Experimental Design and Data Analysis, Lecture 6

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Lecture overview

1. general factorial and incomplete block designs
2. random effects
3. crossover design
4. split-plot design
5. overview anova designs

general factorial and incomplete block designs

General factorial design

- Everything extends to an arbitrary number of factors.
- A practical difficulty is that the number of combinations of factors increases rapidly, so that many experiments are necessary.
- In the decomposition of the population means this becomes visible through many interaction parameters. E.g., given 3 factors there are 3 2nd order and 1 3rd order interactions:

$$\mu_{ijk} = \mu + \alpha_i + \beta_j + \gamma_k + (\alpha\beta)_{ij} + (\alpha\gamma)_{ik} + (\beta\gamma)_{jk} + (\alpha\beta\gamma)_{ijk}.$$

- It is often assumed that higher order interactions are zero. Then lower order interactions can be estimated using fewer experiments (incomplete designs).

Incomplete block designs

⊙ block = fac. that is not of interest but we take into acc.

- In a regular block design every treatment (the factor of interest) is applied at least once within every block.
  - all cells are filled w/ at least 1 data point
- If there are many blocks (in particular if two or more block factors are crossed), then this requires many experiments.
  - → we want treat. to be appl. to each block = becomes diff.
- In an incomplete block design only a subset of the experiments is performed.
  - not each comb. of levels — block has obs. w/ cert. treatment
- It is advisable to choose this subset in a "balanced way".
- Example of incomplete block design with 3 factors (1 treatment factor + 2 block factors): latin squares.

Incomplete designs with 3 factors: latin squares

The setting for a latin square design for 2 block factors is an experiment with:

- a numerical outcome Y (dependent variable).
- a factor of interest that can be fixed at I *levels* (treatment).
- two factors that are *not* of interest, both with fixed *levels* (blocks).

we have 3 fac.s in total

Example of a latin square design for 2 block factors, with levels 1, 2, 3, 4 and I, II, III, IV, and a treatment with levels A, B, C, D

	I	II	III	IV
1	D	C	B	A
2	B	D	A	C
3	C	A	D	B
4	A	B	C	D

we have all treat. for each lvl. of each bl.

The outcome is measured (only) for blocks and treatment combinations (1,I,D), (1,II,C), (1,III,B), (1,IV,A), (2,I,B), etc.: 16 experiments in total.

Every treatment is measured exactly once for every level of both blocks.

4 treatm. = we cannot have each treatm. rep. in each cell b/c we can only have 16 obs.

The analysis assumes the additive model (interactions are assumed to be 0):

$$Y_{ikl} = \mu + \alpha_i + \beta_{1k} + \beta_{2l} + e_{ikl},$$

can't say anything abt. interact.

β_{1k} and β_{2l} are the block effects at levels $k \in \{1,2,3,4\}$ and $l \in \{I, II, II, IV\}$.

```
> lm(y~treatment+block1+block2,data=...)
```

Balanced incomplete block design

A balanced incomplete block design for a block factor with levels b1,...,b10 and a treatment factor with levels A, B, C, D, E, F takes the form

	b1	b2	b3	b4	b5	b6	b7	b8	b9	b10
A		*		*			*	*		*
B	*	*				*	*		*	
C	*	*	*	*	*					
D			*		*		*		*	*
E				*	*	*		*	*	
F	*		*			*		*		*

10 levels (block)

6 levels (treat.)

C & E are present.

$10 \times 6 = 60$ cells → not enough obs per cell

The outcome is measured (only) for the combinations marked by a "*": 30 experiments in total, 3 per block. Every pair of treatments is compared within exactly 2 blocks. The analysis is the same as for an ordinary block design.

each block has 3 treat.

now we can compare all treats w/each other

Ideally a latin square is chosen at random from all possible latin squares, but this is computationally difficult. Instead one may apply a sequence of swaps of randomly chosen pairs of columns or rows.

Advantage of incomplete block designs: great save in experiments; disadvantage: even a rough graphical check on interactions between blocks and treatments is impossible.

no way to say anyth. abt. interacts

random effects (mixed effects models)

The idea of random effects

So far we have considered block effects as fixed effects. That is, we regard the blocks as predetermined, not as a random selection of all availalbe blocks.

Alternatively, we can regard the blocks as a random selection of all possible blocks (the block population). In that case, the effects of the blocks occurring in our experiment are random effects.

since it's rand. we won't draw any infer. but we still take into acc.

EXAMPLE We want to investigate whether exam 1 is more difficult than exam 2. Because math professors may have different grading styles, resulting in different heights of the grades, we take "professor" as block factor. We randomly select 6 math professors from the math professor population. We apply a randomized block design by selecting 10 students for each professor. 5 randomly chosen students per professor make exam 1 (treatment 1) and the other 5 make exam 2 (treatment 2). The treatment effect (exam effect) is a fixed effect, whereas the block effect (professor effect) is a random effect. We are interested in the treatment effect.

by draw. them rand. ly you sort of remove eff. of grading style

Analysis

rand. var.s drawn from norm dist. and have diff. σ's for diff. b's. → we can't est. it b/c it's rand. but we don't need to.

Data (Y_{ibk}) are assumed to follow the model

$$Y_{ibk} = \mu + \alpha_i + \tau_b + e_{ibk}, \quad i = 1, \ldots, I; \quad b = 1, \ldots, B; \quad k = 1, \ldots, N,$$

where the treatment effect (α_i) is a fixed effect, and the block effect (τ_b) is a random effect. That means, we assume the block effects τ_b form a random sample from a centered normal distribution (i.e., with mean 0).

As in 1-way ANOVA we test $H_0 : \alpha_1 = \ldots = \alpha_I = 0$. → no need to test on interact.s or a 2nd fac., just test whether treat. is of influence

We also estimate μ and the α_i's.

Since we have both fixed and random effects, this is called a mixed effects model.

mixed effects model: crossover design

Setting and design

Setting:

An experiment with two numerical outcomes per experimental unit, corresponding to two different treatments. Interest is in a possible difference between the two outcomes. An order effect of the outcomes is suspected.

(The crossover design can be extended to more than 2 outcomes.)

EXAMPLE Comparing pain relief by a dedicated drug or by a placebo. Both treatments are applied to every individual (with recovery time in between).

EXAMPLE Comparing time needed to complete a search task in a tree of webpages as function of the organization of the webpages. Every individual performs a search task with both types of organization.

Design:

- Take a random sample of experimental units from the relevant population.
- Divide the units at random in two equal groups.
- Apply the treatments in one order to the units in the first group, and in the reversed order to the units in the second.

Analysis

Data are $2N$ measurements (on N individuals), which can be classified to belong to one of the 4 entries in the 2×2 table.

		period 1	period 2
sequence	$T_1\,T_2$	T_1	T_2
	$T_2\,T_1$	T_2	T_1

The crossover design assumes that

$$Y_{ispbk} = \mu_{isp} + b_b + e_{ispbk},$$

(b_b: r.v.)

★ we deal w/ppl → blocking var. = every indiv. is diff. and we take it into acc.

whre errors (e_{ispbk}) and random individual effects (b_b) are independent samples from centered normal distributions, and the mean values μ_{isp} is parametrized as

		period 1	period 2
sequence	$T_1\,T_2$	μ	$\mu + \alpha + \beta$
	$T_2\,T_1$	$\mu + \alpha + \gamma$	$\mu + \beta + \gamma$

(general param.)

α the treatment effect ($T_2 - T_1$),
β the learning (or period) effect,
γ the sequence effect.

(e.g. if you are given T1 first & smth happens it might react diff. on T2)

(order of drugs served)

If the effect b_b is random, the model has the 4 mean values (over the 4 cells) and 4 parameters $(\mu, \alpha, \beta, \gamma)$, i.e., identifiable. For example, the parameter α is found as the average $(\mu + \alpha + \beta + \mu + \alpha + \gamma)/2$ of the two T_2 treatments minus the average $(\mu + \mu + \beta + \gamma)/2$ of the two T_1 treatments in the table.

Analysis in R: data input

The rows of the data frame ashinal correspond to 16 subjects and give measures of pain (for chronic headache) when treated with a drug (a) (that inhibits nitric oxide synthase) or a placebo (p). The bigger the outcome pain, the more the measured headache. One of the three columns sequence, treatment and period is redundant, but useful for the analysis.

block var.

```
> ashinal=read.table("ashinal.txt",header=TRUE); ashinal
   pain id sequence treatment period
1  -167  1     pa         a      2
2  -102  1     pa         p      1
3  -127  2     pa         a      2
[ some output deleted ]
30    3 15     ap         p      2
31  -72 16     ap         a      1
32  -36 16     ap         p      2
```

obs. val.

pa = 1st placebo, then active

ap = 1st active, then placebo

you don't really need all 3 of these col.s = take any 2 and the other can be recovered → e.g. from seq. pa and treat. a, we understand that treat. a was given per. 2.

Analysis in R: fixed effects (1)

```
> ashinal$id=factor(ashinal$id); ashinal$period=factor(ashinal$period)
> ashinalm=lm(pain~treatment+period+id,data=ashinal)
> anova(ashinalm)
          Df Sum Sq Mean Sq F value   Pr(>F)
treatment  1  14706 14706.1 10.4624 0.005994 **
period     1   1505  1505.2  1.0709 0.318298
id        15  51137  3409.2  2.4254 0.052870 .
Residuals 14  19679  1405.6
```

seq. is not here b/c we can't have all of them → we have only 4 cells

sig.

not sig.

not sig.

If factor `id` enters the model, we have 5 parameters for 4 groups and the parameters become unidentifiable. The sequence effect is therefore left out, as it cannot then be estimated in a fixed effects model. In the mixed effects model this is possible.

not poss. to recover it

In general (e.g., for unbalanced designs), changing the order of factors in the anova formula gives different *p*-values, as anova performs "sequential tests". To obtain the correct p-value the factor of interest (`treatment`), put this factor last in the formula.

```
> anova(lm(pain~id+period+treatment,data=ashinal)) # treatment last!
          Df Sum Sq Mean Sq F value  Pr(>F)
id        15  51137  3409.2  2.4254 0.05287 .
period     1   4608  4608.0  3.2783 0.09171 .
treatment  1  11603 11603.3  8.2550 0.01228 *
Residuals 14  19679  1405.6
```

right p-val. to look at → changed after changing order

Analysis in R: fixed effects (2)

```
> summary(ashinalm)
[ some output deleted ]
             Estimate Std. Error t value Pr(>|t|)
(Intercept)  -147.08      28.63  -5.137 0.000151 ***
treatmentp     39.33      13.69   2.873 0.012276 *
period2       -14.17      13.69  -1.035 0.318298
id2            51.50      37.49   1.374 0.191150
id3           121.50      37.49   3.241 0.005921 **
[ some output deleted ]
id16           80.50      37.49   2.147 0.049781 *
```

active does smth

diff. b.w. active and placebo

μ

not sig. = no diff. in periods

block fac. is expect. to be imp. → don't pay attent.

The active drug gives 39.33 more pain relief (recall the treatment parameterization p is compared to a). There is no significant learning (=period) effect.

The "fixed effects" analysis given here is not the correct implementation of the model assumptions. The "mixed effects" ought to be used instead with id as random factor. In this case however, the difference between the incorrect "fixed effects" analysis and the correct "mixed effects" analysis on the next slide is minor.

Analysis in R: mixed effects (1)

- lme4 (classic pack.)
- nlml (modern alt. w/diff. synt.)

```
> library(lme4); attach(ashinal)
> ashinalmer=lmer(pain~treatment+sequence+period+(1|id),
+ REML=FALSE,data=ashinal); summary(ashinalmer)
[ some output deleted ]
Random effects:
 Groups   Name        Variance Std.Dev.
 id       (Intercept)  755.91  27.494
 Residual             1229.92  35.070
Fixed effects:
             Estimate Std. Error t value
(Intercept)  -28.50      18.19  -1.567
treatmentp    39.33      12.81   3.071
sequencepa   -31.13      19.12  -1.628
period2      -14.17      12.81  -1.106
```

fixed eff. = we can have all in our model b/c id is random

linear model mixed eff.s

additive rand. eff. = id is decl. as rand.

method that computes est. of σ and coeff.s

for rand. you can only est. variance and not coeff. b/c id is random.

μ

identif. b/c id is rand.

no p-val.s b/c it's not well defined now → you won't see p-val. if you apply ANOVA on model

The R-library `lme4` implements the mixed effects models, another library is `nlml`. The function `lmer` gives the correct implementation of the crossover design, with the individuals as "random effects". The number 755.91 under `Random effects` is the estimated variance of the normal population of the "individual effects" (b_n). The estimated `treatment` and `period` effects under `Fixed effects` are identical to those in the previous slide. The model: $Y_{ispbn} = \mu + \alpha_i + \beta_s + \gamma_p + b_b + e_{ispbn}$.

Analysis in R: mixed effects (2)

≠ ANOVA for mixed effects ≠

we are interest. in treat. eff. → we create 2 models = 1 with treat and other w/out treat.

```
> ashinalmer1=lmer(pain~sequence+period+(1|id),data=ashinal,REML=FALSE)
> anova(ashinalmer1,ashinalmer) # test reduced model inside full model
Models:
ashinalmer1: pain ~ sequence + period + (1 | id)
ashinalmer: pain ~ treatment + sequence + period + (1 | id)
            npar    AIC    BIC  logLik deviance  Chisq Df Pr(>Chisq)
ashinalmer1    5 348.72 356.05 -169.36   338.72
ashinalmer     6 343.31 352.10 -165.65   331.31 7.4161  1   0.006464 **
```

model w/out treat.

we test: does treat. matter or not?

p-val. → corresp.s to importance of treat.

small p-val: treat. is imp. and does influence

The function `lmer` does not automatically produce p-values (and they cannot be extracted by `anova(ashinalmer)`), but these can be found by refitting the model without the effect of interest (in our case `treatment`), and applying anova with 2 arguments (to test the fit of the reduced model without `treatment` inside the full model). Factor `treatment` has a significant effect.

Notation: `1` in `(1|id)` means the the random effect `id` is with respect to the intercept. Note that within this mixed effects model it is also possible to estimate the sequence effect.

mixed effects model: split-plot design

Setting and design

Setting: an experiment with a numerical outcome Y,

- a treatment factor with I levels that is difficult to apply or randomize,
- a treatment factor with J levels that is easy to apply or randomize.
- possibly a block factor.

2 fac.s, 1 is sub-fac. of the other

Interest is as in a two-way factorial experiment.

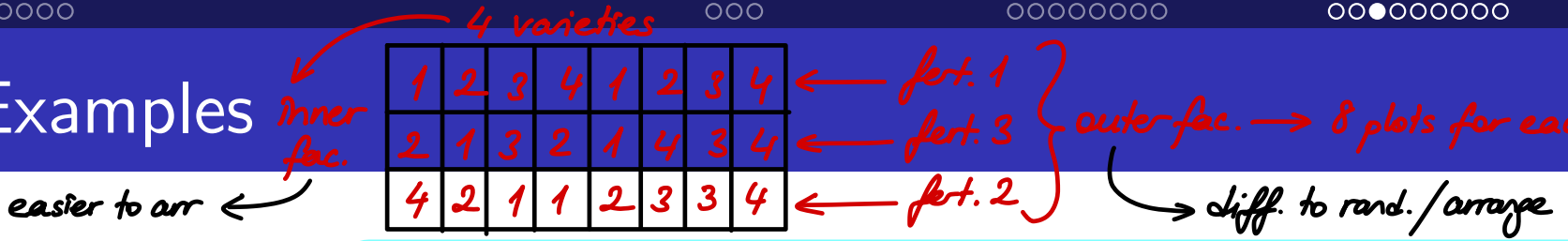
The experimental units are grouped as subplots of whole plots; the levels of the first, outer factor are randomized over the groups (whole plots), whereas the levels of the second, inner factor are randomized over the subplots. The experiment may be repeated within the levels of a block variable.

Design: for each of the B levels of the block factor

- Select I groups of NJ experimental units randomly from the population.
- Randomize the I levels of the ("difficult") outer factor over the I groups.
- Within every group randomize the J levels of the ("easy") inner factor over the NJ units in the group.
- Perform the experiment NIJ times independently.

Instead of "outer" one says "whole plot" and instead of "inner" one says "subplot".

Examples



EXAMPLE To study the yield of 4 varieties of a crop under 3 varieties of fertilizer a large field is subdividided into 3 whole plots, which are subdivided into 8 subplots. The 3 levels of fertilizers are randomized over the 3 whole plots; in each whole plot the 4 varieties are randomized over the 8 subplots. The motivation is that it is hard to apply fertilizer to small, contiguous plots. The experiment is replicated on 2 other fields which serve as blocks. It is suspected that fertilizer influences the yield, i.e., the yields within the same whole plot share more similarity than the yields from different whole plots.

EXAMPLE An experiment to study reaction time to 3 types of stimuli is run in two different experimental set-ups (e.g. room lay-out, furnishings, electronic equipment). Because it is time-consuming to change the set-ups, the experiment is run 6 times, 3 times with both set-ups, in random order, and in each run 18 subjects are randomized to the 3 types of stimuli. It is suspected that measurements within one of the 6 runs share some uncontrolled variables (day of the week, the weather, the experimenter,etc.), more than measurements from different runs.

Analysis

interact. w/ levels of 1st fac. and block → rand b/c block is rand.

The split-plot design assumes that the measurement Y_{ijbk} at levels i and j of the outer and inner factors, of the kth replicate in the bth block, satisfies

$$Y_{ijbk} = \mu_{ij} + b_b + c_{ib} + e_{ijbk}, \quad i = 1, \ldots, I;\ j = 1, \ldots, J;\ b = 1, \ldots, B;\ k = 1, \ldots, N.$$

rand.

for errors (e_{ijbk}), block effects (b_b) and block-whole plot interactions c_{ib} that are independent random samples from centered normal distributions.

avg. for comb. of 1st fac. outer & 2nd fac. = inner

- The variables b_b model dependence between the measurements within blocks.
- The variables c_{ib} model (further) dependence within the groups of experimental units (= "whole plots") within blocks that receive the same treatment of the outer factor.

we assume that there is interact. = block has influence on factor → for each level of fac. we have diff. influence of block var.

As in a two-way lay-out the means μ_{ij} can be decomposed in main and interaction effects as

$$\mu_{ij} = \mu + \alpha_i + \beta_j + \gamma_{ij}.$$

reflects influence of outer fac. (1st fac.)

The same tests and estimates as in 2-way ANOVA are of interest.

Analysis in R: data input

At two farms (= block) a field was subdivided in 3 parts (= whole plot) and the (outer) factor spray was independently randomized over the 3 whole plots. Next, each of the 3 x 2 = 6 whole plots was subdivided in 2 subplots and within every whole plot the (inner) factor variety was randomized over the 2 subplots. Little of this description can be seen from the data matrix wheat.

response var.

```
> wheat
   farm yield spray variety
1    f1    56     2       2
2    f1    64     2       1
3    f1    71     1       1
4    f1    66     1       2
5    f1    84     3       1
6    f1    82     3       2
7    f2    88     3       2
8    f2    97     3       1
9    f2    79     1       2
10   f2    83     1       1
11   f2    77     2       1
12   f2    73     2       2
```

block var.

out. fac.

inner fac.

variety varies w/in spray = It's inside (inner fac.)

* we think that interacts w/spray → rand. eff.

a farm could use certain spray more than the others = interact. b.w. farm + spray

Analysis in R: fixed effects (1)

outer fac. (fixed) — fixed

```
> wheat$spray=factor(wheat$spray); wheat$variety=factor(wheat$variety)
> wheatlm=lm(yield~spray*variety+farm+farm:spray,data=wheat)
> anova(wheatlm)
```

fix. eff. — farm interacting w/spray

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
spray	2	842.17	421.08	76.5606	0.002664	**
variety	1	85.33	85.33	15.5152	0.029157	*
farm	1	456.33	456.33	82.9697	0.002796	**
spray:variety	2	1.17	0.58	0.1061	0.902597	
spray:farm	2	15.17	7.58	1.3788	0.376117	
Residuals	3	16.50	5.50			

no interaction → we can remove both interact.s and go ahead to see whether spray and variety are imp. or not

Interest is in the main and interaction effects of the outer and inner factor. Main effects for spray and variety are significant, whereas interaction effects between these two are not. Here, the model is three-way ANOVA with some interactions included: $Y_{ijbk} = \mu + \alpha_i + \beta_j + \gamma_{ij} + b_b + c_{ib} + e_{ijbk}$.

block. fac. — interact. b.w. block fac. and outer fac.

Analysis in R: fixed effects (2)

```
> summary(wheatlm)
[ some output deleted ]
                 Estimate Std. Error t value Pr(>|t|)
(Intercept)μ       70.750      2.031  34.835  5.2e-05 ***
spray2α2−α1        -7.750      2.872  -2.698   0.0739 .
spray3α3−α1        15.000      2.872   5.222   0.0137 *
variety2           -4.500      2.345  -1.919   0.1508
farmf2             12.500      2.345   5.330   0.0129 *
spray2:variety2    -1.500      3.317  -0.452   0.6818
spray3:variety2    -1.000      3.317  -0.302   0.7827
spray2:farmf2       2.500      3.317   0.754   0.5057
spray3:farmf2      -3.000      3.317  -0.905   0.4324
```

This "fixed effects" analysis is nowadays considered old-fashioned, and preference is for the mixed effects analysis on the next slide.

Analysis in R: mixed effects (1)

```
> wheatlmer=lmer(yield~spray*variety+(1|farm)+(1|farm:spray),
+ data=wheat,REML=FALSE); summary(wheatlmer)
[ some output deleted ]
Random effects:
 Groups      Name        Variance Std.Dev.
 farm:spray (Intercept)  0.52083 0.72169
 farm       (Intercept) 37.39584 6.11521
 Residual                2.75000 1.65831
Fixed effects:
                  Estimate Std. Error t value
(Intercept)          77.000      4.509  17.076
spray2               -6.500      1.808  -3.594
spray3               13.500      1.808   7.465
variety2             -4.500      1.658  -2.714
spray2:variety2      -1.500      2.345  -0.640
spray3:variety2      -1.000      2.345  -0.426
```

rand. fac.

fixed fac.s w/ interact.

rand. interact. b.w. farm = rand. fac. w/ spray = 1st fac. → 1 = additive

rand.

μ

$\alpha_2 - \alpha_1$

$\alpha_3 - \alpha_1$

$\beta_2 - \beta_1$

interact. terms

est. of var. = disappeared + no p-val.s → need to do smth extra to get it

Recall the model: $Y_{ijbk} = \mu + \alpha_i + \beta_j + \gamma_{ij} + b_b + c_{ib} + e_{ijbk}$. The estimates and p-values for the effects of spray and variety (under Fixed effects) are a bit different from the previous slide. The column Variance under random effects gives estimates 0.52, 37.39 and 2.75 for the variances of the (normal) populations of the c_{ib}, b_b and e_{ijbk} in the model.

Analysis in R: mixed effects (2)

if we want to test for variety, we skip it (spray = outer fac.)

```
> wheatlmer1=lmer(yield~spray+(1|farm)+(1|farm:spray),data=wheat,REML=FALSE)
> anova(wheatlmer1,wheatlmer)
Models:
wheatlmer1: yield ~ spray + (1 | farm) + (1 | farm:spray)
wheatlmer: yield ~ spray * variety + (1 | farm) + (1 | farm:spray)
           npar    AIC    BIC  logLik deviance  Chisq Df Pr(>Chisq)
wheatlmer1    6 81.610 84.519 -34.805   69.610
wheatlmer     9 74.316 78.680 -28.158   56.316 13.294  3  0.004042 **
```

small model w/out variety

big model w/ variety

variety is imp.

Recall that we cannot directly run `anova(wheatlmer)` to test for any factor of interest. We need to create a model without that factor and test that model inside the full one. For example, to test the effect of the factor `variety` we fit the mixed effects model again, now without this factor in `wheatlmer1` and test by `anova` its fit within the full model `wheatlmer`. The significance of the difference in the models is computed, which is the effect of the factor `variety`. It appears that the effect of `variety` is significant.

overview anova designs so far

Overview designs so far (1)

- 1-way anova (completely randomized) → only 1 fac.
  - Design: select NI units simultaneously.
  - Model: $Y_{ik} = \mu + \alpha_i + e_{ik}$, fixed effects.
- 2-way anova (completely randomized)
  - Design: select NIJ units simultaneously.
  - Model: $Y_{ijk} = \mu + \alpha_i + \beta_j + \gamma_{ij} + e_{ijk}$, fixed effects.

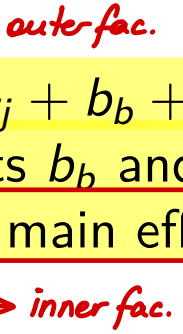
  (α_i: 1st fac., β_j: 2nd fac., γ_{ij}: interact b.w.)
- Randomized block design
  - Design: select NI units from each block population.
  - Model: $Y_{ibk} = \mu + \alpha_i + \beta_b + e_{ibk}$, fixed effects, no interactions.

  (α_i: treat. fac. = of interest; β_b: block fac. = not of interest)
- Repeated measures
  - Design: select B units (which serve as block). → diff. measures done on units → units were treat. as block fac.
  - Model: $Y_{ib} = \mu + \alpha_i + \beta_b + e_{ib}$, fixed effects, no interactions.

  (α_i: treat. = of interest)

Overview designs so far (2)

- General factorial and incomplete block designs
- Mixed effects: crossover design (2 fixed effects + 1 random ind. effect)
  - Design: select N units and divide in two "sequence" groups.
  - Model: $Y_{ispbk} = \mu + \alpha_i + \beta_s + \gamma_p + b_b + e_{ispbk}$, mixed effects with fixed treatment effect α, fixed period effect β, fixed sequence effect γ (but effectively 2 fixed effects), and one random individual effect b_b.
- Mixed effects: split-plot design (2 treatments + one random block factor + random interaction with one treatment)
  - Design: for each block select I (outer) groups of size NJ units from the block population.
  - Model: $Y_{ijbk} = \mu + \alpha_i + \beta_j + \gamma_{ij} + b_b + c_{ib} + e_{ijbk}$, mixed effects with random block effects b_b and random block-whole plot interactions (c_{ib}) and fixed main effects (α_i, β_j) and fixed interaction effects (γ_{ij}).



To finish

Today we discussed:

- general factorial and incomplete block designs
- random effects
- crossover design
- split-plot design
- overview anova designs

Next time: contingency tables, linear regression.