LGN 5822 - Biometrical Genetics

L09 – Factorial Experiments

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Introduction

• You may be interested in comparing two different sets of treatments

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• You may be interested in comparing two different sets of treatments

- You can fix one level of a treatment and study the other, or you may compare both simultaneously
- Treatment designs that combine two (or more) treatment factors are factorial designs

 Factorial experiments involve simultaneously more than one factor and each factor is at two or more levels

Introduction

Factorial Experiments: Objective

 Effect of different factors that influence the variable under study and the relationship between them

 The main idea of a factorial experiment is that it allows you to evaluate not only the individual effect of each factor, but also how these factors interact



 Several factors affect simultaneously the characteristic under study in factorial experiments

 The researcher is interested in the main effects and the interaction effects among different factors

Experimental Design X Factorial Arrangement

- Experimental Design: It is the manner in which levels of a factor or treatments are distributed to experimental units
 - Experiment design defines the error structure

Completely Randomized Design (CRD)

- Randomized Complete Block Design (RCBD)
- Latin Square (LS)
- Factorial arrangement: It is the way in which the combination of the levels of the factors under study is organized in experimental units

What is the difference?

Experimental Design X Factorial Arrangement

 Factorial experiments are set up according to a type of design experimental, such as: CRD, RCBD, LS

• The choice of design depends on the homogeneity of the experimental unit



Treatment Design

• In factorial experiments, treatments are obtained by combinations factor levels

 Complete factorial design, each level of a factor combines with all levels of the other factors

Treatment Design

- The symbology commonly used for factorial experiments is to indicate the product of the levels of the factors under test ("x")
 - *e.g.* Factorial Experimente 2x4x6
 - in the experiment were tested simultaneously 3 factors. The first has 2 levels, the second 4 levels and the third 6 levels
- When the number of levels is the same for all factors, the following symbols can be used: n^F
 - where F is the number of factors and n is the number of levels of each factor
 - e.g. 4³: the experiment has 3 factors with 4 levels each

Treatment Design

- Factorial designs can include multiple levels of a larger number of treatments
 - *E.g.* if three factors are under investigation, the design is an *m × n × o* factorial arrangement

 If the numbers of factors and/or levels are moderately large, the size of the experiment can be a limiting factor



Effects

 Main Effect: is the effect of each factor, independent of the effect of other factors

- Interaction Effect: is effect of factors on the variable in study
 - The interaction between factors occurs when the effects of the levels of one factor are modified by the levels of the other factor



Is there interaction?

• Factorial: 3x2

Effects



No interaction

Is there interaction?

• Factorial: 3x2

Effects



Interaction

Data Table

- Factors A and B, with I and levels, respectively, according to the CRD
 - K replicates

	A1	A2	AI	
Repetition	B1 B2 BJ	B1 B2 BJ		B1 B2 BJ
1	Y ₁₁₁ Y ₁₂₁ Y _{1J1}	Y_{211} Y_{221} Y_{2J1}		Y _{I11} Y _{I21} Y _{IJ1}
2	$Y_{112} \ Y_{122} \ \dots \ Y_{1J2}$	${\sf Y}_{212} {\sf Y}_{222} {\sf Y}_{2J2}$	•••	${\sf Y}_{{\sf I}12} \ {\sf Y}_{{\sf I}22} \ \dots \ {\sf Y}_{{\sf I}J2}$
K	Y _{11K} Y _{12K} Y _{1JK}	Y _{21K} Y _{22K} Y _{2JK}		$Y_{I1K} \hspace{0.1in} Y_{I2K} \hspace{0.1in} \dots \hspace{0.1in} Y_{IJK}$
Total	Y _{11•} Y _{12•} Y _{1J•}	Y ₂₁ , Y ₂₂ ,, Y ₂ ,		Y _{I1} , Y _{I2} , Y _{IJ} ,

Data Table

- Number of experimental units: $N = I \times J \times K$
- Total of the *ij*-th treatment: $AB_{ij} = \sum_{k=1}^{\kappa} Y_{ijk} = Y_{ij.}$

• Total of the *i*-th level of factor A:
$$A_i = \sum_{j=1,k=1} Y_{ijk} = Y_{i..}$$

• Total of the *j*-th level of factor B:
$$B_j = \sum_{i=1,k=1}^{i,k} Y_{ijk} = Y_{.j.}$$

Data Table

• Mean of the *i*-th level of factor A: $\widehat{m}_{Ai} = \frac{A_i}{IK}$

• Mean of the *j*-th level of factor B:
$$\widehat{m}_{Bj} = \frac{B_j}{IK}$$

• General mean:
$$\widehat{m} = \frac{G}{N}$$

• Number of experimental units: $N = I \times J \times K$

Data Table: Total Treatments

Factor A	B1 B2 BJ	Total
A1	Y ₁₁ , Y ₁₂ ,, Y ₁ ,	A ₁
A2	Y ₂₁ , Y ₂₂ ,, Y ₂ J.	A ₂
AI	Y _{I1.} Y _{I2.} Y _{IJ.}	A
Totais	B ₁ B ₂ B _j	G

Statistical Model

Consider a factorial experiment, with two factors: factor T with i levels and factor G with j levels, installed according to the DIC, with K repetitions

Statistical Model

Model

• In a CRD, data can be described with the following model:

$$y_{ijk} = \mu + \tau_i + \gamma_i + (\tau\gamma)_{ij} + \varepsilon_{ijk}$$

where τ_i is the effect of treatment T, γ_i is the effect of treatment G and $(\tau \gamma)_{ij}$ represents the interaction of the two factors

Statistical Model

Model

• In a RCBD, data can be described with the following model:

$$y_{ijk} = \mu + \tau_i + \gamma_i + (\tau\gamma)_{ij} + \omega_k + \varepsilon_{ijk}$$

where τ_i is the effect of treatment T, γ_i is the effect of treatment G and $(\tau \gamma)_{ij}$ represents the interaction of the two factors

Statistical Model

• The effects τ_i of treatment T and γ_i of treatment G are called *main effects*

Statistical Model

We assume that:

•
$$\varepsilon_{ij} \sim N(0, \sigma^2)$$
, for $i = 1, ..., t$ and $j = 1, ..., g$ and $k = 1, ..., r$

•
$$cov\left(\varepsilon_{ijk},\varepsilon_{i'j'k'}\right)=0$$

Errors are independent and identically distributed (i.i.d)

The corresponding ANOVA table

Source of Variation	Degrees of Freedom	Sum of Squares	Mean Square
Т	t-1	SST	$MS_T = \frac{SS_T}{t-1}$
G	g-1	SS_G	$MS_G = \frac{SS_G}{g-1}$
$T\timesG$	(t-1)(g-1)	$SS_{T\timesG}$	$MS_{T \times G} = \frac{SS_{T \times G}}{(t-1)(g-1)}$
Within	tg(r-1)	SS_{Within}	$MS_{Within} = \frac{SS_{Within}}{tg(r-1)}$
Total	tgr - 1	SS_Total	-

• If treatments T and G are random:

Source of Variation	Degrees of Freedom	Mean Square	Expected Mean Square
Т	t - 1	MS_T	$\sigma^2 + r\sigma_{tg}^2 + rg\sigma_t^2$
G	g-1	MS_G	$\sigma^2 + r\sigma_{tg}^2 {+} rt\sigma_g^2$
$T\timesG$	(t-1)(g-1)	$MS_{T\timesG}$	$\sigma^2 + r \sigma_{tg}^2$
Within	tg(r-1)	MS _{Within}	σ^2
Total	tgr - 1		-

The expected mean squares are the expected values of these terms with the specified model

Mixed Models

- For mixed effects models, we will use REML estimates, the likelihood ratio test and model selection criteria such as AIC/BIC
- From now on, we deal with fixed effects only



• If T is fixed and G is random:

Source of	Degrees of	Mean	Expected
Variation	Freedom	Square	Mean Square
Т	t - 1	MS _T	$\sigma^2 + r\sigma_{tg}^2 + \frac{rg}{t-1}\sum_i \tau_i^2$
G	g-1	MS_{G}	$\sigma^2 + rt\sigma_g^2$
$T\timesG$	(t-1)(g-1)	$MS_{T\timesG}$	$\sigma^2 + r \sigma_{tg}^2$
Within	tg(r-1)	MS_{Within}	σ^2
Total	tgr - 1		-

• If treatments T and G are fixed:

Source of Variation	Degrees of Freedom	Mean Square	Expected Mean Square
Т	t-1	MS_T	$\sigma^2 + \frac{rg}{t-1}\sum_i \tau_i^2$
G	g-1	MS_G	$\sigma^2 + \frac{rt}{g-1} \sum_j \gamma_j^2$
$T\timesG$	(t-1)(g-1)	$MS_{T\timesG}$	$\sigma^2 + \frac{r}{(t-1)(g-1)} \sum_{ij} (\tau \gamma)$
Within	tg(r-1)	MS_{Within}	σ^2
Total	tgr - 1		

Hypothesis Testing

- The null hypothesis of no effect of treatment T is H_0 : $\tau_i = 0$ for all i
- Similarly, the null hypothesis of no effect of treatment G is $H_0: \tau_j = 0$ for all j

• The null hypothesis of no interaction effects is

 $H_0: + (\tau \gamma)_{ij} = 0$ for all i, j

Hypothesis Testing

Source of	Degrees of	Mean	Expected	F-Statistic
Variation	Freedom	Square	Mean Square	
т	t - 1	MS _T	$\sigma^2 + \frac{rg}{t-1} \sum_i \tau_i^2$	$F = \frac{MS_T}{MS_{Within}}$
G	g-1	MS_G	$\sigma^2 + rac{rt}{g-1} \sum_j \gamma_j^2$	$F = \frac{MS_G}{MS_{Within}}$
$T \times G$	(t-1)(g-1)	$MS_{T\timesG}$	$\sigma^2 + \frac{r}{(t-1)(g-1)} \sum_{ij} (\tau \gamma)_{ij}^2$	$F = \frac{MS_{T \times G}}{MS_{Within}}$
Within	tg(r-1)	MS_{Within}	σ^2	
Total	tgr - 1			

Interaction

Possible results for the F test of the interaction

Interaction

Possible results for the F test of the interaction

Note

• Non-significant interaction, the effects of the factors are independent

Interaction

Possible results for the F test of the interaction

Note

- A significant interaction means that the effect of one treatment is dependent on the levels of another
- Interpretation of treatment effects can be difficult, especially when there are many interactions
- The effect of one factor depends on the level of the other factor

Example: Interaction

 Suppose we are investigating the effect of m = 4 different culture mediums (solution) with the growth rate of n = 2 strains

• We can plot cell means to construct the interaction plot

Example: Interaction



Absence of interaction

Example: Interaction



Quantitative interaction

Example: Interaction



Qualitative interaction

Multiple Comparasions

- In the absence of interaction, we can contrast the main (average) effects of both treatment factors
 - Compare the levels of treatment T and/or
 - Compare the levels of treatment G

Multiple Comparasions

 If interaction if significant, we compare the levels of treatment T within each level of treatment G (and vice versa)

Advantages of a factorial experiment

 It allows the study of main effects and the effect of the interaction between factors

The number of degrees of freedom associated with the residue is high when compared to simple experiments on the same factors, which contributes to reducing the residual variance, increasing the precision of the experiment

Disadvantage of a factorial experiment

 Requires a greater number of experimental units in relation to simple experiments



- The data set consists of dry matter measurements (in mg) in Aspergillus nidulans
- Dry matter yield from ten different strains was measured in two contrasting conditions: mediums with and without nicotinic acid
- The experiment was conducted as an RCB design with two blocks
- These data come from Favraud & Azevedo. ESALQ/USP.

- Use the R function read.csv to import the data
- Fit the model with fixed (and/or random) effects
- Check if model assumptions are met



- Build the ANOVA table and test the null hypotheses of no difference between strains, no difference between nicotinic acid treatments and no interaction between both factors
- Draw the interaction plot
- Use multiple comparisons to assess pairwise differences

		 • 			-
>	dados				
	strain	nicot_acid	treatment	block	dry_matter
1	MSE	no	MSE_no	B1	47.2
2	MSE	no	MSE_no	в2	38.2
3	MSE	yes	MSE_yes	B1	140.0
4	MSE	yes	MSE_yes	в2	152.0
5	MSEsu1	no	MSEsu1_no	B1	37.6
6	MSEsu1	no	MSEsu1_no	в2	44.4
7	MSEsu1	yes	MSEsu1_yes	B1	79.6
8	MSEsu1	yes	MSEsu1_yes	в2	74.0
9	MSEsu2	no	MSEsu2_no	B1	103.2
1	0 MSEsu2	no	MSEsu2_no	в2	106.0
1	1 MSEsu2	yes	MSEsu2_yes	B1	102.6
1	2 MSEsu2	yes	MSEsu2_yes	в2	112.0
1	3 MSEsu3	no	MSEsu3_no	в1	163.6



"xyplot" is a function from the "lattice" package. This function is used to create scatter plots





```
fm1 <- lm(dry_matter ~ treatment, data = dados)
anova(fm1)</pre>
```

```
fm2 <- lm(dry_matter ~ strain * nicot_acid, data = dados)
anova(fm2)</pre>
```

```
fm3 <- lm(dry_matter \sim block + treatment, data = dados)
anova(fm3)
```

```
> fm2 <- lm(dry_matter ~ strain * nicot_acid, data = dados)
> anova(fm2)
Analysis of Variance Table
```

```
      Response: dry_matter
      Df Sum Sq Mean Sq F value
      Pr(>F)

      strain
      9
      45653
      5072.5
      131.205
      8.517e-16
      ***

      nicot_acid
      1
      9967
      9966.6
      257.796
      6.819e-13
      ***

      strain:nicot_acid
      9
      14560
      1617.8
      41.845
      4.938e-11
      ***

      Residuals
      20
      773
      38.7
      ---

      Signif. codes:
      0
      '***'
      0.001
      '**'
      0.05
      '.'
      0.1<'<'</td>
      1
```

```
> fm3 <- lm(dry_matter ~ block + treatment, data = dados)
> anova(fm3)
Analysis of Variance Table
```

```
Response: dry_matter

Df Sum Sq Mean Sq F value Pr(>F)

block 1 64 64.0 1.7148 0.206

treatment 19 70179 3693.6 98.9537 4.403e-15 ***

Residuals 19 709 37.3

---

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
fm5 <- lm(dry_matter ~ block + strain + nicot_acid: strain + nicot_acid, data = dados)
anova(fm5)</pre>
```

```
> fm5 <- lm(dry_matter ~ block + strain + nicot_acid: strain + nicot_acid, data = dados)
> anova(fm5)
Analysis of Variance Table
```

Response: dry_matt	ter					
	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
block	1	64	64.0	1.7148	0.206	
strain	9	45653	5072.5	135.8943	2.552e-15	* * *
nicot_acid	1	9967	9966.6	267.0099	1.210e-12	* * *
strain:nicot_acid	9	14560	1617.8	43.3402	8.815e-11	***
Residuals	19	709	37.3			
Signif. codes: 0	(<u>*</u> *	**' 0.00)1'**'(0.01'*'(0.05'.'0.	.1''1

```
fm6 <- lm(dry_matter ~ block + strain * nicot_acid, data = dados)
anova(fm6)</pre>
```

```
> fm6 <- lm(dry_matter ~ block + strain * nicot_acid, data = dados)
> anova(fm6)
Analysis of Variance Table
```

```
      Response: dry_matter
      Df Sum Sq Mean Sq F value Pr(>F)

      block
      1
      64
      64.0
      1.7148
      0.206

      strain
      9
      45653
      5072.5
      135.8943
      2.552e-15
      ***

      nicot_acid
      1
      9967
      9966.6
      267.0099
      1.210e-12
      ***

      strain:nicot_acid
      9
      14560
      1617.8
      43.3402
      8.815e-11
      ***

      Residuals
      19
      709
      37.3
      ---
      Signif. codes:
      0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Graph to analyze interaction



Multiple comparisons

≻ fm_mea	ans				
strain	emmean	SE	df	lower.CL	upper.CL
MSE	94.3	3.11	20	87.9	100.8
MSEsul	58.9	3.11	20	52.4	65.4
MSEsu2	106.0	3.11	20	99.5	112.4
MSEsu3	147.2	3.11	20	140.7	153.6
MSEsu4	141.8	3.11	20	135.3	148.3
MSEsu5	132.6	3.11	20	126.1	139.1
MSEsu6	89.1	3.11	20	82.6	95.6
MSEsu7	71.0	3.11	20	64.5	77.5
MSEsu8	142.6	3.11	20	136.1	149.0
MSEsu9	55.2	3.11	20	48.8	61.7

Multiple comparisons

Results are avera	aged over	the	٦e	/els of:	nicot_acio
Confidence level	used: 0.9	45 - C			
> pairs(fm_means))				
contrast	estimate	SE	df	t.ratio	p.value
MSE – MSEsul	35.45	4.4	20	8.063	<.0001
MSE – MSEsu2	-11.60	4.4	20	-2.638	0.2628
MSE – MSEsu3	-52.80	4.4	20	-12.009	<.0001
MSE – MSEsu4	-47.45	4.4	20	-10.792	<.0001
MSE – MSEsu5	-38.25	4.4	20	-8.700	<.0001
MSE – MSEsu6	5.25	4.4	20	1.194	0.9650
MSE – MSEsu7	23.35	4.4	20	5.311	0.0011
MSE – MSEsu8	-48.20	4.4	20	-10.963	<.0001
MSE – MSEsu9	39.10	4.4	20	8.893	<.0001
MSEsul - MSEsu2	-47.05	4.4	20	-10.701	<.0001
MSEsul - MSEsu3	-88.25	4.4	20	-20.072	<.0001
	00 00	a a	20		~~~+

References

 Chapters 7 (Analysis of Variance II: Multiway Classifications) and 15 (Analysis of Variance III: Factorial Experiments)¹ (for a more classical view)

1. Steel, R. G. & Torrie, J. H. Principles and Procedures of Statistics: A Biometrical Approach. 2nd Edition. (1980)