

# 3. Design Experiments and Variance Analysis

**Isabel M. Rodrigues**

## 3.1. Completely randomized experiment.

- ▶ Experimentation allows an investigator to find out what happens to the output variables when the settings of the input variables in a system are purposely changed.
- ▶ In many investigations, e.g. in social sciences, in economics, in ecological field studies, there is no control over the way that data arise. No interventions are made, we simply observe. These are observational studies. The standard methods of analysis (ANOVA, regression etc.) are valid but the wider applicability of conclusions is limited.
- ▶ In experiments, such as laboratory experiments, we can deliberately vary the conditions and observe the changing responses. Such planned experiments allow conclusions to be drawn which can not be drawn from observational studies, e.g. about cause and effect.

## 3.1. Completely randomized experiment.

- ▶ In the **Observational Studies** is investigate the characteristics of an output variable  $y$ , and conceptually, once a unit  $i$  is selected, there is a fixed (non-random) value  $y_i$  of the output to be obtained.
- ▶ In **Experimental Design Studies**, the values of input variables are carefully chosen and controlled, and the output variables are regarded as random in that the values of the output variables will change over repeated experiments under the same setting of the input variables. Experimental design was introduced by Sir Ronald Fisher, in the context of agricultural experiments at Rothamstead Experimental Station. When Fisher joined Rothamstead, RES employees knew that their fields had fertility gradients, different exposures to sunlight, and that yield could be affected by crops and practices used in previous seasons.

## 3.1. Completely randomized experiment.

- ▶ It was not sufficient to pick one field at random and use, say, fertilizer A, and another at random and use fertilizer B, then compare the yields. The observed difference could be due to sunlight exposure or previous crops.
- ▶ In principle one could pick many fields at random for fertilizer A, and many fields at random for fertilizer B, and then compare the results.
- ▶ But it is even better if you can pick the fields at random in such a way that the choice controls for possible confounding factors; e.g., it would be good if equal numbers of fertilizer A fields and fertilizer B fields were in bright sunshine (or shaded), or had good drainage (or not), and so forth.

## 3.1. Completely randomized experiment.

- ▶ We also assume that the setting of the input variables determines the distribution of the output variables, in a way to be discovered. The population under study is the collection of all possible quantitative settings behind each setting of experimental factors and is (at least conceptually) infinite.
- ▶ **Experimental Design Terminology:** Because these methods are used in a wide range of areas of application, a standard terminology is used.

## 3.1. Completely randomized experiment.

- ▶ **Experimental Unit:** The basic set of conditions/materials on which a single element of the experiment is carried out (e.g. patient, blood sample, piece of material etc.).
- ▶ **Treatment:** What we do to the experimental unit. In various situations a treatment can be a type of drug, a catalyst, a type of fertilizer, a methodology etc.
- ▶ **Trial:** A single, independent application of a treatment to an experimental unit.
- ▶ **Response:** The outcome of a trial - also known as an observation, or collectively as data.
- ▶ **Block:** A set of experimental units with some common property, e.g. patients with similar characteristics.
- ▶ **Factor:** A controllable experimental variable that is thought to influence the response.

## 3.1. Completely randomized experiment.

- ▶ **Nuisance factor** : As above but outside the control of the experimenter, e.g. environmental variables.
- ▶ **Level**: Specific value of a factor.
- ▶ **Interaction**: Existence of joint factor effects in which the effect of each factor depends on the levels of the other factors.
- ▶ **Replication**: Repetition of an entire experiment or a portion of an experiment under two or more sets of conditions. Most experiments have several replications. To be genuine replications, each replication must be carried out independently on distinct sets of experimental units.

## 3.1. Completely randomized experiment.

### Completely Randomized Design

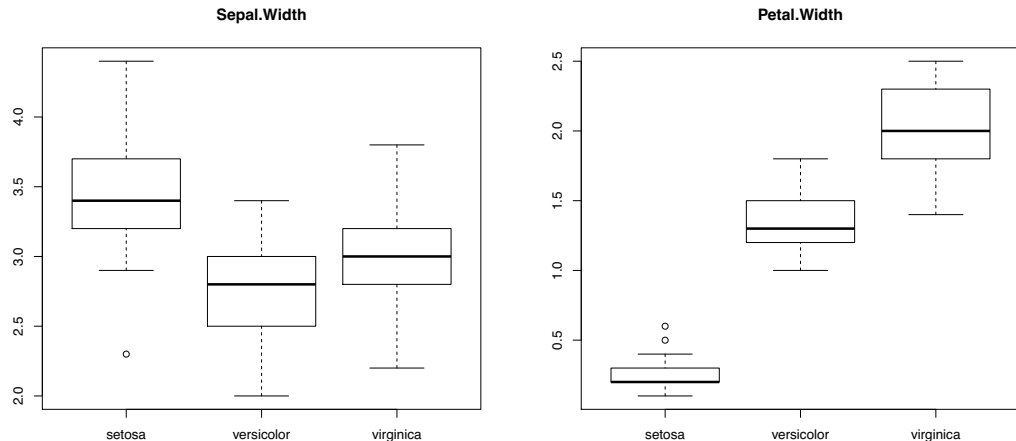
A completely randomized design is a design for which independent random samples of experimental units are selected for each treatment. The **ANOVA** is used to test whether or not different levels (qualitative or quantitative) of  $a > 2$  treatments involved in populations cause property change. For examples:

1. An experiment to study the effects of five different brands of gasoline on auto mobile engine operating efficiency (mpg);
2. An experiment to study the effects of the presence of four different sugar solutions (glucose, sucrose, fructose, and a mixture of the three) on bacterial growth;
3. An experiment to study the effects of the four different training methods for the course of statistics on the scores of examination.



## 3.2. Single-factor analysis variance, (one-way ANOVA).

- ▶ The ANOVA methodology was proposed by Sir Ronald Fisher in the Rothamstead Experimental Station.
- ▶ The aim is to see if there is any difference between groups on some variable. As an example let us see the **IRIS** data set with the variables **Sepal Width** and **Petal Width** by the groups **Setosa**, **Versicolor** and **Virginica**.



- ▶ The variable Petal Width looks like different for the three groups.

## 3.2. Single-factor analysis variance, (one-way ANOVA).

- ▶ Suppose there are  $a > 2$  treatments. For each treatment  $i$  there are  $n_i$  independent experiment runs. A design is called balanced if  $n_1 = n_2 = \dots n_a$ . For a balanced single factor design the total number of runs is  $N = na$ . A completely randomized design would randomly assign  $a$  runs to treatment 1,  $a$  runs to treatment 2, etc.
- ▶ Some Notation:
  - ▶  $a$ : is the number of treatments;
  - ▶  $y_{ij}$ : is the measurement on the  $j$ th unit receiving treatment  $i$ ;
  - ▶  $n_i$ : is the number of experimental units that received treatment  $i$ ;
  - ▶  $N$ : is the total number of observations;
  - ▶  $y_i$ . is the sum of all measurements for units receiving treatment  $i$ ;
  - ▶  $\bar{y}_i$ .: is the average of all measurements for units receiving treatment  $i$ ;
  - ▶  $\bar{y}_{..}$ .: is the average of all measurements.

## 3.2. Single-factor analysis variance, (one-way ANOVA).

- ▶ The analysis of variance (ANOVA) works by splitting up the variation between the data into components which are assigned to various sources. In the one-way ANOVA these sources include differences among the population means and random errors.

### Model one-way ANOVA

$$Y_{ij} = \mu_i + \varepsilon_{ij} = \mu + \tau_i + \varepsilon_{ij}$$

- ▶ In each case the errors  $\varepsilon_{ij}$  are independent and identically distributed  $N(0, \sigma^2)$ . In the second parametrization  $\mu$  is an overall mean and  $\tau_i$  is a treatment effect. In order not to have too many parameters we apply the constraint  $\sum_{i=1}^a \tau_i = 0$ . Alternatively we may make  $\mu$  represent the mean for the first population and set  $\tau_1 = 0$ . In this case  $\tau_2, \dots, \tau_a$  represent differences of the other population means from the first.

## 3.2. Single-factor analysis variance, (one-way ANOVA).

- ▶ Note that we thus have three key assumptions assumed in all populations:
  1. normality,
  2. independence,
  3. equal variances.

Our primary interest is to test if the treatment means are all the same, i.e. to test:

$$H_0 : \mu_1 = \mu_2 = \cdots = \mu_a \text{ vs } H_1 : \mu_i \neq \mu_j \text{ for some } (i, j),$$

or in the equivalent formulation

$$H_0 : \tau_1 = \tau_2 = \cdots = \tau_a = 0 \text{ vs } H_1 : \tau_i \neq 0 \text{ for some } i.$$

## 3.2. Single-factor analysis variance, (one-way ANOVA).

- ▶ The strategy in making an ANOVA test is to partition the total variation in the data into components attributable to different effects.
- ▶ In the case of one-way ANOVA, we divide the total sum of squares ( $SST$ ) into the part attributable to differences between the treatment means ( $SSTR$ ) and the part attributable to differences within treatment groups, or the sum of squares due to pure error ( $SSE$ ),  $SST = SSTR + SSE$ .

- ▶ 
$$SST = \sum_i^a \sum_j^{n_i} (y_{ij} - \bar{y}_{..})^2 = \sum_i^a \sum_j^{n_i} y_{ij}^2 - \frac{y_{..}^2}{N}$$

- ▶ Between-treatment: 
$$SSTR = \sum_i^a n_i (\bar{y}_{i.} - \bar{y}_{..})^2 = \sum_i^a \frac{y_{i.}^2}{n_i} - \frac{y_{..}^2}{N}$$

- ▶ Within-treatment: 
$$SSE = \sum_i^a \sum_j^{n_i} (y_{ij} - \bar{y}_{i.})^2.$$

## 3.2. Single-factor analysis variance, (one-way ANOVA).

► Anova Table:

Source of variation	$SS$	$df$	$MS$
Treatments	$SSTR$	$a - 1$	$MSTR = \frac{SSTR}{a-1}$
Error	$SSE$	$N - a$	$MSE = \frac{SSE}{N-a}$
Total	$SST$	$N - 1$	

## 3.2. Single-factor analysis variance, (one-way ANOVA).

- ▶ It is possible to show that  $\hat{\sigma}^2 = MSE$  and is an unbiased estimator:

$$E[MSE] = \sigma^2 \quad \text{and} \quad \frac{SSE}{\sigma^2} \sim \chi^2_{(N-a)}.$$

On the other hand:

$$E[MSTR] = \sigma^2 + \frac{1}{a-1} \sum_{i=1}^a n_i (\mu_i - \mu)^2.$$

- ▶ Hence, if  $H_0$  is true, we have

$$E[MST] = \sigma^2 \quad \text{and} \quad \frac{SST}{\sigma^2} \sim \chi^2_{(N-1)}.$$

- ▶ If  $H_0$  is true we have that  $E[MSTR] = \sigma^2$  and  $\frac{SSTR}{\sigma^2} \sim \chi^2_{(a-1)}$ , on the other hand if  $H_1$  is true  $E[MSTR] > E[MSE]$ .

## 3.2. Single-factor analysis variance, (one-way ANOVA).

Test Statistic-equality of effects:

$$F_0 = \frac{MSTR}{MSE} \stackrel{H_0}{\sim} F_{(a-1, N-a)}$$

- ▶ If  $H_0$  is not true,  $MSTR$  will become quite large. Hence, if the value of  $F_0 \gg 1$ , we will reject  $H_0$ . Accordingly, we will perform upper-tailed  $F$ -test.



## 3.2. Single-factor analysis variance, (one-way ANOVA).

Balanced Design:  $N = an$

- ▶ Choosing a balanced design has two important advantages:
  1. ANOVA is relatively insensitive to small departures from the assumption of equality of variances if the sample sizes are equal. This is not the case for unequal sample sizes.
  2. The power of the test is maximized if the samples are of equal size.

## 3.3. Multiple comparisons.

- ▶ The ANOVA is a powerful procedure for test the homogeneity of a set of means. However, if we reject the null hypothesis and accept the stated alternative that the means are not all equal we still do not know which of the population means are equal and which are different. We can analyse how the treatments differers.

Inferences for a single mean value:  $\mu_i$ . Since  $\bar{Y}_{i.} \sim N(\mu_i, \frac{\sigma^2}{n_i})$ ,

we have the pivotal variable: 
$$\frac{\bar{Y}_{i.} - \mu_i}{\sqrt{\frac{MSE}{n_i}}} \sim t_{(N-a)}$$

- ▶  $C.I. \cdot (1-\alpha) \times 100\%(\mu_i) = \left( \bar{Y}_{i.} \pm t_{1-\frac{\alpha}{2}}(N-a) \sqrt{\frac{MSE}{n_i}} \right)$ .

## 3.3. Multiple comparisons.

Paired Comparison-inference for  $(\mu_i - \mu_j)$

From

$$\bar{Y}_{i.} - \bar{Y}_{j.} \sim N\left(\mu_i - \mu_j, \frac{\sigma^2}{n_i} + \frac{\sigma^2}{n_j}\right),$$

we have the pivotal variable:

$$\frac{\bar{Y}_{i.} - \bar{Y}_{j.} - (\mu_i - \mu_j)}{\sqrt{MSE \left( \frac{1}{n_i} + \frac{1}{n_j} \right)}} \sim t_{(N-a)}$$

- ▶ The  $(1 - \alpha) \times 100\%$  confidence interval for  $(\mu_i - \mu_j)$  is given by:

$$\left( (\bar{Y}_{i.} - \bar{Y}_{j.}) \pm t_{1-\frac{\alpha}{2}, (N-a)} \sqrt{MSE \left( \frac{1}{n_i} + \frac{1}{n_j} \right)} \right).$$

### 3.3. Multiple comparisons.

- ▶ As a general rule, if the CI does not contain zero, then these two means can be considered statistically different (with confidence level  $(1 - \alpha)$ ).
- ▶ With  $a$  treatment there are  $g = a(a - 1)/2$  pairs of means to be compared and we want the overall confidence level for all intervals to be “correct”  $(1 - \alpha) \times 100\%$  of the times.
- ▶ For example, if we construct many 95% confidence intervals, the chance that they all contain the true values of the parameters that they estimate will be lower than 95%. For  $g$  independent confidence intervals we have  $P(\text{all confidence intervals cover their parameters}) = 0.95^g$ .

$g$	1	2	3	...	10	...	100
$0.95^g$	0.9500	0.9025	0.8574	...	0.5987	...	0.0059

### 3.3. Multiple comparisons.

- ▶ One possible correction for the two by two investigate differences is the follow: the par of means  $\mu_i$  and  $\mu_j$  are declared significantly different if

$$|\bar{y}_{i.} - \bar{y}_{j.}| > LSD,$$

where  $LSD = z \sqrt{MSE \left( \frac{1}{n_i} + \frac{1}{n_j} \right)}$  and  $z = t_{1 - \frac{\alpha}{2g}}(N-a)$  where  $g$  is the total number of comparisons under study. This is called Bonferroni correction.

- ▶ Residuals are  $e_{ij} = y_{ij} - \bar{y}_{i.}$ . The residuals analysis and model checking can be performed as we did in multiple regression, e.g., qq-plots, plots of  $e_{ij}$  vs  $\bar{y}_{i.}$  and  $e_{ij}$  vs factor levels.

## Iris data set with

- ▶ Two equivalent ways: `aov` command

```
> iris.aov= aov(Petal.Width ~ Species, data=iris)
Call:
  aov(formula = Petal.Width ~ Species, data = iris)

Terms:
              Species Residuals
Sum of Squares 80.41333   6.15660
Deg. of Freedom      2       147

Residual standard error: 0.20465
Estimated effects may be unbalanced
anova(Petal.Width ~ Species, data=iris)

> summary(iris.aov)
              Df Sum Sq Mean Sq F value Pr(>F)
Species      2  80.41   40.21    960 <2e-16 ***
Residuals   147   6.16    0.04
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

# one-way ANOVA with R

- ▶ Two equivalent ways: `lm` and `anova` commands

```
> lmiris=lm(Petal.Width ~ Species, data=iris)
> summary(lmiris)

Call:
lm(formula = Petal.Width ~ Species, data = iris)

Residuals:
    Min       1Q   Median       3Q      Max
-0.626 -0.126 -0.026  0.154  0.474

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)    0.24600    0.02894     8.50 1.96e-14 ***
Speciesversicolor  1.08000    0.04093    26.39 < 2e-16 ***
Speciesvirginica  1.78000    0.04093    43.49 < 2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.2047 on 147 degrees of freedom
Multiple R-squared:  0.9289,    Adjusted R-squared:  0.9279
F-statistic:  960 on 2 and 147 DF,  p-value: < 2.2e-16

> anova(lmiris)
Analysis of Variance Table

Response: Petal.Width
      Df Sum Sq Mean Sq F value    Pr(>F)
Species    2  80.413   40.207  960.01 < 2.2e-16 ***
Residuals 147   6.157    0.042
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

# one-way ANOVA with R

- ▶ We can obtain the estimates of  $\mu_1$ ,  $\tau_2$  and  $\tau_3$  with the command `coef`:

```
coef(iris.aov)
(Intercept) Speciesversicolor Speciesvirginica
0.246          1.080          1.780
```

- ▶  $\hat{\mu}_1 = 0.246$ : Petal Width mean for species Setosa;  
 $\hat{\tau}_2 = 1.080$ , increment of Petal Width mean for species Versicolor related to Petal Width mean for species Setosa;  
 $\hat{\tau}_3 = 1.780$ , increment of Petal Width mean for species Virginica related to Petal Width mean for species Setosa.



# one-way ANOVA with R

- ▶ To confirm let calculate the total mean and the mean by group:  
command `model.tables`

```
> model.tables(iris.aov , type="mean")
Tables of means
Grand mean

1.199333

Species
Species
  setosa versicolor virginica
  0.246    1.326    2.026
```

**Pairwise comparisons:**  
Library(`asbio`)  
command: `pairw.anova`

```
library(asbio)
pairw.anova(iris[,4],iris[,5], method="bonf")
```

95% Bonferroni confidence intervals

	Diff	Lower	Upper	Decision	Adj. p-value
musetosa-muversicolor	-1.08	-1.17912	-0.98088	Reject H0	0
musetosa-muvirginica	-1.78	-1.87912	-1.68088	Reject H0	0
muversicolor-muvirginica	-0.7	-0.79912	-0.60088	Reject H0	0

## 3.4. Two-factors analysis variance, (two-way ANOVA).

- ▶ The response variable  $Y$  is continuous.
- ▶ There are now two categorical explanatory variables (factors). Call them factor  $A$  and factor  $B$ .
- ▶ **Data for Two-way ANOVA:**
  - ▶  $Y$ , the response variable;
  - ▶ Factor  $A$  with levels  $i = 1, \dots, a$ ;
  - ▶ Factor  $B$  with levels  $j = 1, \dots, b$ ;
  - ▶ A particular combination of levels is called a treatment or a cell. There are  $ab$  treatments;
  - ▶  $Y_{ijk}$  is the  $k$ -th observation for treatment  $(i, j)$ ,  $k = 1, \dots, n$ .
- ▶ We will assume equal sample size in each treatment combination,  $n_{ij} = n > 1$  and  $N = abn$ . We have a balanced design.

## 3.4. Two-factors analysis variance, (two-way ANOVA).

### Notation

- ▶ For  $Y_{ijk}$  the subscripts are interpreted as follows:
  - ▶  $i$  denotes the level of the factor  $A$ , with  $i = 1, \dots, a$  levels of factor  $A$ ;
  - ▶  $j$  denotes the level of the factor  $B$ , with  $j = 1, \dots, b$  levels of factor  $B$ ;
  - ▶  $k$  denotes the  $k$ -th observation in cell or treatment  $(i, j)$ , with  $k = 1, \dots, n$  observations in cell  $(i, j)$ .

## 3.4. Two-factors analysis variance, (two-way ANOVA).

### Model Assumptions

- ▶ As a consequence of the assumptions to the error model, we have that the response variable observations are independent, and normally distributed with a mean that may depend on the levels of the factors  $A$  and  $B$ , and a variance that does not (is constant).

$$\text{Cell Means Model: } Y_{ijk} = \mu_{ij} + \epsilon_{ijk}$$

- ▶  $\mu_{ij}$  is the theoretical mean or expected value of all observations in cell  $(i, j)$ ;
- ▶ The errors are i.i.d.  $\epsilon_{ijk} \sim N(0; \sigma^2)$ ;
- ▶  $Y_{ijk} \sim N(\mu_{ij}; \sigma^2)$  and independent.

## 3.4. Two-factors analysis variance, (two-way ANOVA).

### Alternative:

**Factor Effects Model:**  $Y_{ijk} = \mu + \tau_i + \beta_j + (\tau\beta)_{ij} + \varepsilon_{ijk}$

- ▶  $\mu$  is the overall (grand) mean;
- ▶  $\tau_i$  is the main effect of Factor  $A$ ;
- ▶  $\beta_j$  is the main effect of Factor  $B$ ;
- ▶  $(\tau\beta)_{ij}$  is the interaction effect between  $A$  and  $B$ . Note that  $(\tau\beta)_{ij}$  is the name of a parameter and does not refer to the product of  $\tau$  and  $\beta$ .
- ▶ A model without the interaction term, i.e.,  $\mu_{ij} = \mu + \tau_i + \beta_j$  is called an additive model.

## 3.4. Two-factors analysis variance, (two-way ANOVA).

### Parameters Definition:

- ▶ The overall mean:  $\mu = \frac{\sum_i^a \sum_j^b \mu_{ij}}{ab}$ .
- ▶ The mean for the  $i$ -th level of  $A$  is  $\mu_{i\cdot} = \frac{\sum_j^b \mu_{ij}}{b}$ .
- ▶ The mean for the  $j$ -th level of  $B$  is  $\mu_{\cdot j} = \frac{\sum_i^a \mu_{ij}}{a}$ .
- ▶ So,  $\mu_{i\cdot} = \mu + \tau_i$  and  $\mu_{\cdot j} = \mu + \beta_j \Rightarrow$   
$$\tau_i = \mu_{i\cdot} - \mu \quad \text{and} \quad \beta_j = \mu_{\cdot j} - \mu.$$
- ▶  $(\tau\beta)_{ij} = \mu_{ij} - (\mu + \tau_i + \beta_j) = \mu_{ij} - \mu_{i\cdot} - \mu_{\cdot j} + \mu.$

## 3.4. Two-factors analysis variance, (two-way ANOVA).

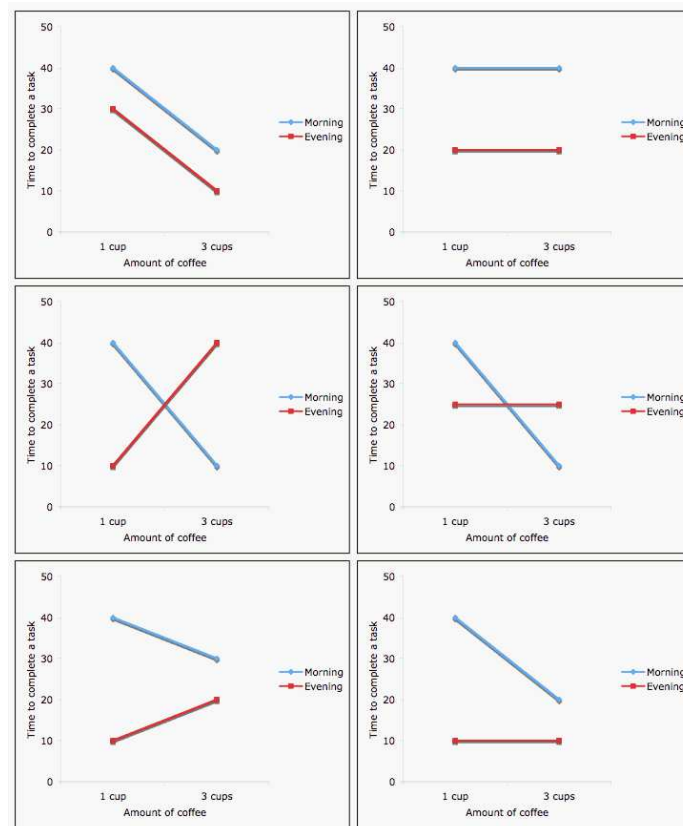
### Parameters Interpretation

- ▶  $\tau_i$  is an adjustment for level  $i$  of  $A$  and  $\beta_j$  is an adjustment for level  $j$  of  $B$ , related to the overall mean  $\mu$ . They are called the **principal effects**.
- ▶  $(\tau\beta)_{ij}$  is an additional adjustment that takes into account both levels  $i$  and  $j$ . This is called the **interaction effect**. Non interaction effect  $\Rightarrow$  additive model.



## 3.4. Two-factors analysis variance, (two-way ANOVA).

### Analyse existence of interaction effect:



## 3.4. Two-factors analysis variance, (two-way ANOVA).

### Zero-sum Constraints

- ▶ As in the one-way model, we now have too many parameters and need now several constraints:

1.  $\tau_{\cdot} = \sum_{i=1}^a \tau_i = 0;$
2.  $\beta_{\cdot} = \sum_{j=1}^b \beta_j = 0;$
3.  $(\tau\beta)_{\cdot j} = \sum_{i=1}^a (\tau\beta)_{ij} = 0, \quad \forall j;$
4.  $(\tau\beta)_{i \cdot} = \sum_{j=1}^b (\tau\beta)_{ij} = 0, \quad \forall i.$

### Estimates (LS) for Factor-effects model:

- ▶  $\hat{\mu} = \bar{Y}_{\dots} = \frac{\sum_i^a \sum_j^b \sum_k^n y_{ijk}}{abn}, \hat{\mu}_{i \cdot} = \bar{Y}_{i \cdot}, \hat{\mu}_{\cdot j} = \bar{Y}_{\cdot j};$
- ▶  $\hat{\tau}_i = \bar{Y}_{i \cdot} - \bar{Y}_{\dots}$  and  $\hat{\beta}_j = \bar{Y}_{\cdot j} - \bar{Y}_{\dots};$
- ▶  $(\hat{\tau\beta})_{ij} = \bar{Y}_{ij \cdot} - \bar{Y}_{i \cdot} - \bar{Y}_{\cdot j} + \bar{Y}_{\dots}.$

## 3.4. Two-factors analysis variance, (two-way ANOVA).

### SS for ANOVA Table

$$SSA = \sum_i^a \sum_j^b \sum_k^n \hat{\tau}_i^2 = \sum_i^a \frac{y_{i..}^2}{bn} - \frac{y_{...}^2}{abn};$$

$$SSB = \sum_i^a \sum_j^b \sum_k^n \hat{\beta}_j^2 = \sum_j^b \frac{y_{.j.}^2}{an} - \frac{y_{...}^2}{abn};$$

$$SSAB = \sum_i^a \sum_j^b \sum_k^n (\tau\hat{\beta})_{ij}^2 = \sum_i^a \sum_j^b \frac{y_{ij.}^2}{n} - \frac{y_{...}^2}{abn} - SSA - SSB;$$

$$SSE = \sum_i^a \sum_j^b \sum_k^n (Y_{ijk} - \bar{Y}_{ij.})^2;$$

$$\begin{aligned} SST &= \sum_i^a \sum_j^b \sum_k^n (Y_{ijk} - \bar{Y}_{...})^2 = \sum_i^a \sum_j^b \sum_k^n y_{ijk}^2 - \frac{y_{...}^2}{abn} \\ &= SSA + SSB + SSAB + SSE. \end{aligned}$$

## 3.4. Two-factors analysis variance, (two-way ANOVA).

### ANOVA Table

Source of variation	SS	df	MS
A Treatments	$SSA = \sum_i^a \frac{y_{i..}^2}{bn} - \frac{y_{...}^2}{abn}$	$a - 1$	$MSA = \frac{SSA}{a-1}$
B Treatments	$SSB = \sum_j^b \frac{y_{.j.}^2}{an} - \frac{y_{...}^2}{abn}$	$b - 1$	$MSB = \frac{SSB}{b-1}$
Interaction	$SSAB = \sum_i^a \sum_j^b \frac{y_{ij.}^2}{n} - \frac{y_{...}^2}{abn} - SSA - SSB$	$(a - 1)(b - 1)$	$MSAB = \frac{SSAB}{(a-1)(b-1)}$
Error	$SSE = \sum_i^a \sum_j^b \sum_k^n (y_{ijk} - \bar{y}_{ij.})^2$	$ab(n - 1)$	$MSE = \frac{SSE}{ab(n-1)}$
Total	$SST = \sum_i^a \sum_j^b \sum_k^n y_{ijk}^2 - \frac{y_{...}^2}{abn}$	$abn - 1$	

## 3.4. Two-factors analysis variance, (two-way ANOVA).

### Test Hypotheses for two-way ANOVA

- ▶ Test for factor A effect:

$$H_0 : \mu_{1.} = \mu_{2.} = \cdots = \mu_{a.} \text{ vs } H_1 : \mu_{i.} \neq \mu_{j.} \exists_{(i,j)}$$

$$\Rightarrow H_0 : \tau_i = 0, \forall i \text{ vs } H_1 : \tau_i \neq 0, \exists i$$

Under  $H_0$  we have that  $F_0 = \frac{MSA}{MSE} \stackrel{H_0}{\sim} F_{(a-1, ab(n-1))}$ .

- ▶ We reject  $H_0$  in the upper-tailed of the  $F_{(a-1, ab(n-1))}$  distribution.

## 3.4. Two-factors analysis variance, (two-way ANOVA).

- ▶ Test for factor B effect:

$$H_0 : \mu_{\cdot 1} = \mu_{\cdot 2} = \cdots = \mu_{\cdot b} \text{ vs } H_1 : \mu_{\cdot i} \neq \mu_{\cdot j} \exists_{(i,j)}$$

$$\Rightarrow H_0 : \beta_j = 0, \forall j \text{ vs } H_1 : \beta_j \neq 0, \exists j$$

Under  $H_0$  we have that  $F_0 = \frac{MSB}{MSE} \stackrel{H_0}{\sim} F_{(b-1, ab(n-1))}$ .

- ▶ We reject  $H_0$  in the upper-tailed of the  $F_{(b-1, ab(n-1))}$  distribution.

## 3.4. Two-factors analysis variance, (two-way ANOVA).

- ▶ Test for interaction Effect:

$$H_0 : (\tau\beta)_{ij} = 0, \forall(i, j) \text{ vs } H_1 : (\tau\beta)_{ij} \neq 0, \exists(i, j)$$

Under  $H_0$  we have that  $F_0 = \frac{MSAB}{MSE} \stackrel{H_0}{\sim} F_{((a-1)(b-1), ab(n-1))}$ .

- ▶ We reject  $H_0$  in the upper-tailed of the  $F_{((a-1)(b-1), ab(n-1))}$  distribution.

## Weightgain Data set (in library(HSAUR)) with

```
library(HSAUR)
data(weightgain)
```

package:HSAUR

R Documentation

Gain in Weight of Rats

Description:

The data arise from an experiment to study the gain in weight of rats fed on four different diets, distinguished by amount of protein (low and high) and by source of protein (beef and cereal).

Usage:

```
data("weightgain")
```

Format:

A data frame with 40 observations on the following 3 variables.

'source' source of protein given, a factor with levels 'Beef' and 'Cereal'.

'type' amount of protein given, a factor with levels 'High' and 'Low'.

'weightgain' weight gain in grams.

Details:

Ten rats are randomized to each of the four treatments. The question of interest is how diet affects weight gain.



## Weightgain Data set (in library(HSAUR)) with

```
> head(weightgain)

  source type weightgain
1  Beef  Low          90
2  Beef  Low          76
3  Beef  Low          90
4  Beef  Low          64
5  Beef  Low          86
6  Beef  Low          51

> summary(weightgain)
  source      type      weightgain
Beef  :20   High:20   Min.   : 51.00
Cereal:20   Low :20   1st Qu.: 75.50
                        Median : 88.50
                        Mean   : 87.25
                        3rd Qu.: 98.00
                        Max.   :118.00
```

# Two-way ANOVA with R

```
> weightgain.aov= aov(weightgain ~type+source+ type * source, data =
weightgain)
> summary(weightgain.aov)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
type	1	1300	1299.6	5.812	0.0211 *
source	1	221	220.9	0.988	0.3269
type:source	1	884	883.6	3.952	0.0545 .
Residuals	36	8049	223.6		

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

# Two-way ANOVA with R

```
> model.tables(weightgain.aov, type="mean")
Tables of means
Grand mean

87.25

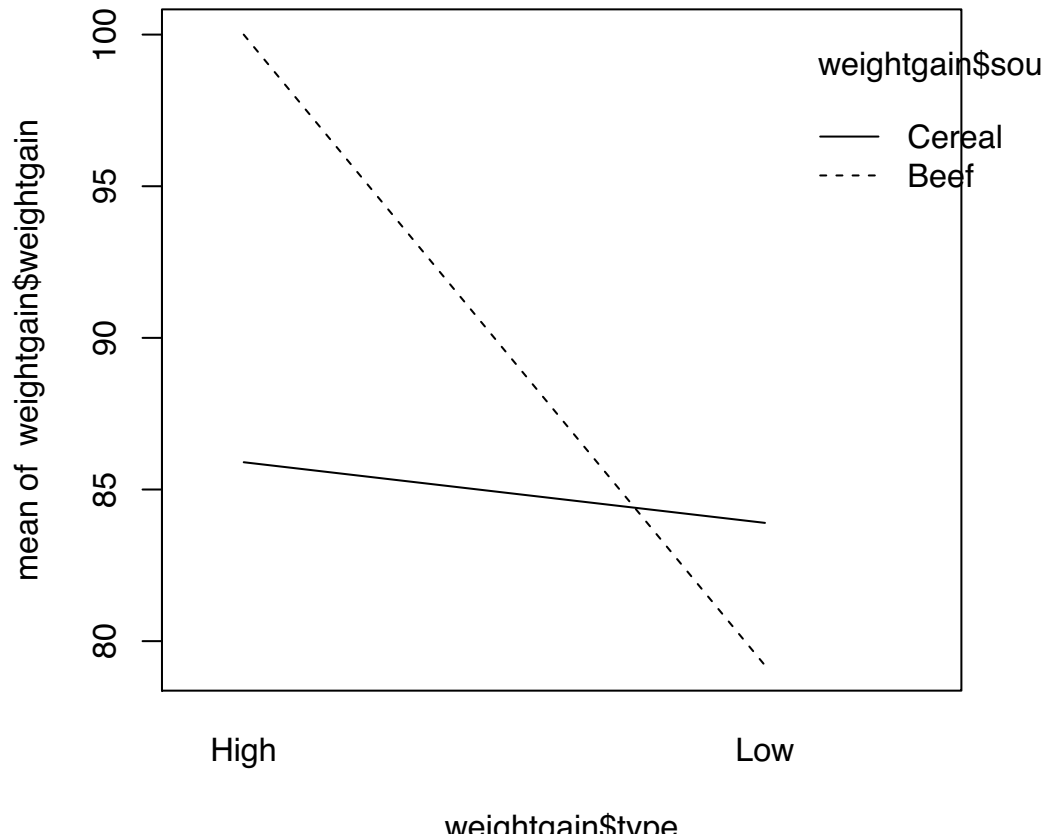
  type
type
  High  Low
92.95 81.55

  source
source
  Beef Cereal
  89.6  84.9

type:source
  source
type  Beef  Cereal
High 100.0 85.9
Low  79.2 83.9
```

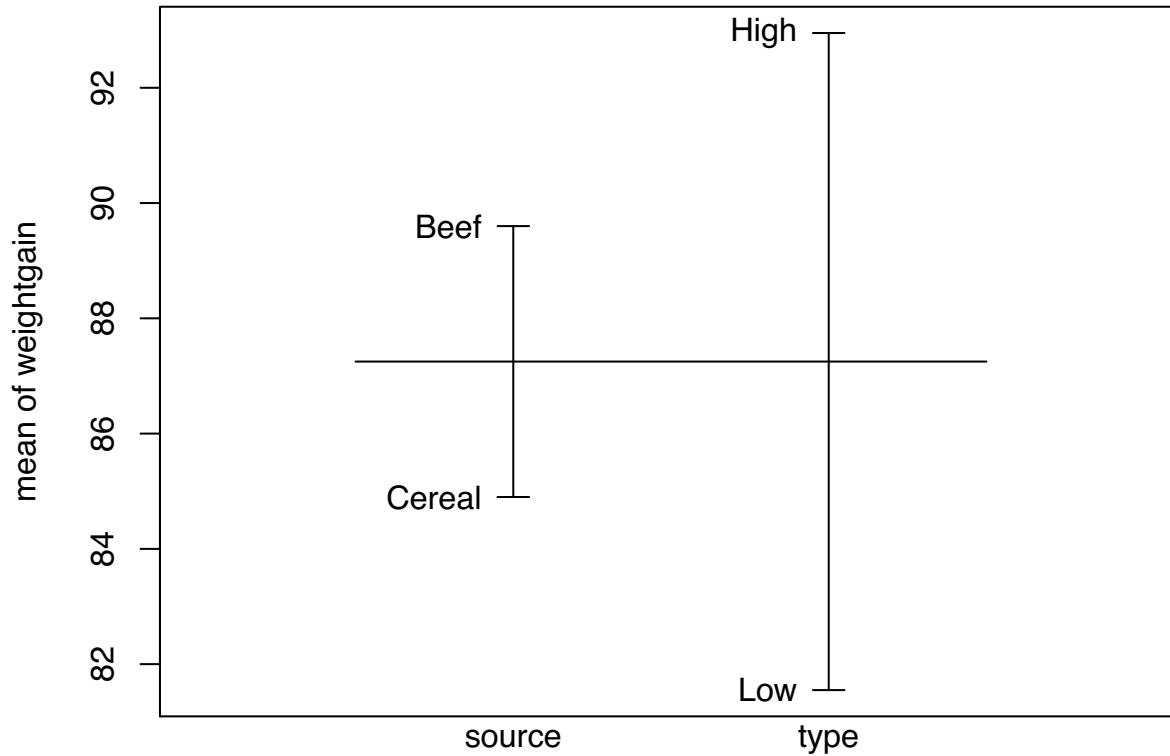
# Two-way ANOVA with R

`interaction.plot(weightgain$type,  
weightgain$source,weightgain$weightgain)`



# Two-way ANOVA with R

`plot.design(weightgain)`



# Two-way ANOVA with R

```
> pairw.anova(weightgain$weightgain, weightgain$type, method="bonf")
```

```
95% Bonferroni confidence intervals
```

	Diff	Lower	Upper	Decision	Adj. p-value
muHigh-muLow	11.4	1.46412	21.33588	Reject H0	0.025649

```
> pairw.anova(weightgain$weightgain, weightgain$source, method="bonf")
```

```
95% Bonferroni confidence intervals
```

	Diff	Lower	Upper	Decision	Adj. p-value
muBeef-muCereal	4.7	-5.80501	15.20501	FTR H0	0.370788