Week 14 Tuesday notes
Recall example
18 subj. Group 1
Group 2

Source of EMS

\[ G_i : 1 \sigma_i^2 + 2 \sigma_i^2 + 1 \beta \sigma_i^2 \]
\[ Subj: 1 \sigma_i^2 + 2 \sigma_i^2 \]
\[ Treat: 1 \sigma_i^2 + 1 \beta \delta \]
\[ Time: 1 \sigma_i^2 + 1 \beta \delta \text{Time} \]
\[ Error: 1 \sigma_i^2 + \frac{1}{2} \text{Subj/group} \]

Recall: Not complete design, i.e., some combinations of Treat, Time, and Group not considered. Looks like a Latin square.

Confounding:

\[ \text{Treat} = \text{Group} \times \text{Time} \]
\[ \text{Group} = \text{Treat} \times \text{Time} \]
\[ \text{Time} = \text{Group} \times \text{Treat} \]

Back to $2^3$
Treat combinations
(a,b,c ac bc ab)
A -1 1 -1 -1 -1 1
B 1 A C
C -1 -1 1
ABC
Suppose run $2^3$, all pts. (full design)

**Source df**
- A: 1
- B: 1
- C: 1
- AB: 1
- AC: 1
- BC: 1
- ABC: 1
- Error: 0

**Options**
1. Delete ABC (into error)
2. Problem: $F_{1,15} = 161$
3. Need nest
4. Most SNR

Option 2: delete all interactions from model.

**Source df**
- A: 1
- B: 1
- C: 1

Can test all main effects

Problem: Tests are conservative.

Error 4 p-values

Since F-tests are conservative, if have significance, we are sure it is real.

**Option 3:** Kind of clever,
calculate "Effect" for each term in ANOVA table.

Recall contrasts:

<table>
<thead>
<tr>
<th>$Y$</th>
<th>$Y$</th>
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<th>$Y$</th>
<th>$Y$</th>
<th>$Y$</th>
<th>$Y$</th>
<th>$Y$</th>
<th>$Y$</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>-1</td>
<td>-1</td>
<td>-1</td>
<td>-1</td>
<td>-1</td>
<td>-1</td>
<td>-1</td>
<td>-1</td>
</tr>
<tr>
<td>$\overline{Y}<em>{A</em>{hi}} - \overline{Y}<em>{A</em>{hj}}$ = Effect of A</td>
<td></td>
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</tbody>
</table>

Can calculate an effect for any term in the model.

<table>
<thead>
<tr>
<th>$Y$</th>
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<th>$Y$</th>
<th>$Y$</th>
<th>$Y$</th>
<th>$Y$</th>
<th>$Y$</th>
</tr>
</thead>
<tbody>
<tr>
<td>ABC</td>
<td>-1</td>
<td>-1</td>
<td>-1</td>
<td>-1</td>
<td>-1</td>
<td>-1</td>
<td>-1</td>
<td>-1</td>
</tr>
<tr>
<td>$\overline{Y}<em>{ABC</em>{hi}} - \overline{Y}<em>{ABC</em>{hj}}$ = &quot;Effect of ABC&quot;</td>
<td></td>
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</tbody>
</table>
So what? Calculating effects is like orthogonal change of basis. If no term is significant, then the Effects of all terms in the Model are i.i.d. $\mathcal{N}(0, \sigma^2)$, $\sigma^2$ depends on # factors & $\sigma_0^2$.

If we plot the Effects on normal quantile plot, Is $H_0$ true for all terms.

If we see a point not on the line, then the Effect that it corresponds to is "significant".

How to get p-value?
Usual way, drop other terms from the model.
Source df can get p-value:

What can go wrong with this?
Usual thing done is to pool higher order interactions.
Better still. Get more B replications...

Replication can mean 2 things:

1) within cell replication

2) Blocking

Analysis of CRB

Source df

D 1
B 1
A 1
AB 1
B C 1
AB C 1

Error 5

Suppose have constraint, can only run 8 obs/time:

Block

A 1
B 1
C 1

X X X

X X X

X X X

Usual solution: pool Block*Test

Source df

Error 7

\( F_{1,1,05} = 16! \)
Contrasts are useful!!
Another use: Incomplete Blocks.
Suppose for $2^3$ design, can only run 4 observations at a time. Run 2 incomplete blocks of 4 obs. each.

Block must be in our ANOVA table a has 1 df.
What is block confounded with?
Design the confounding.
Pick a term to confound with block

<table>
<thead>
<tr>
<th>Source</th>
<th>df</th>
<th>Options</th>
</tr>
</thead>
<tbody>
<tr>
<td>Block/ABC</td>
<td>1</td>
<td>1) Pool interactions into error</td>
</tr>
<tr>
<td>A</td>
<td>1</td>
<td>2) Normal plot</td>
</tr>
<tr>
<td>B</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td>C</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td>AB</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td>AC</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td>BC</td>
<td>1</td>
<td></td>
</tr>
</tbody>
</table>

$\begin{array}{l|l}
ABC & \text{a, b, c, ab, ac, bc, abc} \\
\hline
-1 & 1 & -1 & 1 & -1 & -1 & 1 \\
\text{Block/ABC} & 1 & 1 & 1 & 1 & 1 & 1 & 1 & 1 \\
\text{(a), (b), (c), (a, b, c, abc)} & \end{array}$