# Experimental Design and Data Analysis, Lecture 6

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# Lecture Overview

1. Friedman test
2. incomplete block design
3. random effects
4. crossover design
5. split-plot design
6. overview block designs

# Friedman test

# Setting and design

Setting and design for the Friedman test are either as in a randomized block design with $N = 1$ or as in repeated measures. An experiment with:

- a numerical outcome $Y$ ("dependent variable").
- a factor of interest that can be fixed at $I$ *levels.* ("treatment").
- a number of blocks or units that are measured at *every* treatment level.

Data

| | block1 | block2 | ... | blockB |
|---|---|---|---|---|
| level 1: | $Y_{11}$, | $Y_{12}$, | ..., | $Y_{1B}$ |
| level 2: | $Y_{21}$, | $Y_{22}$, | ..., | $Y_{2B}$ |
| ⋮ | | | | |
| level $I$: | $Y_{I1}$, | $Y_{I2}$, | ..., | $Y_{IB}$ |

Data ($Y_{ib}$) are not assumed to come from a normal distribution.

We want to test the null hypothesis of no treatment effect taking the blocks into account, by using ranks.

The Friedman test computes the ranks of the $i^{th}$ measurement within each block. Under $H_0$ the rank of $Y_{ib}$ should lie randomly between 1 and $I$ for each $b$. If the average rank of $Y_{ib}$ (averaged over blocks) is lower/higher than expected, then this indicates that $H_0$ might not be true. This is the underlying idea of this test. A $p$-value is output.

# Analysis in R — data input

The dataset `itch.tx` contains the numbers of hours subjects were itching after treatment with 7 different drugs (incl. `No_Drag` and `Placebo`) against itching.

```
> itch=read.table("itch.txt",header=TRUE,sep=","); itch
```

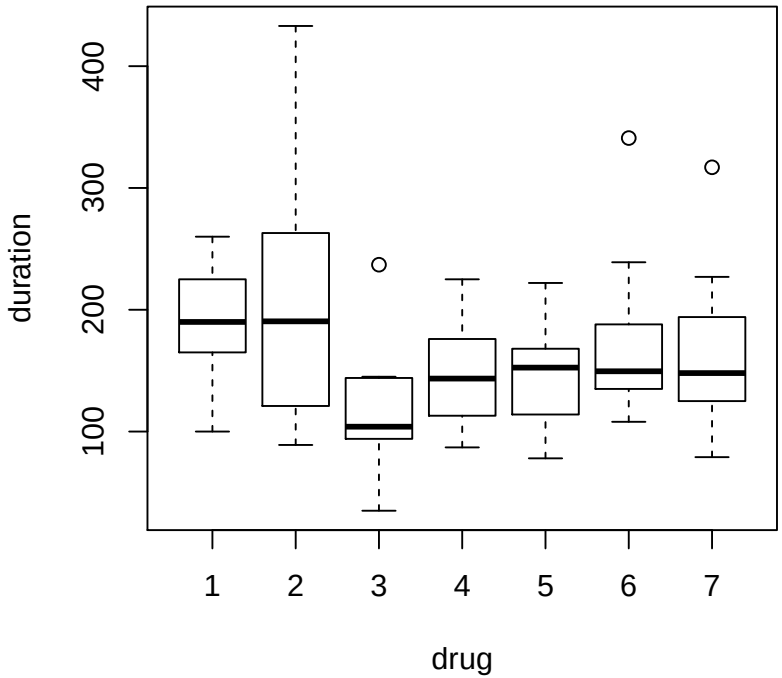
| | Subject | No_Drug | Placebo | Papaverine | Morphine | Aminophylline | Pentabarbital | Tripelennamine |
|---|---|---|---|---|---|---|---|---|
| 1 | BG | 174 | 263 | 105 | 199 | 141 | 108 | 141 |
| 2 | JF | 224 | 213 | 103 | 143 | 168 | 341 | 184 |
| 3 | BS | 260 | 231 | 145 | 113 | 78 | 159 | 125 |
| 4 | SI | 225 | 291 | 103 | 225 | 164 | 135 | 227 |
| 5 | BW | 165 | 168 | 144 | 176 | 127 | 239 | 194 |
| 6 | TS | 237 | 121 | 94 | 144 | 114 | 136 | 155 |
| 7 | GM | 191 | 137 | 35 | 87 | 96 | 140 | 121 |
| 8 | SS | 100 | 102 | 133 | 120 | 222 | 134 | 129 |
| 9 | MU | 115 | 89 | 83 | 100 | 165 | 185 | 79 |
| 10 | OS | 189 | 433 | 237 | 173 | 168 | 188 | 317 |

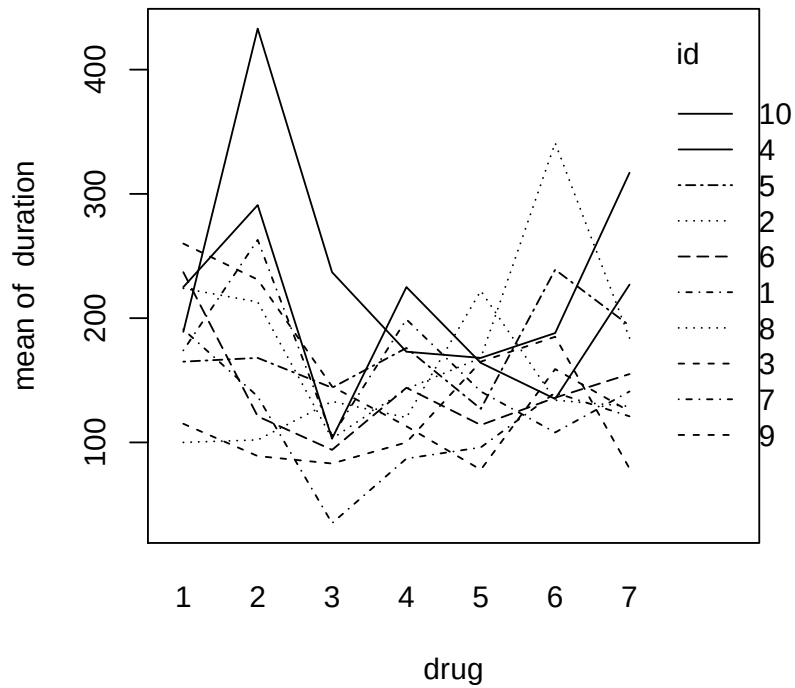
Create a data frame with `duration` as 1st, `id` as 2d, and `drug` as 3d columns.

```
> duration=as.vector(as.matrix(itch[,2:8]))
> id=as.factor(rep(1:10,7)); drug=as.factor(rep(1:7,each=10))
> itchdata=data.frame(cbind(duration,id,drug)); itchdata[1:3,]
  duration id drug
1      174  1    1
2      224  2    1
3      260  3    1
```

# Analysis in R — graphics

```
> boxplot(duration~drug,xlab="drug",ylab="duration")
> interaction.plot(drug,id,duration)
```




Parallel lines in the interaction plot indicate that there is no significant interaction effect. But beware that we're dealing with $N = 1$.

# Analysis in R — testing (1)

```
> friedman.test(duration,drug,id,data=itchdata)

        Friedman rank sum test

data:  duration, drug and subject
Friedman chi-squared = 14.2796, df = 6, p-value = 0.02666
```

Command `friedman.test(duration,drug,id,data=itchdata)` performs the Friedman test, testing the relevance of factor `drug` taking into account the blocking factor `id`. The $p$-value for testing ($H_0$ : no treatment effect) is 0.02666, so $H_0$ is rejected, there is a treatment effect.

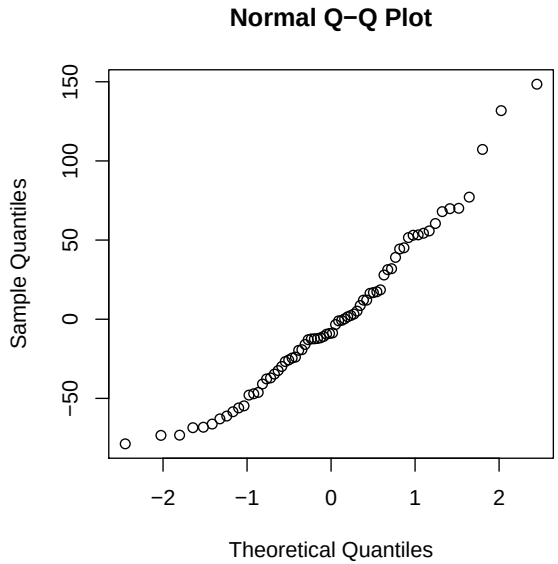
# Analysis in R — testing (2)

Compare the Friedman test results to results for the repeated measures design:

```
> itchaov=lm(duration~drug+subject); anova(itchaov)
Analysis of Variance Table
Response: duration
          Df Sum Sq Mean Sq F value   Pr(>F)
drug       6  51487  8581.2  2.7893 0.019494 *
subject    9 101253 11250.3  3.6569 0.001261 **
Residuals 54 166127  3076.4
```

```
> qqnorm(itchaov$residuals)
```

In a randomized block design we also find a significant treatment effect. The QQ-plot looks ok, perhaps slightly bowed.



# incomplete block designs

# Incomplete block designs

In a regular block design every treatment is applied at least once within every block. If there are many blocks (in particular if two or more block factors are crossed), then this requires many experiments.

In an incomplete block design only a subset of the experiments is performed. For full inference it is advisable to choose this subset in a "balanced way".

# Latin square

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).

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 |

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

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

$\beta_{1k}$ and $\beta_{2l}$ 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 | * | | * | | | * | | * | | * |

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.

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: great save in experiments. Disadvantage: even a rough graphical check on interactions between blocks and treatments is impossible.

# 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.

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.

# Analysis

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

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

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

As in 1-way ANOVA we test $H_0 : \alpha_1 = \ldots = \alpha_I = 0$.

We also estimate $\mu$ and the $\alpha_i$'s.

Since we have both fixed and random effects, this is called a 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 $2 \times 2$ 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

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

for errors ($e_{ispbn}$) and random individual effects ($b_b$) that are independent random samples from centered normal populations, and the *mean values* $\mu_{isp}$ given by

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

$\alpha$ the treatment effect ($T_2 - T_1$),
$\beta$ the learning (or period) effect,
$\gamma$ the sequence effect.

The model leaves the 4 mean values free (4 parameters for 4 means). The parameter $\alpha$ is 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.

```
> 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
```

# 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
```

The sequence effect is left out, because it cannot be estimated in a fixed effects model. If factor `id` enters the model, we have 5 parameters for 4 groups and the parameters become unidentifiable. We do not have enough information to estimate all effects as fixed effects from the data. In the mixed effects model this is possible.

Changing the order of factors in the anova formula gives different $p$-values, because `anova` performs "sequential tests". To use it correctly, put the factor of interest last in the formula, e.g., `anova(lm(pain~id+period+treatment,data=ashinal))` produces the desired p-value for `treatment`, which is "corrected" for the other factors.

# 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 *
```

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 given here and the correct "mixed effects" analysis on the next slide is minor.

# Analysis in R — mixed effects (1)

```
> library(lme4); attach(ashinal)
> ashinalmer=lmer(pain~treatment+sequence+period+(1|id),REML=FALSE)
> 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
```

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)

```
> 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 **
```

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.

# 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.

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 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

The split-plot design assumes that the measurement $Y_{ijnb}$ at levels $i$ and $j$ of the outer and inner factors, of the $n$th replicate in the $b$th block, satisfies the model

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

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

- 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.

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

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

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`.

```
> 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
```

# Analysis in R — fixed effects (1)

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

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: $Y_{ijbn} = \mu + \alpha_i + \beta_j + \gamma_{ij} + b_b + c_{ib} + e_{ijbn}$.

# Analysis in R — fixed effects (2)

```
> summary(wheatlm)
[ some output deleted ]
                 Estimate Std. Error t value Pr(>|t|)
(Intercept)        70.750      2.031  34.835  5.2e-05 ***
spray2             -7.750      2.872  -2.698   0.0739 .
spray3             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
```

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 $e_{ijnb}$ in the model. Recall the model: $Y_{ijbn} = \mu + \alpha_i + \beta_j + \gamma_{ij} + b_b + c_{ib} + e_{ijbn}$.

# Analysis in R — mixed effects (2)

```
> 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 **
```

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 (block) designs so far

# Overview designs so far (1)

- 1-way anova (completely randomized)
  - design: select NI units simultaneously
  - model: $Y_{in} = \mu + \alpha_i + e_{in}$, fixed effects
- 2-way anova (completely randomized)
  - design: select NIJ units simultaneously
  - model: $Y_{ijn} = \mu + \alpha_i + \beta_j + \gamma_{ij} + e_{ijn}$, fixed effects
- randomized block design
  - design: select NI units from each block population
  - model: $Y_{ibn} = \mu + \alpha_i + \beta_b + e_{ibn}$, fixed effects, no interactions
- repeated measures
  - design: select B units (which serve as block)
  - model: $Y_{ib} = \mu + \alpha_i + \beta_b + e_{ib}$, fixed effects, no interactions

# Overview designs so far (1)

- incomplete block design
  - design: select less than NIJ units in a balanced way
  - model: $Y_{ijn} = \mu + \alpha_i + \beta_j + e_{ijn}$, fixed effects, no interactions
- crossover design (2 treatments)
  - design: select N units, and divide in two "sequence" groups
  - model: $Y_{ispbn} = \mu + \alpha_i + \beta_s + \gamma_p + b_b + e_{ispbn}$, mixed effects with random individual effects $b_b$ and fixed treatment effect $\alpha$, fixed period effect ($\beta$) and fixed sequence effect ($\gamma$)
- split-plot design (with block factor)
  - design: for each block: select I (outer) groups of size NJ units from the block population
  - model: $Y_{ijbn} = \mu + \alpha_i + \beta_j + \gamma_{ij} + b_b + c_{ib} + e_{ijbn}$, mixed effects with random block effects $b_b$ and random block-whole plot interactions ($c_{ib}$) and fixed main effects ($\alpha_i$, $\beta_j$) and fixed interaction effects ($\gamma_{ij}$)

# To finish

Today we discussed:

- Friedman test
- incomplete block design
- random effects
- crossover design
- split-plot design
- overview block designs

Next time: contingency tables, linear regression.