ORIGIN ≡ 1

ANOVA Randomized Block Design

ANOVA designs involving "randomized blocks with replicates", also termed ANOVA "repeated measures designs with replicates", are an extension of the approach in *Biostatistics* Worksheet 300 by adding replicate sets of mached observations. Whereas before, individuals (or objects) comprised "blocks" by themselves, now a block contains replicate sets that are considered more similar to each other (i.e., correlated) than to observations taken from other blocks. The objective of the ANOVA analysis is to control for these correlations when assessing treatment effect. This approach is an example of "mixed-model" (Type III) ANOVA. Shown here is the traditional approach to this problem using a standard two-way ANOVA table and modified Mean Squares F-ratios as specified by Zar's Table 12.3 p. 262 and *Biostatistics* Worksheet 310. More modern approaches to mixed model ANOVA, utilizing liklihood estimation and ANOVA full versus reduced model tests, have largely supplanted the methods presented here. Data is from JC Pinhiero & DM Bates 2004 *Mixed-Effects Models in S and S-Plus* p. 21.

Data Structure:

k treatments exactly matched within individuals (objects). Typically, the order in which specific treatments are presented to individuals is randomized with n replicates for each combination of treatment and block.

Let index i,j indicate the ith column (treatment class) and jth row (block). For each i,j combination, there are n replicates.

ANOVA Randomized Block Design					
	Treatment Classes:				
Blocks	#1	#2	#3	...	#k
1	n	n	n		n
2	n	n	n		n
3	n	n	n		n
...					
b	n	n	n		n
means:	X1bar	X2bar	X3bar	...	Xkbar

Model:

$X_{i,j} = \mu + \rho_j + \alpha_i + \alpha_i\rho_j + \varepsilon_{i,j}$ **< where:**

μ is the grand mean of all objects.
ρ_j is a random effect for each block j
α_i is a constant effect for each treatment i.
$\alpha_i\rho_j$ is the interaction between treatment and block
$\varepsilon_{i,j}$ is the error term specific to each object i,j

Restriction:

$\sum_i \alpha_i := 0 \quad \sum_j \rho_j := 0 \quad \sum_i \alpha\rho_{ij} := 0$

^ allows estimation of parameters.

Assumptions:

ρ_j are a random sample ~ N(0, σ_ρ^2)
ε_{ij} are a random sample ~ N(0,σ^2), spherical
ρ_j and ε_{ij} are independent.

Number & Means:

M := READPRN("c:/DATA/Biostatistics/machines.txt")

$Y := M^{\langle 3\rangle}$ **< measurement variable**

$k := 3$ **< number of treatments (machines)**

$b := 6$ **< number of blocks (workers)**

$n := 3$ **< number of replicates**

$N := 54$ **< total number of observations**

PB Machines example:

M =

	1	2	3
1	1	1	52
2	1	1	52.8
3	1	1	53.1
4	2	1	51.8
5	2	1	52.8
6	2	1	53.1
7	3	1	60
8	3	1	60.2
9	3	1	58.4
10	4	1	51.1
11	4	1	52.3
12	4	1	50.3
13	5	1	50.9
14	5	1	51.8
15	5	1	51.4
16	6	1	46.4

$GM := \frac{1}{N} \cdot \left(\sum Y \right)$ $\quad GM = 59.65$ **< grand mean - sample estimate of μ**

$j := 1 .. k \cdot b$ $\quad A1_j := \left(M^{\langle 3 \rangle} \right)_j$

$A2_j := \left(M^{\langle 3 \rangle} \right)_{j+k \cdot b}$

$A3_j := \left(M^{\langle 3 \rangle} \right)_{j+2 \cdot k \cdot b}$

$$A_1 = \begin{pmatrix} 52 \\ 52.8 \\ 53.1 \\ 51.8 \\ 52.8 \\ 53.1 \\ 60 \\ 60.2 \\ 58.4 \\ 51.1 \\ 52.3 \\ 50.3 \\ 50.9 \\ 51.8 \\ 51.4 \\ 46.4 \\ 44.8 \\ 49.2 \end{pmatrix} \quad A_2 = \begin{pmatrix} 62.1 \\ 62.6 \\ 64 \\ 59.7 \\ 60 \\ 59 \\ 68.6 \\ 65.8 \\ 69.7 \\ 63.2 \\ 62.8 \\ 62.2 \\ 64.8 \\ 65 \\ 65.4 \\ 43.7 \\ 44.2 \\ 43 \end{pmatrix} \quad A_3 = \begin{pmatrix} 67.5 \\ 67.2 \\ 66.9 \\ 61.5 \\ 61.7 \\ 62.3 \\ 70.8 \\ 70.6 \\ 71 \\ 64.1 \\ 66.2 \\ 64 \\ 72.1 \\ 72 \\ 71.1 \\ 62 \\ 61.4 \\ 60.5 \end{pmatrix}$$

< treatments

$$A_{bar} := \begin{pmatrix} \text{mean}(A_1) \\ \text{mean}(A_2) \\ \text{mean}(A_3) \end{pmatrix} \qquad A_{bar} = \begin{pmatrix} 52.35556 \\ 60.32222 \\ 66.27222 \end{pmatrix}$$

< means for treatments

$$B_1 := \begin{pmatrix} 52 \\ 52.8 \\ 53.1 \\ 62.1 \\ 62.6 \\ 64 \\ 67.5 \\ 67.2 \\ 66.9 \end{pmatrix} \quad B_2 := \begin{pmatrix} 51.8 \\ 52.8 \\ 53.1 \\ 59.7 \\ 60 \\ 59 \\ 61.5 \\ 61.7 \\ 62.3 \end{pmatrix} \quad B_3 := \begin{pmatrix} 60 \\ 60.2 \\ 58.4 \\ 68.6 \\ 65.8 \\ 69.7 \\ 70.8 \\ 70.6 \\ 71 \end{pmatrix} \quad B_4 := \begin{pmatrix} 51.1 \\ 52.3 \\ 50.3 \\ 63.2 \\ 62.8 \\ 62.2 \\ 64.1 \\ 66.2 \\ 64 \end{pmatrix} \quad B_5 := \begin{pmatrix} 50.9 \\ 51.8 \\ 51.4 \\ 64.8 \\ 65 \\ 65.4 \\ 72.1 \\ 72 \\ 71.1 \end{pmatrix} \quad B_6 := \begin{pmatrix} 46.4 \\ 44.8 \\ 49.2 \\ 43.7 \\ 44.2 \\ 43 \\ 62 \\ 61.4 \\ 60.5 \end{pmatrix}$$

< blocks

$$B_{bar} := \begin{pmatrix} \text{mean}(B_1) \\ \text{mean}(B_2) \\ \text{mean}(B_3) \\ \text{mean}(B_4) \\ \text{mean}(B_5) \\ \text{mean}(B_6) \end{pmatrix} \qquad B_{bar} = \begin{pmatrix} 60.91111 \\ 57.98889 \\ 66.12222 \\ 59.57778 \\ 62.72222 \\ 50.57778 \end{pmatrix}$$

< means for blocks

$$AB_{11} := \begin{pmatrix} 52 \\ 52.8 \\ 53.1 \end{pmatrix} \quad AB_{12} := \begin{pmatrix} 51.8 \\ 52.8 \\ 53.1 \end{pmatrix} \quad AB_{13} := \begin{pmatrix} 60 \\ 60.2 \\ 58.4 \end{pmatrix} \quad AB_{14} := \begin{pmatrix} 51.1 \\ 52.3 \\ 50.3 \end{pmatrix} \quad AB_{15} := \begin{pmatrix} 50.9 \\ 51.8 \\ 51.4 \end{pmatrix} \quad AB_{16} := \begin{pmatrix} 46.4 \\ 44.8 \\ 49.2 \end{pmatrix}$$

$$AB_{21} := \begin{pmatrix} 62.1 \\ 62.6 \\ 64 \end{pmatrix} \quad AB_{22} := \begin{pmatrix} 59.7 \\ 60 \\ 59 \end{pmatrix} \quad AB_{23} := \begin{pmatrix} 68.6 \\ 65.8 \\ 69.7 \end{pmatrix} \quad AB_{24} := \begin{pmatrix} 63.2 \\ 62.8 \\ 62.2 \end{pmatrix} \quad AB_{25} := \begin{pmatrix} 64.8 \\ 65 \\ 65.4 \end{pmatrix} \quad AB_{26} := \begin{pmatrix} 43.7 \\ 44.2 \\ 43 \end{pmatrix}$$

< cells

$$AB_{31} := \begin{pmatrix} 67.5 \\ 67.2 \\ 66.9 \end{pmatrix} \quad AB_{32} := \begin{pmatrix} 61.5 \\ 61.7 \\ 62.3 \end{pmatrix} \quad AB_{33} := \begin{pmatrix} 70.8 \\ 70.6 \\ 71 \end{pmatrix} \quad AB_{34} := \begin{pmatrix} 64.1 \\ 66.2 \\ 64 \end{pmatrix} \quad AB_{35} := \begin{pmatrix} 72.1 \\ 72 \\ 71.1 \end{pmatrix} \quad AB_{36} := \begin{pmatrix} 62 \\ 61.4 \\ 60.5 \end{pmatrix}$$

$$AB := \begin{pmatrix} \text{mean}(AB_{11}) & \text{mean}(AB_{21}) & \text{mean}(AB_{31}) \\ \text{mean}(AB_{12}) & \text{mean}(AB_{22}) & \text{mean}(AB_{32}) \\ \text{mean}(AB_{13}) & \text{mean}(AB_{23}) & \text{mean}(AB_{33}) \\ \text{mean}(AB_{14}) & \text{mean}(AB_{24}) & \text{mean}(AB_{34}) \\ \text{mean}(AB_{15}) & \text{mean}(AB_{25}) & \text{mean}(AB_{35}) \\ \text{mean}(AB_{16}) & \text{mean}(AB_{26}) & \text{mean}(AB_{36}) \end{pmatrix} \qquad AB = \begin{pmatrix} 52.6333 & 62.9 & 67.2 \\ 52.5667 & 59.5667 & 61.8333 \\ 59.5333 & 68.0333 & 70.8 \\ 51.2333 & 62.7333 & 64.7667 \\ 51.3667 & 65.0667 & 71.7333 \\ 46.8 & 43.6333 & 61.3 \end{pmatrix}$$

< cell means

Sums of Squares:

SSA for Treatment:

$i := 1 .. k$

$$SSA := n \cdot b \cdot \sum_i \left(A_{bar_i} - GM\right)^2 \qquad SSA = 1755.2633$$

SSB for factor B:

$j := 1 .. b$

$$SSB := n \cdot k \cdot \sum_j \left(B_{bar_j} - GM\right)^2 \qquad SSB = 1241.895$$

SSAB for Interaction AB:

$$SSAB := n \cdot \sum_i \sum_j \left(AB_{j,i} - A_{bar_i} - B_{bar_j} + GM\right)^2 \qquad SSAB = 426.53$$

SS Total:

$kk := 1 .. N$

$$SSTO := \sum_{kk} \left(Y_{kk} - GM\right)^2 \qquad SSTO = 3456.975$$

SSE for Error:

$$SSE := SSTO - SSAB - SSA - SSB \qquad SSE = 33.2867$$

Randomized Block NOVA Table:

Sum of Squares:	Degrees of Freedom:		Mean Squares:	
$SSA = 1755.2633$	$df_A := k - 1$	$df_A = 2$	$MSA := \frac{SSA}{df_A}$	$MSA = 877.6317$
$SSB = 1241.895$	$df_B := (b - 1)$	$df_B = 5$	$MSB := \frac{SSB}{df_B}$	$MSB = 248.379$
$SSAB = 426.53$	$df_{AB} := (k - 1) \cdot (b - 1)$	$df_{AB} = 10$	$MSAB := \frac{SSAB}{df_{AB}}$	$MSAB = 42.653$
$SSE = 33.2867$	$df_E := k \cdot b \cdot (n - 1)$	$df_E = 36$	$MSE := \frac{SSE}{df_E}$	$MSE = 0.9246$
$SSTO = 3456.975$	$df_T := n \cdot k \cdot b - 1$	$df_T = 53$		

Omnibus F Test for 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:

$F := \frac{MSA}{MSAB}$ $F = 20.5761$ **< Ratio of "treatment" versus "interaction" Mean Squares**

Sampling Distribution of the test Statistic F:

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

Critical Value of the Test:

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

$C := qF(1 - \alpha, df_A, df_{AB})$ $C = 4.1028$

Decision Rule:

IF F > C, THEN REJECT H_0 OTHERWISE ACCEPT H_0

Probability Value:

$P_A := 1 - pF(F, df_A, df_{AB})$ $P_A = 0.0002855$

Omnibus F Test for Block Effect:

Hypotheses:

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

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

Test Statistic:

$F := \frac{MSB}{MSE}$ $F = 268.6254$ **< Ratio of "block" versus "error" Mean Squares**

Sampling Distribution of the test Statistic F:

If Assumptions hold and H_0 is true then F ~$F_{(dfB,dfE)}$

Critical Value of the Test:

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

$C := qF(1 - \alpha, df_B, df_E)$ $C = 2.4772$

Decision Rule:

IF F > C, THEN REJECT H_0 OTHERWISE ACCEPT H_0

Probability Value:

$P_A := 1 - pF(F, df_B, df_E)$ $P_A = 0$

F Test for Treatment X Block Interaction:

Hypotheses:

H_0: $\alpha\rho_{ij}$ = 0 *for all ij* **< All treatment class deviations from the grand mean are 0**
H_1: *At least one* $\alpha\rho_{ij} \neq 0$ **< Two sided test**

Test Statistic:

$F := \frac{MSAB}{MSE}$ $F = 46.1298$ **< Ratio of "interaction" versus "error" Mean Squares**

Sampling Distribution of the test Statistic F:

If Assumptions hold and H_0 is true then F ~$F_{(dfAB,dfE)}$

Critical Value of the Test:

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

$C := qF(1 - \alpha, df_{AB}, df_E)$ $C = 2.1061$

Decision Rule:

IF F > C, THEN REJECT H_0 OTHERWISE ACCEPT H_0

Probability Value:

$P_A := 1 - pF(F, df_{AB}, df_E)$ $P_A = 0$

Prototype in R:

```
#ANOVA FOR RANDOMIZED BLOCKS WITH REPLICATES

M=read.table("C:/DATA/Biostatistics/machinesR.txt",header=TRUE)
M
attach(M)
fMachine=factor(Machine)
fWorker=factor(Worker)

LM=lm(score~fMachine*fWorker)
anova(LM)

alpha = 0.05
MSA=anova(LM)[1,3]
MSB=anova(LM)[2,3]
MSAB=anova(LM)[3,3]
MSE=anova(LM)[4,3]
dfA=anova(LM)[1,1]
dfB=anova(LM)[2,1]
dfAB=anova(LM)[3,1]
dfE=anova(LM)[4,1]
```

```
> anova(LM)
Analysis of Variance Table

Response: score
                 Df  Sum Sq Mean Sq F value    Pr(>F)    
fMachine          2 1755.26  877.63  949.17 < 2.2e-16 ***
fWorker           5 1241.89  248.38  268.63 < 2.2e-16 ***
fMachine:fWorker 10  426.53   42.65   46.13 < 2.2e-16 ***
Residuals        36   33.29    0.92                      
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#OMNIBUS F TEST FOR TREATMENT EFFECT:
F=MSA/MSAB
F
C=qf(1-alpha,dfA,dfAB)
C
P=1-pf(F,dfA,dfAB)
P
```

```
> F
[1] 20.57608
> C
[1] 4.102821
> P
[1] 0.0002855485
```

```
#OMNIBUS F TEST FOR BLOCK EFFECT:
F=MSB/MSE
F
C=qf(1-alpha,dfB,dfE)
C
P=1-pf(F,dfB,dfE)
P
```

```
> F
[1] 268.6254
> C
[1] 2.477169
> P
[1] 0
```

```
#F TEST FOR TREATMENT BY BLOCK INTERACTION:
F=MSAB/MSE
F
C=qf(1-alpha,dfAB,dfE)
C
P=1-pf(F,dfAB,dfE)
P
```

```
> F
[1] 46.12982
> C
[1] 2.106054
> P
[1] 0
```