Course 02402 Introduction to Statistics

Lecture 12: Two-way Analysis of Variance, ANOVA

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Overview

1. Intro: Small example and TV-data from B&O

2. Model

3. Computation - decomposition and the ANOVA table

4. Hypothesis test (F-test)

5. Post hoc analysis

6. Model control / model validation

7. A complete example - from the book

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TV set development at Bang & Olufsen

Sound and image quality is measured by th human perceptual instrument:

Bang & Olufsen data in R

```
# Get the B&O data from the lmerTest-package
library(lmerTest)

## Error in library(lmerTest): there is no package called 'lmerTest'

data(TVbo)

## Warning in data(TVbo): data set 'TVbo' not found

# Each of 8 assessors scored each of 12 combinations 2 times.
# Take a look at the sharpness scores for one single picture
# and one of the two repetitions
TVbo_sub <- subset(TVbo, Picture == 1 & Repeat == 1)[, c(1, 2, 9)]

## Error in subset(TVbo, Picture == 1 & Repeat == 1): objekt 'TVbo' blev
ikke fundet

sharp <- matrix(TVbo_sub$Sharpness, nrow = 8, byrow = T)

## Error in matrix(TVbo_sub$Sharpness, nrow = 8, byrow = T): objekt
'TVbo_sub' blev ikke fundet

colnames(sharp) <- c("TV3", "TV2", "TV1")
```

```
## Error in colnames(sharp) <- c("TV3", "TV2", "TV1"): objekt 'sharp'
blev ikke fundet
```

Bang & Olufsen data in R

```
## Error in library(lmerTest): there is no
package called 'lmerTest'
## Warning in data(TVbo): data set 'TVbo' not
found
## Error in subset(TVbo, Picture == 1 & Repeat
== 1): objekt 'TVbo' blev ikke fundet
## Error in matrix(TVbo_sub$Sharpness, nrow =
8, byrow = T): objekt 'TVbo_sub' blev ikke
fundet
## Error in colnames(sharp) <- c("TV3", "TV2",
"TV1"): objekt 'sharp' blev ikke fundet
## Error in rownames(sharp) <- c("Person 1",
"Person 2", "Person 3", "Person 4", : objekt
```

```
'sharp' blev ikke fundet
## Error in xtable(sharp): objekt 'sharp' blev
```

Two-way ANOVA - example

- Same data as for one-way, but now we know that the experiment was split into blocks:

	Group A	Group B	Group C
Block 1	2.8	5.5	5.8
Block 2	3.6	6.3	8.3
Block 3	3.4	6.1	6.9
Block 4	2.3	5.7	6.1

  - Hence three *groups* on four *blocks*,
  - or three *treatments* on four *persons*,
  - or three *varieties* on four *fields* (hence blocks),
  - or something similar.

- *One-way* vs. *two-way* ANOVA

- *Completely randomized design* vs. *Randomized block design*

Two-way ANOVA - example

- Same data as for one-way, but now we know that the experiment was split into blocks:

	Group A	Group B	Group C
Block 1	2.8	5.5	5.8
Block 2	3.6	6.3	8.3
Block 3	3.4	6.1	6.9
Block 4	2.3	5.7	6.1

- Question: Is there a significant difference (in means) between the groups A, B and C?

- ANOVA can be used if the observations in each group are (approximately) normal distributed or if the n_is are large enough (CLT).

The toy data in R

```r
# Observations
y <- c(2.8, 3.6, 3.4, 2.3,
       5.5, 6.3, 6.1, 5.7,
       5.8, 8.3, 6.9, 6.1)

# Treatments (groups, varieties)
treatm <- factor(c(1, 1, 1, 1,
                   2, 2, 2, 2,
                   3, 3, 3, 3))

# Blocks (persons, fields)
block <- factor(c(1, 2, 3, 4,
                  1, 2, 3, 4,
                  1, 2, 3, 4))

# No. of treatments and no. of blocks (for later formulas)
(k <- length(unique(treatm)))
(l <- length(unique(block)))

# Box plots by treatment
plot(treatm, y, xlab = "Treatment", ylab = "y")

# Box plots by  block
plot(block, y, xlab = "Block", ylab="y")
```

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Two-way ANOVA, model

- The model may be formulated as

$$Y_{ij} = \mu + \alpha_i + \beta_j + \varepsilon_{ij},$$

  where the errors are i.i.d. with

$$\varepsilon_{ij} \sim N(0, \sigma^2).$$

  - μ is the overall mean
  - α_i is the effect of treatment i
  - β_j is the level for block j
  - There are k treatments and l blocks

Estimates of parameters in the model

- We can compute the estimates of the parameters ($\hat{\mu}$, $\hat{\alpha}_i$, and $\hat{\beta}_j$)

$$\hat{\mu} = \bar{y} = \frac{1}{k \cdot l} \sum_{i=1}^{k} \sum_{j=1}^{l} y_{ij}$$

$$\hat{\alpha}_i = \left(\frac{1}{k} \sum_{j=1}^{k} y_{ij} \right) - \hat{\mu}$$

$$\hat{\beta}_j = \left(\frac{1}{l} \sum_{i=1}^{l} y_{ij} \right) - \hat{\mu}$$

```r
# Sample mean
(mu_hat <- mean(y))

# Sample mean deviation for each treatment
(alpha_hat <- tapply(y, treatm, mean) - mu_hat)

# Sample mean deviation for each block
(beta_hat <- tapply(y, block, mean) - mu_hat)
```

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Two-way ANOVA, decomposition and the ANOVA table, Theorem 8.20

- With the model

$$Y_{ij} = \mu + \alpha_i + \beta_j + \varepsilon_{ij}, \quad \varepsilon_{ij} \overset{\text{i.i.d.}}{\sim} N(0, \sigma^2)$$

  the <u>total variation in the data can be decomposed</u>:

$$SST = SS(Tr) + SS(Bl) + SSE$$

- 'Two-way' refers to the fact that there are two factors (grouping variables) in the experiment.

- The method is called <u>analysis of variance</u>, because hypothesis testing is carried out by comparing certain variances.

Formulas for sums of squares

- Total sum of squares (or "the total variance", same as for one-way)

$$SST = \sum_{i=1}^{k} \sum_{j=1}^{l} (y_{ij} - \hat{\mu})^2$$

- Treatment sum of squares (or "variance explained by the treatment part of the model")

$$SS(Tr) = l \cdot \sum_{i=1}^{k} \hat{\alpha}_i^2$$

Formulas for sums of squares

- Sum of squares for blocks/persons ("variance explained by the block part of the model")

$$SS(Bl) = k \cdot \sum_{j=1}^{l} \hat{\beta}_j^2$$

- Sum of squares for the residuals ("residual variance after model fit")

$$SSE = \sum_{i=1}^{k} \sum_{j=1}^{l} (y_{ij} - \hat{\alpha}_i - \hat{\beta}_j - \hat{\mu})^2$$

Overview

Two-way ANOVA: Hypothesis of no effect of treatment, Theorem 8.22

- We want to compare (more than 2) means $\mu + \alpha_i$ in the model

$$Y_{ij} = \mu + \alpha_i + \beta_j + \varepsilon_{ij}, \quad \varepsilon_{ij} \overset{\text{i.i.d.}}{\sim} N(0, \sigma^2)$$

- The hypothesis of no difference between treatment means may be formulated as

$$H_{0,Tr}: \quad \alpha_i = 0 \quad \text{for all } i$$
$$H_{1,Tr}: \quad \alpha_i \neq 0 \quad \text{for at least one } i$$

- Under $H_{0,Tr}$ the following is true:

$$F_{Tr} = \frac{SS(Tr)/(k-1)}{SSE/((k-1)(l-1))}$$

is F-distributed with $k-1$ and $(k-1)(l-1)$ degrees of freedom.

Two-way ANOVA: hypothesis of no effect of blocks/persons, Theorem 8.22

- We want to compare (more than 2) means $\mu + \beta_j$ in the model

$$Y_{ij} = \mu + \alpha_i + \beta_j + \varepsilon_{ij}, \quad \varepsilon_{ij} \overset{\text{i.i.d.}}{\sim} N(0, \sigma^2)$$

- The hypothesis of no difference between block means may be formulated as

$$H_{0,Bl}: \quad \beta_j = 0 \quad \text{for all } j$$
$$H_{1,Bl}: \quad \beta_j \neq 0 \quad \text{for at least one } j$$

- Under $H_{0,Bl}$ the following is true:

$$F_{Bl} = \frac{SS(Bl)/(l-1)}{SSE/((k-1)(l-1))}$$

follows an F-distribution with $l-1$ and $(k-1)(l-1)$ degrees of freedom.

F-distribution and treatment hypothesis

```r
# Plot density of relevant F-distribution. Remember that this is "under H0"
# (computed as if H0 were true)
xseq <- seq(0, 10, by = 0.1)
plot(xseq, df(xseq, df1 = k-1, df2 = (k-1)*(l-1)), type = "l")

# Show critical value (5% signif. level) for test of treatment hypothesis
critical_value <- qf(0.95, df1 = k-1, df2 = (k-1)*(l-1))
abline(v = critical_value, col = "red")

# Compute value of the  test statistic
(FTr <- (SSTr/(k-1)) / (SSE/((k-1)*(l-1))))

# Compute p-value for the test
1 - pf(FTr, df1 = k-1, df2 = (k-1)*(l-1))
```

F-distribution and block hypothesis

```
# Plot density of relevant F-distribution. Remember that this is "under H0"
# (computed as if H0 were true)
xseq <- seq(0, 10, by = 0.1)
plot(xseq, df(xseq, df1 = l-1, df2 = (k-1)*(l-1)), type = "l")

# Show critical value (5% signif. level) for test of treatment hypothesis
critical_value <- qf(0.95, df1 = l-1, df2 = (k-1)*(l-1))
abline(v = critical_value, col = "red")

# Compute value of the  test statistic
(FBl <- (SSBl/(l-1)) / (SSE/((k-1)*(l-1))))

# Compute p-value for the test
1 - pf(FBl, df1 = l-1, df2 = (k-1)*(l-1))
```

The two-way ANOVA table

Source of variation	Deg. of freedom	Sums of squares	Mean sum of squares	Test-statistic F	p-value
Treatment	$k-1$	$SS(Tr)$	$MS(Tr) = \frac{SS(Tr)}{k-1}$	$F_{\mathrm{Tr}} = \frac{MS(Tr)}{MSE}$	$P(F > F_{\mathrm{Tr}})$
Block	$l-1$	$SS(Bl)$	$MS(Bl) = \frac{SS(Bl)}{l-1}$	$F_{\mathrm{Bl}} = \frac{MS(Bl)}{MSE}$	$P(F > F_{\mathrm{Bl}})$
Residual	$(k-1)(l-1)$	SSE	$MSE = \frac{SSE}{(k-1)(l-1)}$		
Total	$n-1$	SST			

```
anova(lm(y ~ treatm + block))

## Analysis of Variance Table
##
## Response: y
##            Df Sum Sq Mean Sq F value  Pr(>F)
## treatm      2  30.79   15.40   74.40 5.8e-05 ***
## block       3   3.95    1.32    6.37   0.027 *
## Residuals   6   1.24    0.21
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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Post hoc confidence interval

- Like for one-way ANOVA (use methods 8.9 and 8.10) but substitute $n-k$ degrees of freedom with $(k-1)(l-1)$ (and use MSE from the two-way ANOVA).

- Can be done with either treatments or blocks.

- A single pre-planned CI for the difference between treatment i and j:

$$\bar{y}_i - \bar{y}_j \pm t_{1-\alpha/2} \sqrt{\frac{SSE}{(k-1)(l-1)}\left(\frac{1}{n_i} + \frac{1}{n_j}\right)} \qquad (1)$$

where $t_{1-\alpha/2}$ is based on the t-distribution with $(k-1)(l-1)$ degrees of freedom.

- If all $M = k(k-1)/2$ combinations of pairwise confidence intervals are found use the formula M times but each time with $\alpha_{\mathrm{Bonferroni}} = \alpha/M$.

Post hoc pairwise hypothesis test

- A single pre-planned level α hypothesis tests:

$$H_0 : \mu_i = \mu_j, \ H_1 : \mu_i \neq \mu_j$$

is carried out as:

$$t_{\text{obs}} = \frac{\bar{y}_i - \bar{y}_j}{\sqrt{MSE \left(\frac{1}{n_i} + \frac{1}{n_j} \right)}} \qquad (2)$$

and:

$$p - \text{value} = 2P(t > |t_{\text{obs}}|)$$

where the t-distribution with $(k-1)(l-1)$ degrees of freedom is used.

- If all $M = k(k-1)/2$ combinations of pairwise confidence intervals are found use the formula M times but each time with $\alpha_{\text{Bonferroni}} = \alpha/M$.

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Model validation: Variance homogeneity

Make box plots of the *residuals* to check whether the variability seems different across the groups.

```
# Save the  fitted model
fit <- lm(y ~ treatm + block)

# Make box plots of residuals
par(mfrow = c(1,2))
plot(treatm, fit$residuals, xlab = "Treatment")
plot(block, fit$residuals, xlab = "Block")
```

Model validation: Normality

Make a normal QQ-plot to check whether the distribution of the residuals seems normal.

```
# Normal QQ-plot of the residuals
qqnorm(fit$residuals)
qqline(fit$residuals)
```
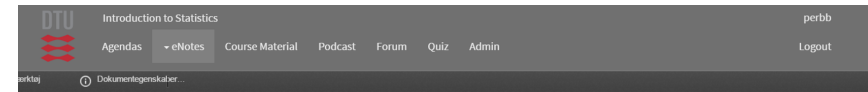
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0.3.5 A complete worked through example: Car tires

‖‖ **Example 8.26**   **Car tires**

In a study of 3 different types of tires ("treatment") effect on the fuel economy, drives of 1000 km in 4 different cars ("blocks") were carried out. The results are listed in the following table in km/l.

	Car 1	Car 2	Car 3	Car 4	*Mean*
Tire 1	22.5	24.3	24.9	22.4	22.525
Tire 2	21.5	21.3	23.9	18.4	21.275
Tire 3	22.2	21.9	21.7	17.9	20.925
Mean	21.400	22.167	23.167	19.567	21.575

Let us analyse these data with a two-way ANOVA model, but first some explorative plotting:

Collecting the data in a data frame

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