ORIGIN ≡ 1

Two-Way ANOVA without Replication

As described previously, One-Way ANOVA with Fixed Effects Model (also termed "Single Factor" or "Between Groups" ANOVA) represents an extension of the Two-Sample t-Test with equal variance to analyses involving $k \geq 2$ groups (often termed "treatments" or "factor levels"). The ANOVA extensions of the Paired t-Test, in which data are matched exactly across groups ("treatments" or "factor levels"), are called Repeated One-Way ANOVA designs (also termed "Within-Subjects" Single-Factor ANOVA). They are also sometimes called "Radomized Block" studies emphasizing the importance of proper experimental design in the presentation of treatments to multiple individuals ("objects" or "replicates") within the study. Such concerns were also present in the Paired t-Test but become much more so in Repeated-Measures ANOVA.   In considering the Assumption section below, it is useful to note that this test represents a simple example of a linear mixed model, or "Type III" ANOVA, as described in *Biostatistics* Worksheet 310.

Data Structure:

k groups (treatments) exactly matched within individuals (objects). Typically, the order in which specific treatments are presented to individuals is randomized and exactly matched over the n replicates.

Let index i,j indicate the ith column (treatment class) and jth row (object, or block).

Repeated Measures One-Way ANOVA					
	Treatment Classes:				
Objects (Replicates)	#1	#2	#3	…	#k
1					
2					
3					
…					
n	n	n	n		n
means:	X1bar	X2bar	X3bar	…	Xkbar

Model:

$$X_{i,j} = \mu + \rho_j + \alpha_i + \varepsilon_{i,j}$$

< where:

μ is the grand mean of all objects.
ρ_j is a random effect for each object (replicate) j
α_i is a constant effect for each treatment i.
$\varepsilon_{i,j}$ is the error term specific to each object i,j

Restriction:

$$\sum_i \alpha_i := 0$$

< allows estimation of k parameters.

Assumptions:

ρ_j are a random sample $\sim N(0, \sigma_\rho^2)$

ε_{ij} are a random sample $\sim N(0,\sigma^2)$, spherical

ρ_j and ε_{ij} are independent.

Number & Means:

ZAR := READPRN("c:/DATA/Biostatistics/ZarEX12.4R.txt")

$Y := ZAR^{\langle 2 \rangle}$

a := 3　　**< number of treatments**

b := 5　　**< number of blocks (objects repeatedly measured)**

n := 15　　**< total number of measures = 5 objects X 3 treatments**

Zar Example 12.4:

	time	treatment	block
1	8.25	1	1
2	11	1	2
3	10.25	1	3
4	9.5	1	4
5	8.75	1	5
6	11.25	2	1
7	12.5	2	2
8	12	2	3
9	9.75	2	4
10	11	2	5
11	10.75	3	1
12	11.75	3	2
13	11.25	3	3
14	9	3	4
15	10	3	5

$$GM := \frac{1}{n} \cdot \left(\sum Y \right) \qquad GM = 10.4667 \qquad \text{< grand mean - sample estimate of } \mu$$

$$A_1 := \begin{pmatrix} 8.25 \\ 11 \\ 10.25 \\ 9.5 \\ 8.75 \end{pmatrix} \qquad A_2 := \begin{pmatrix} 11.25 \\ 12.5 \\ 12 \\ 9.75 \\ 11 \end{pmatrix} \qquad A_3 := \begin{pmatrix} 10.75 \\ 11.75 \\ 11.25 \\ 9 \\ 10 \end{pmatrix} \qquad \text{< treatments}$$

$$A_{bar} := \begin{pmatrix} \text{mean}(A_1) \\ \text{mean}(A_2) \\ \text{mean}(A_3) \end{pmatrix} \qquad A_{bar} = \begin{pmatrix} 9.55 \\ 11.3 \\ 10.55 \end{pmatrix} \qquad \text{< means for treatments}$$

$$B_1 := \begin{pmatrix} 8.25 \\ 11.25 \\ 10.75 \end{pmatrix} \quad B_2 := \begin{pmatrix} 11.0 \\ 12.5 \\ 11.75 \end{pmatrix} \quad B_3 := \begin{pmatrix} 10.25 \\ 12 \\ 11.25 \end{pmatrix} \quad B_4 := \begin{pmatrix} 9.5 \\ 9.75 \\ 9 \end{pmatrix} \quad B_5 := \begin{pmatrix} 8.75 \\ 11 \\ 10 \end{pmatrix} \quad \text{< blocks}$$

$$B_{bar} := \begin{pmatrix} \text{mean}(B_1) \\ \text{mean}(B_2) \\ \text{mean}(B_3) \\ \text{mean}(B_4) \\ \text{mean}(B_5) \end{pmatrix} \qquad B_{bar} = \begin{pmatrix} 10.0833 \\ 11.75 \\ 11.1667 \\ 9.4167 \\ 9.9167 \end{pmatrix} \qquad \text{< means for blocks}$$

$$Y = \begin{pmatrix} 8.25 \\ 11 \\ 10.25 \\ 9.5 \\ 8.75 \\ 11.25 \\ 12.5 \\ 12 \\ 9.75 \\ 11 \\ 10.75 \\ 11.75 \\ 11.25 \\ 9 \\ 10 \end{pmatrix}$$

Sums of Squares:

$$SS_{TOT} := \sum (Y - GM)^2 \qquad\qquad SS_{TOT} = 21.7333 \qquad \text{< Total Sum of Squares}$$

$$i := 1 .. a$$

$$SS_A := b \cdot \left[\sum_i \left(A_{bar_i} - GM \right)^2 \right] \qquad SS_A = 7.7083 \qquad \text{< Sums of Squares for treatments}$$

$$j := 1 .. b$$

$$SS_B := a \cdot \sum_j \left(B_{bar_j} - GM \right)^2 \qquad SS_B = 11.0667 \qquad \text{< Sums of Squares for blocks (objects or subjects)}$$

$$SS_E := SS_{TOT} - SS_A - SS_B \qquad SS_E = 2.9583 \qquad \text{< Between (treatment) Sum of Squares}$$

Two-Way ANOVA without Replication Table:

Source:	SS	df		MS	
Treatments	$SS_A = 7.7083$	$df_A := a - 1$	$df_A = 2$	$MS_A := \dfrac{SS_A}{df_A}$	$MS_A = 3.8542$
Blocks	$SS_B = 11.0667$	$df_B := b - 1$	$df_B = 4$	$MS_B := \dfrac{SS_B}{df_B}$	$MS_B = 2.7667$
Error	$SS_E = 2.9583$	$df_E := (a - 1) \cdot (b - 1)$	$df_E = 8$	$MS_E := \dfrac{SS_E}{df_E}$	$MS_E = 0.3698$
TOTAL	$SS_{TOT} = 21.7333$	$df_T := n - 1$	$df_T = 14$		

F Test for Overall Comparison of Treatment Effect:

Hypotheses:

H_0: $\alpha_i = 0$ *for all* **i**   **< All treatment class deviations from the grand mean are 0**

H_1: *At least one* $\alpha_i \neq 0$ **< Two sided test**

Test Statistic:

$$F := \frac{MS_A}{MS_E} \qquad F = 10.4225 \qquad \text{< Ratio of "treatment" versus "error" Mean Squares}$$

Sampling Distribution of the test Statistic F:

If Assumptions hold and H_0 is true then F $\sim F_{(dfA, dfE)}$

Critical Value of the Test:

$\alpha := 0.05$ **< Probability of Type I error must be explicitly set**

$C := qF\left(1 - \alpha, df_A, df_E\right)$ $C = 4.459$

Decision Rule:

IF F > C, THEN REJECT H_0 OTHERWISE ACCEPT H_0

Probability Value:

$P_A := 1 - pF\left(F, df_A, df_E\right)$ $P_A = 0.0059166$

Prototype in R:

```
#BALANCED TWO-WAY ANOVA
#FIXED EFFECTS (ANOVA MODEL I)
#WITHOUT REPLICATION
#ZAR EXAMPLE 12.4
ZAR=read.table("c:/DATA/Biostatistics/ZarEX12.4R.txt")
ZAR
attach(ZAR)
Y=time
A=factor(treatment)
B=factor(block)

options(digits=12)
anova(lm(Y~A*B))
```

```
Analysis of Variance Table

Response: Y
          Df        Sum Sq      Mean Sq  F value Pr(>F)
A          2   7.708333333  3.854166667
B          4  11.066666667  2.766666667
A:B        8   2.958333333  0.369791667
Residuals  0   0.000000000
Warning message:
In anova.lm(lm(Y ~ A * B)) :
  ANOVA F-tests on an essentially perfect fit are unreliable
```

^ SS, df & MS are correct.

$$MS_A = 3.8542$$

$$MS_E = 0.3698$$

```
#CALCULATING ANOVA F:
F=3.854166667/0.369791667
F
alpha=0.05
dfA=2
dfE=8
C=qf(1-alpha,dfA,dfE)
C
P=1-pf(F,dfA,dfE)
P
```

$$F := \frac{MS_A}{MS_E} \qquad F = 10.422535211$$

^ In this case we have to conduct the test on our own by pulling out the appropriate numbers from the ANOVA table and calculating F.

$$C := qF\left(1 - \alpha, df_A, df_E\right) \qquad C = 4.458970108$$

```
> F
[1] 10.4225352028

> C
[1] 4.45897010752

> P
[1] 0.0059166180575
```