or *blocks* of g EU's.
- *Random* assignment of a complete set of treatments to the EU's in each block.

The blocks represent a *non-treatment* factor which is crossed with the treatment factor or factors.

With non-random assignment, it's not RCB

Example of non-RCB:

"Treatment" factor = type of family member, Mother, Father, son, daughter

Sample r households with this family structure in neighborhood.

A family might be a block, but it's not a RCB; you can't randomly select a family member to be mother, say.

Example of RCB:

An experiment studied the difference in effects of 5 cardioactive drugs on etherized cats.

The response was $y = x/(\text{heart wt})^{.7}$ where x was dose required to get a specific response

Only 5 cats could be studied on a day, so it was natural to block on days.

On each of 10 days, treatments were randomly assigned to 5 cats and y was determined.

Since blocks are a non-treatment factor, there is no interest in making inference about the difference between blocks.

Among-block variability may be useful for

- Checking to see that blocks did reduce variability
- plan for future experiments.

Should blocks be considered random of fixed in this experiment?

Probably random is OK, but it really doesn't matter.

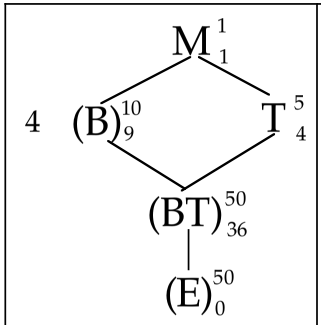
Without interaction in the model

M^{1}_{1} 1 B^{10}_{9} T^{5}_{4} $(E)^{50}_{36}$ **Fixed**	$EMS_B = 5Q_B + \sigma^2$ $EMS_T = 10Q_T + \sigma^2$ $EMS_E = \sigma^2$ Denominator for T: MS_E Denominator for B: MS_E

M^{1}_{1} 3 $(B)^{10}_{9}$ T^{5}_{4} $(E)^{50}_{36}$ **Random**	$EMS_B = 5\sigma_\beta^2 + \sigma^2$ $EMS_T = 10Q_T + \sigma^2$ $EMS_E = \sigma^2$ Denominator for T: MS_E Denominator for B: MS_E

With no interaction, $MS_E = MS_{BT}$ is the denominator for F for testing H_0: $Q_T = 0$.

With interaction in the model



$EMS_B = 5\sigma_\beta^2 + \sigma^2$

$EMS_T = 10Q_T + \sigma_{\alpha\beta}^2 + \sigma^2$

$EMS_{BT} = \sigma_{\alpha\beta}^2 + \sigma^2$

Denominator for T: MS_{BT}

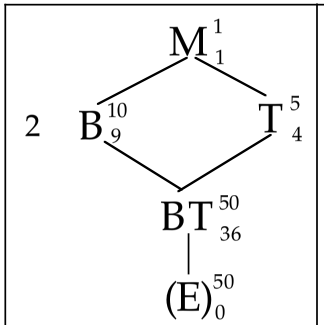
Denominator for B: none

When there is interaction and blocks are random (case 4), the denominator is MS_{BT} which is the same as MS_E when no interaction is assumed.

So, with fixed *or* random blocks no interaction, or with random blocks with interaction, the F-statistic is always the same

$$F_{g-1,(g-1)(r-1)} = MS_T/MS_{BT} = MS_T/MS_E$$

Fixed blocks with interaction



$EMS_B = 5Q_B + \sigma^2$

$EMS_T = 10Q_T + \sigma^2$

$EMS_{BT} = Q_{BT} + \sigma^2$

Denominator for T: None

Denominator for B: None

This is the only problematic case: There really is no error term. If there really is interaction ($Q_{BT} > 0$), then MS_{BT} will tend to be too large, and your $F = MS_T/MS_{BT}$ will be conservative.

The randomization test will work here in testing H_0: drugs have identical effects . This implies any interaction effects are identical in each block ($\alpha\beta_{1j} = \ldots = \alpha\beta_{gj}$). The randomization distribution of $F = MS_T/MS_{BT}$ will be close to $F_{t-1,(t-1)(b-1)}$

```
Cmd> data <- read("","bliss11_11")
bliss11_11      50     3  columns format
) Data derived from Table 11.11 in Statistics in Biology
) by Chester I Bliss,
) Comparative toxicities in etherized cats of five cardioactive
) grugs in mugram/g^.7 of year.
) Table 11.11 gives y = .6 + log10(toxicity).  These values were
) computed as round(10^(y-.6),3)
) Col. 1: Day number (1-10) corresponding to 6-9,13,14,16,
)         21,24,27 Mar 1939
) Col. 2: Drug (1-5), drugs A, B, C, D, E
) Col. 3: Toxicity in mugram/g^.7
Read from file "TP1:DataFromStPaul:Bliss:Bliss.mat"

Cmd> makecols(data, day,drug,toxicity)

Cmd> day <- factor(day); drug <- factor(drug)
```

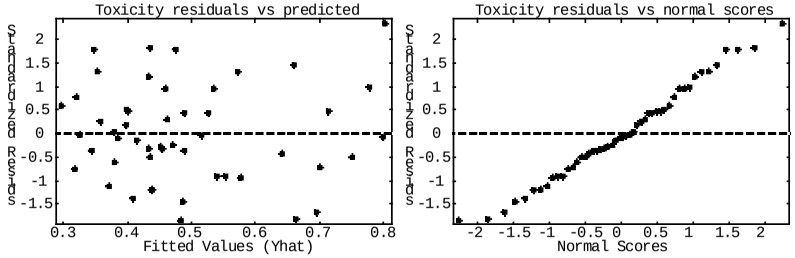
Day = block, Drug = treatment

```
Cmd> anova("toxicity=day + drug",fstat:T)
Model used is toxicity=day + drug
             DF          SS          MS          F     P-value
CONSTANT      1      12.076      12.076  2798.23109  9.8404e-36
day           9     0.15642     0.01738     4.02726   0.0012398
drug          4     0.74132     0.18533     42.94569  3.1431e-13
ERROR1       36     0.15536   0.0043155
```

drug is highly significant.

```
Cmd> resvsyhat(title:"Toxicity residuals vs predicted")

Cmd> resvsrankits(title:"Toxicity residuals vs normal scores")
```



Plots show nothing obviously wrong.

Let's check for non-additivity by 1-dofna.

```
Cmd> muhat <- coefs(1);z <- (toxicity - RESIDUALS - muhat)^2/2

Cmd> anova("toxicity=day + drug + z",pval:T)
Model used is toxicity=day + drug + z
WARNING: summaries are sequential
             DF          SS          MS     P-value
CONSTANT      1      12.076      12.076  1.3741e-35
day           9     0.15642     0.01738  0.00072045
drug          4     0.74132     0.18533  1.5517e-13
z             1    0.015865    0.015865    0.053854
ERROR1       35     0.13949   0.0039855
```

z is close to significant. You probably should consider transforming.

```
Cmd> 1 - muhat*coefs(z) # suggested power
(1)    -0.28539
```

This is a lot closer to 0 (log) than to 1.

```
Cmd> y <- log10(toxicity)

Cmd> anova("y=day + drug",fstat:T)
Model used is y=day + drug
             DF          SS          MS           F     P-value
CONSTANT      1      5.3051      5.3051  1658.20712  1.0405e-31
day           9     0.12011    0.013345     4.17132  0.00095014
drug          4     0.48506     0.12126    37.90326  1.9334e-12
ERROR1       36     0.11518   0.0031993

Cmd> muhat <- coefs(1);z <- (y - RESIDUALS - muhat)^2/2

Cmd> anova("y=day + drug + z",pval:T)
Model used is y=day + drug + z
WARNING: summaries are sequential
             DF          SS          MS     P-value
CONSTANT      1      5.3051      5.3051  7.2376e-31
day           9     0.12011    0.013345   0.0012502
drug          4     0.48506     0.12126  4.2991e-12
z             1  9.7873e-10  9.7873e-10     0.99957
ERROR1       35     0.11518   0.0032907
```

1-dofna is effectively 0.

Redo **anova()** without z.

```
Cmd> anova("y=day + drug",fstat:T)
Model used is y=day + drug
             DF          SS          MS           F     P-value
CONSTANT      1      5.3051      5.3051  1658.20712  1.0405e-31
day           9     0.12011    0.013345     4.17132  0.00095014
drug          4     0.48506     0.12126    37.90326  1.9334e-12
ERROR1       36     0.11518   0.0031993
```

Use **pairwise()** to compare treatment effects.

```
Cmd> pairwise("drug",.05,hsd:T)
  |         1   -0.104
  | |       2  -0.0721
    | |     3  -0.0171
      |     4   0.0147
            5    0.179
```

Drug 1 is significantly different from drugs 3, 4 and 5.

Drug 2 is significantly different from drugs 4 and 5.

Drug 3 us significantly different from drugs 1 and 5.

Drug 3 us significantly different from drugs 5 and drugs 1 and 2.

Drug 5 is significantly different from all.

It would make no sense to compare block effects.

Was blocking worthwhile? What would have happened if this had been done as a CRD (completely randomized design) experiment? Would the estimated error be smaller or larger?

You can't know for sure, but you can estimate the MS_E you would have gotten if it had been CRD.

$\hat{\sigma}_{crd}^2 = ((r-1)MS_{blocks}+r(g-1)MS_E)/(r-1+r(g-1))$

This is a weighted average of MS_{blocks} and MS_E.

$r(g-1) = DF_{error}$ in CRD.

$r-1+r(g-1) = r-1+g-1 + (g-1)(r-1)$

$= DF_{block} + DF_{treat} + DF_{error}$ in RCB

You might think $\hat{\sigma}_{crd}^2$ *should* be $((r-1)MS_{blocks}+ (g-1)(r-1)MS_E)/r(g-1) =$ $SS_E/r(g-1)$ but that's not correct

```
Cmd> g <- 5; r <- 10

Cmd> MS <- SS/DF; MS # MS from ANOVA
    CONSTANT         day        drug      ERROR1
      5.3051    0.013345     0.12126   0.0031993

Cmd> sigmasq_crd <-\
 (DF[2]*MS[2] + (DF[3]+DF[4])*MS[4])/(DF[2]+DF[3]+DF[4])

Cmd> sigmasq_crd
(1)   0.0050629
```

The **efficiency** of design 1 relative to design 2 is the ratio of the error variances $Eff_{1:2} = \sigma_2^2/\sigma_1^2$.

The smaller σ_1^2 is as compared to σ_2^2 the more efficient design 1 is.

A crude measure of estimated efficiency is $\hat{\sigma}_{crd}^2/\hat{\sigma}_{rcb}^2$.

```
Cmd> sigmasq_rcb <- MS[4]

Cmd> sigmasq_crd/sigmasq_rcb # Crude efficiency
(1)      1.5825      158%
```

A more refined measure takes into account the fact that $DF_E = (g-1)(r-1)$ in RCB is smaller than $DF_E = g(r-1)$ in CRD

$$\text{Efficiency} = \text{correction} \times (\hat{\sigma}_{crd}^2/\hat{\sigma}_{rcb}^2)$$

$$\text{correction} = \frac{(df_{err,crd} + 3)/(df_{err,crd} + 1)}{(df_{err,rcb} + 3)/(df_{err,rcb} + 1)}$$

```
Cmd> dfe_crd <- g*(r-1); dfe_rcb <- DF[4] # (g-1)(r-1)

Cmd> correction <-\
     ((dfe_crd+3)/(dfe_crd+1))/((dfe_rcb+3)/(dfe_rcb+1))

Cmd> correction
(1)     0.98997

Cmd> correction*sigmasq_crd/MS[4]
(1)      1.5666
```

The correction for degrees of freedom is so close to 1 that it doesn't make any appreciable effect.

Here are the expected mean squares as computed by MacAnova for the 4 types of models

Case 1: Blocks fixed, no interaction

```
Cmd> ems("y=day+drug",NULL) # no random factors
EMS(CONSTANT) = V(ERROR1) + 50Q(CONSTANT)
EMS(day) = V(ERROR1) + 5Q(day)
EMS(drug) = V(ERROR1) + 10Q(drug)
EMS(ERROR1) = V(ERROR1)
```

ERROR1 is error term for drug

Case 1: Blocks fixed, interaction

```
Cmd> ems("y=day*drug",NULL) # no random factors
EMS(CONSTANT) = V(ERROR1) + 50Q(CONSTANT)
EMS(day) = V(ERROR1) + 5Q(day)
EMS(drug) = V(ERROR1) + 10Q(drug)
EMS(day.drug) = V(ERROR1) + 1Q(day.drug)
EMS(ERROR1) =  cannot be estimated
```

No error term for drug

```
Cmd> ems("y=day+drug",vector("day"))
EMS(CONSTANT) = V(ERROR1) + 5V(day) + 50Q(CONSTANT)
EMS(day) = V(ERROR1) + 5V(day)
EMS(drug) = V(ERROR1) + 10Q(drug)
EMS(ERROR1) = V(ERROR1)
```

ERROR1 is error term for drug

```
Cmd> ems("y=day*drug",vector("day"))
EMS(CONSTANT) = V(ERROR1) + 5V(day) + 50Q(CONSTANT)
EMS(day) = V(ERROR1) + 5V(day)
EMS(drug) = V(ERROR1) + 1V(day.drug) + 10Q(drug)
EMS(day.drug) = V(ERROR1) + 1V(day.drug)
EMS(ERROR1) =  cannot be estimated
```

day.drug is error term for drug