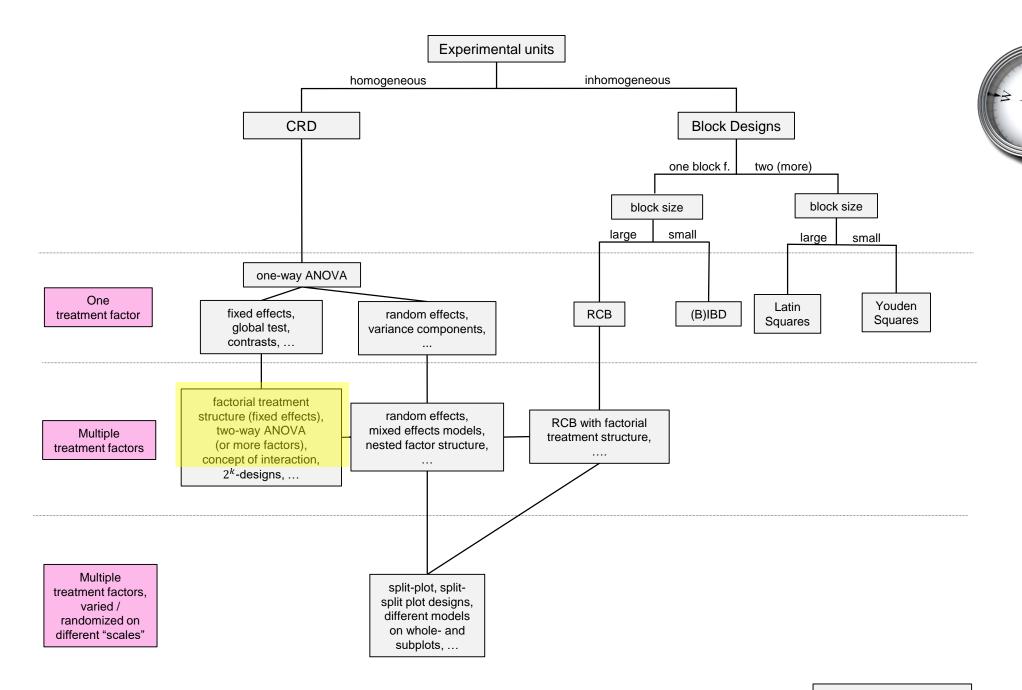


Factorial Treatment Structure: Part I

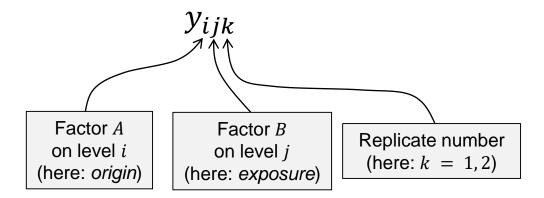


Factorial Treatment Structure

- So far (in CRDs), the treatments had no "structure".
- So called factorial treatment structure exists if the g treatments are the combination of the levels of two or more factors.
- In the case that we see all the possible combinations of the levels of the two factors, we call the factors crossed.
- Examples
 - Biomass of crop: Different fertilizers and different crop varieties.
 - Battery life: Different temperature levels and different plate material (Montgomery, 1991, Example 7-3.1).
 - **...**

Example (Linder, A. und W. Berchtold, 1982)

- Response: Needleweight of 20 three-week old pine seedlings [in 1/100 g].
- Two factors:
 - *A*: "origin" with levels {Taglieda, Pfyn, Rheinau}
 - B: "exposure to light" with levels {short, long, permanent}
- We denote by y_{ijk} the kth response of the treatment formed by the ith level of factor A and the jth level of factor B.



Two Factor Design: Generic Data Table

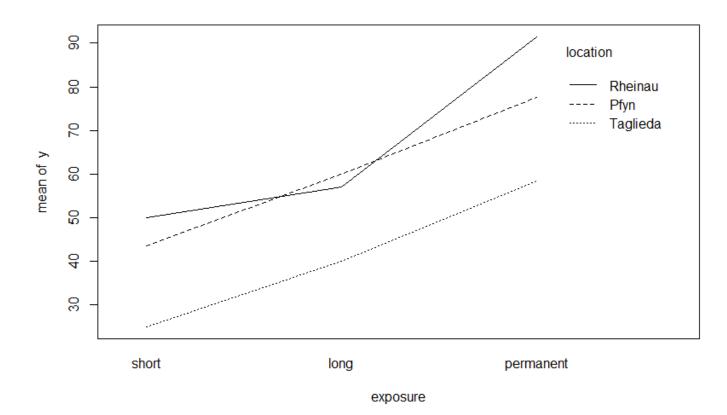
	B_1	B_2	B_3	
A_1	y ₁₁₁ y ₁₁₂ y ₁₁₃ y ₁₁₄	y ₁₂₁ y ₁₂₂ y ₁₂₃ y ₁₂₄	y ₁₃₁ y ₁₃₂ y ₁₃₃ y ₁₃₄	
A_2	y ₂₁₁ y ₂₁₂ y ₂₁₃ y ₂₁₄	У ₂₂₁ У ₂₂₂ У ₂₂₃ У ₂₂₄	$y_{231} \ y_{232} \ y_{233} \ y_{234}$	
	•••		•••	

Data Table of Our Example

	Short	Long	Permanent
Taglieda	25	42	62
	25	38	55
Pfyn	45	62	80
	42	58	75
Rheinau	50	52	88
	50	62	95

Visualization

- As for one-way ANOVA situation
 - for all treatment combinations
 - factor-wise summaries ("marginal summaries")
- More useful: Interaction plot (see R-code)



Factorial Treatment Structure

- The structure of the treatment influences the analysis of the data.
- Setup:
 - Factor A with a levels
 - Factor B with b levels
 - n>1 replicates for **every** combination \longleftarrow a so called **balanced design**
 - Total of $N = a \cdot b \cdot n$ observations
- We could analyze this with the usual cell means model (ignoring the special treatment structure).
- Typically, we have research questions about both factors and their possible interaction (interplay).

Factorial Treatment Structure

- Examples:
 - "Is effect of light exposure location specific?"
 (→ interaction between light exposure and location)
 - "What is the effect of light exposure averaged over all locations?"
 (→ main effect of light exposure)
 - "What is the effect of location averaged over all exposure levels?"
 (→ main effect of location)
- We could use the cell means (one-way ANOVA) model and try to answer these questions with appropriate contrasts (→ complicated).
- Easier: Use a model that incorporates the factorial structure of the treatments.

Factorial Model

because two factors involved

The two-way ANOVA model with interaction is

$$Y_{ijk} = \mu + \alpha_i + \beta_j + (\alpha\beta)_{ij} + \epsilon_{ijk}$$

where

- α_i is the **main effect** of factor A at level i.
- β_i is the **main effect** of factor B at level j.
- $(\alpha\beta)_{ij}$ is the **interaction effect** between A and B for level combination i, j (**not** the product $\alpha_i \beta_i!$)
- ϵ_{iik} are i.i.d. $N(0, \sigma^2)$ errors.
- Typically, sum-to-zero constraints are being used, i.e.
 - $\sum_{i=1}^{a} \alpha_i = 0$, $\sum_{i=1}^{b} \beta_i = 0$.

 $\rightarrow a-1$ and b-1 degrees of freedom

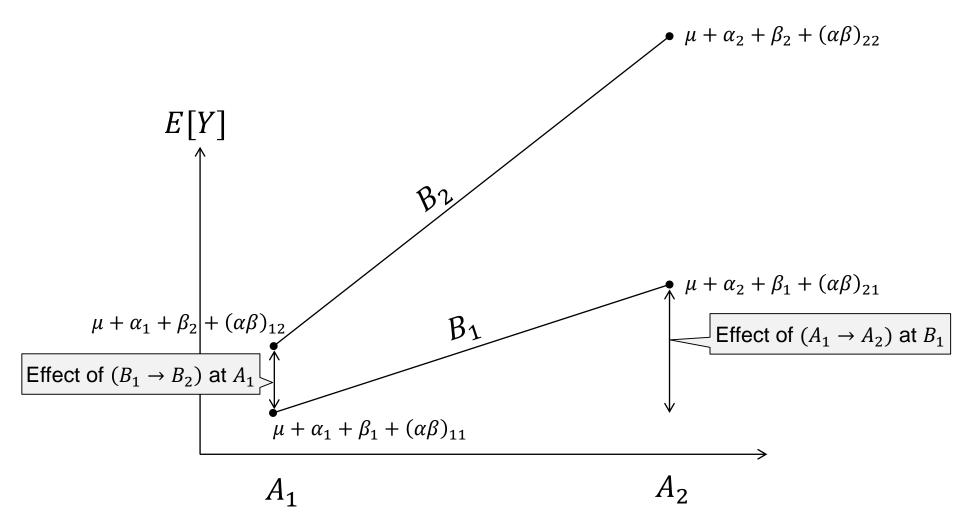
Interpretation of Main Effects

- Main effects are nothing else than the average effect when moving from row to row (column to column).
- The interaction effect is the difference to the main effects model, i.e. it
 measures how far the treatment means differ from the main effects model.
- If there is **no interaction**, the effects are **additive**.
- In our example it would mean: "No matter what location we are considering, the effect of light exposure is always the same."

Visualization of the Model

 $E[Y_{ijk}] = \mu + \alpha_i + \beta_j + (\alpha\beta)_{ij}$

Factor *A*, factor *B* with two levels each:

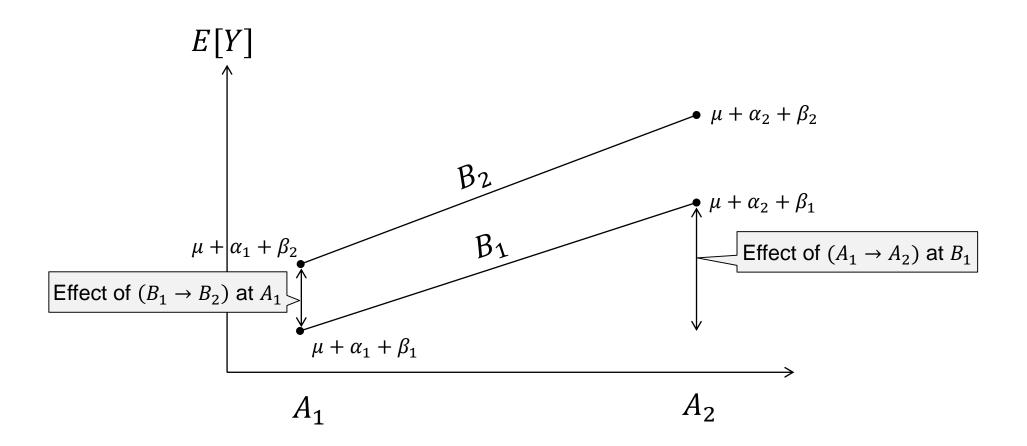


Visualization of the Model

$$E[Y_{ijk}] = \mu + \alpha_i + \beta_j$$

If no interaction is present, lines will be parallel.

An Interaction plot is nothing else than the empirical version of this plot.



Two-Way ANOVA Step By Step

	Short	Long	Permanent
Taglieda	25	42	62
	25	38	55
Pfyn	45	62	80
	42	58	75
Rheinau	50	52	88
	50	62	95

		Short	Long	Permanent
	Taglieda	μ μ	μ μ	μ μ
	Pfyn	μ μ	μ μ	μ μ
1	Rheinau	μ μ	μ μ	μ μ

,		Short	Long	Permanent	
	Taglieda	$egin{array}{c} lpha_1 \ lpha_1 \end{array}$	$egin{array}{c} lpha_1 \ lpha_1 \end{array}$	$egin{pmatrix} lpha_1 & & & \ lpha_1 & & & \ \end{pmatrix}$	//
	Pfyn	$rac{lpha_2}{lpha_2}$	$rac{lpha_2}{lpha_2}$	$\begin{array}{c} \alpha_2 \\ \alpha_2 \end{array}$	/
	Rheinau	$lpha_3 lpha_3$	$lpha_3 lpha_3$	$\begin{array}{ccc} \alpha_3 & \lambda \\ \alpha_3 & \end{array}$]

	Short	Long	Permanent	_
Taglieda	$egin{pmatrix} eta_1 \ eta_1 \end{matrix}$	$eta_2 \ eta_2$	$eta_3 \ eta_3$	
Pfyn	$eta_1 eta_1$	$eta_2 \ eta_2$	$eta_3 \ eta_3$	
Rheinau	$egin{array}{c} eta_1 \ eta_1 \end{array}$	$eta_2 \ eta_2$	$eta_3 \ eta_3$	J
		+		
	Short	Long	Permanent	,
Taglieda	$(\alpha\beta)_{11} \\ (\alpha\beta)_{11}$	$(\alpha\beta)_{12} \\ (\alpha\beta)_{12}$	$(\alpha\beta)_{13} \ (\alpha\beta)_{13}$	
Pfyn	$(\alpha\beta)_{21} \\ (\alpha\beta)_{21}$	$(\alpha\beta)_{22} \ (\alpha\beta)_{22}$	$(\alpha\beta)_{23}$ $(\alpha\beta)_{23}$	
Rheinau	$(\alpha\beta)_{31} (\alpha\beta)_{31}$	$(\alpha\beta)_{32} \ (\alpha\beta)_{32}$	$(\alpha\beta)_{33}$ $(\alpha\beta)_{33}$	J
		+		
	Short	Long	Permanent	ſ
Taglieda	$\epsilon_{111} \\ \epsilon_{112}$	$\epsilon_{121} \ \epsilon_{122}$	ϵ_{131} ϵ_{132}	
Pfyn	$\epsilon_{211} \ \epsilon_{212}$	ϵ_{221} ϵ_{222}	$\epsilon_{231} \ \epsilon_{232}$	
Rheinau	ϵ_{311} ϵ_{312}	ϵ_{321} ϵ_{322}	ϵ_{331} ϵ_{332}	J



Parameter Estimates

Estimates for the balanced case (with sum-to-zero constraints) are:

Parameter	Estimator
μ	$\hat{\mu} = \bar{y}_{}$
$lpha_i$	$\hat{\alpha}_i = \bar{y}_{i\cdots} - \bar{y}_{\cdots}$
eta_j	$\hat{\beta}_j = \bar{y}_{\cdot j \cdot} - \bar{y}_{\cdot \cdot \cdot}$
$(\alpha\beta)_{ij}$	$(\widehat{\alpha}\widehat{\beta})_{ij} = \overline{y}_{ij} - \widehat{\mu} - \widehat{\alpha}_i - \widehat{\beta}_j$

 This means: We estimate the main effects as if the other factors wouldn't be there (see next slides).

Main Effect of Location

Original data-set:

	Short	Long	Permanent
Taglieda	25	42	62
	25	38	55
Pfyn	45	62	80
	42	58	75
Rheinau	50	52	88
	50	62	95

Ignore factor "exposure", estimate effect as in one-way ANOVA model:

Taglieda	Pfyn	Rheinau
25	45	50
25	42	50
42	62	52
38	58	62
62	80	88
55	75	95

Main Effect of Light Exposure

Original data-set:

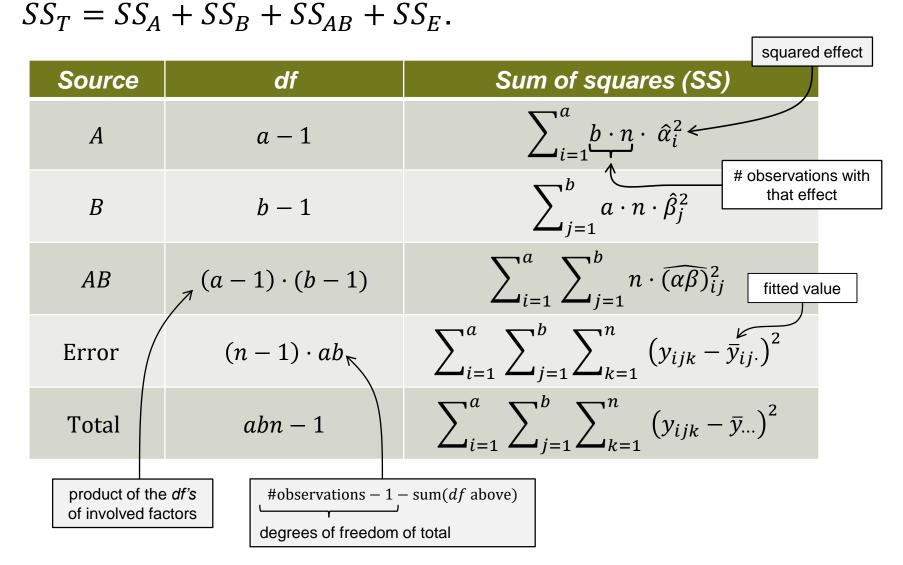
	Short	Long	Permanent
Taglieda	25	42	62
	25	38	55
Pfyn	45	62	80
	42	58	75
Rheinau	50	52	88
	50	62	95

Ignore factor "location", estimate effect as in one-way ANOVA model:

Short	Long	Permanent
25	42	62
25	38	55
45	62	80
42	58	75
50	52	88
50	62	95

Sum of Squares

Again, total sum of squares can be partitioned into different sources, i.e.



ANOVA Table

As before, we can construct an ANOVA table:

Source	df	SS	MS	F
A	a-1	SS_A	$\frac{SS_A}{a-1}$	$\frac{MS_A}{MS_E}$
В	b-1	SS_B	$\frac{SS_B}{b-1}$	$rac{MS_B}{MS_E}$
AB	$(a-1)\cdot(b-1)$	SS_{AB}	$\frac{SS_{AB}}{(a-1)(b-1)}$	$rac{MS_{AB}}{MS_{E}}$
Error	$ab \cdot (n-1)$	SS_E	$\frac{SS_E}{(n-1)ab}$	

Under the corresponding (global) null-hypotheses, the F-ratios are again F-distributed with degrees of freedom defined through the numerator and the denominator, respectively.

F-Tests: Overview

Interaction AB

- H_0 : $(\alpha\beta)_{ij} = 0$ for **all** i, j
- H_A : At least one $(\alpha\beta)_{ij} \neq 0$
- Under H_0 : $\frac{MS_{AB}}{MS_E} \sim F_{(a-1)(b-1), ab(n-1)}$

Main effect A

- $H_0: \alpha_i = 0 \text{ for all } i$
- H_A : At least one $\alpha_i \neq 0$
- Under H_0 : $\frac{MS_A}{MS_E} \sim F_{(a-1), ab(n-1)}$

Main effect B

- $H_0: \beta_j = 0$ for **all** j
- H_A : At least one $\beta_i \neq 0$
- Under H_0 : $\frac{MS_B}{MS_E} \sim F_{(b-1), ab(n-1)}$

Analyzing the ANOVA Table

- Typically, the F-tests are analyzed from bottom to top (in the ANOVA table).
- Here, this means we start with the F-test of the interaction.
- If we reject:
 - Conclude that we need an interaction in our model, i.e. the effect of A depends on the level of B.
 - Don't continue testing the main-effects (principle of hierarchy).
 - Perform individual analysis for every level of factor A (or B), error of full model can be re-used (see later).
 - Have a look at the interaction plot to get a better understanding of what is going on.
 - The interaction might be based on a single cell.
 - Transformation might help in getting rid of the interaction.
- If we can't reject, continue testing the main effects.

Two-Way ANOVA model in R

Define model with interaction in formula interface

```
> fit <- aov(y ~ location * exposure, data = data)
> summary(fit)
                 Df Sum Sq Mean Sq F value
location
                      2053
                            1026.4 69.981 3.28e-06 ***
                      4074
                            2037.1 138.890 1.72e-07 ***
exposure
location:exposure 4 183
                              45.7
                                    3.117 0.0722 .
Residuals
                             14.7
                     132
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

We can also use the following equivalent notation

```
> fit <- aov(y ~ location + exposure + location:exposure, data = data) ## equivalent version
```

More than Two Factors

- Model can be easily extended to more than two factors, e.g. A, B, C.
- Model then includes higher-order interactions:

with ϵ_{ijkl} i.i.d. $N(0, \sigma^2)$ and the usual sum-to-zero constraints.

- Two-way interaction describes how a main-effect depends on the level of the other factor.
- Three-way interaction describes how a two-way interaction depends on the level of the third factor ...

Interpretation

- The higher-order interactions are quite difficult to interpret.
- Parameter estimation as before.
- Degrees of freedom of an interaction is the product of the df's of the involved factors (as usual).
- E.g., for the three-way interaction:

$$(a-1)\cdot(b-1)\cdot(c-1)$$