Nested and nonnested grouping factors

Peter Hoff
Duke STA 610

Nested groups

Non-nested groups

Nested groups

In some situations there are multiple grouping factors that are *nested*, having observations within groups within groups, etc:

- students within classrooms within schools within counties;
- cities within counties within states;
- medical measurements within patients within hospitals.

We will want to allow for across-group heterogeneity at each level of the hierarchy.

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Nested groups - ET example

A study examined the effects of two different instructional methods on three different exams.

- `itype` $\in \{1, 2\}$, instruction type, an unordered categorical factor.
- `etype` $\in \{1, 2, 3\}$, exam type, an unordered categorical factor.

Experimental design:

- $m_1 = 8$ different sessions (on 8 different days);
- $m_2 = 10$ subjects on each day (subjects were different across days);
- `itype=1` was given on odd days, `itype=2` was on even;
- Each subject given one of two instruction types; took all three exams.

Exercise: Draw the design on the board.

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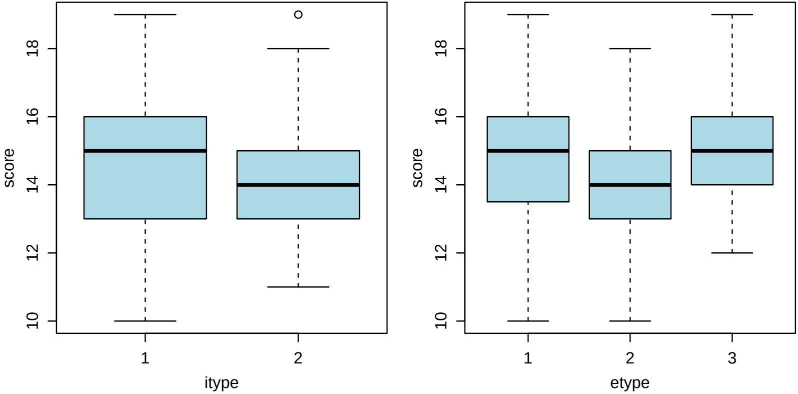
Nested groups

```
etest[1:25,]

##    session itype subject sub.ses etype score
## 1        1     1       1       1     1    17
## 2        1     1       1       1     2    16
## 3        1     1       1       1     3    17
## 4        1     1       2       2     1    17
## 5        1     1       2       2     2    18
## 6        1     1       2       2     3    18
## 7        1     1       3       3     1    17
## 8        1     1       3       3     2    16
## 9        1     1       3       3     3    17
## 10       1     1       4       4     1    16
## 11       1     1       4       4     2    15
## 12       1     1       4       4     3    16
## 13       1     1       5       5     1    15
## 14       1     1       5       5     2    13
## 15       1     1       5       5     3    14
## 16       1     1       6       6     1    15
## 17       1     1       6       6     2    14
## 18       1     1       6       6     3    16
## 19       1     1       7       7     1    14
## 20       1     1       7       7     2    17
## 21       1     1       7       7     3    15
## 22       1     1       8       8     1    17
## 23       1     1       8       8     2    14
## 24       1     1       8       8     3    15
## 25       1     1       9       9     1    16
```

Nested groups

```
etest[20:45,]

##    session itype subject sub.ses etype score
## 20       1     1       7       7     2    17
## 21       1     1       7       7     3    15
## 22       1     1       8       8     1    17
## 23       1     1       8       8     2    14
## 24       1     1       8       8     3    15
## 25       1     1       9       9     1    16
## 26       1     1       9       9     2    16
## 27       1     1       9       9     3    15
## 28       1     1      10      10     1    16
## 29       1     1      10      10     2    13
## 30       1     1      10      10     3    16
## 31       2     2       1      11     1    15
## 32       2     2       1      11     2    14
## 33       2     2       1      11     3    15
## 34       2     2       2      12     1    13
## 35       2     2       2      12     2    11
## 36       2     2       2      12     3    12
## 37       2     2       3      13     1    13
## 38       2     2       3      13     2    15
## 39       2     2       3      13     3    16
## 40       2     2       4      14     1    15
## 41       2     2       4      14     2    13
## 42       2     2       4      14     3    15
## 43       2     2       5      15     1    16
## 44       2     2       5      15     2    13
## 45       2     2       5      15     3    15
```

Preliminary analysis



Preliminary analysis

```
anova(lm(score ~ as.factor(itype) + as.factor(etype) ,data=etest)  )

## Analysis of Variance Table
##
## Response: score
##                   Df Sum Sq Mean Sq F value   Pr(>F)
## as.factor(itype)   1  10.00 10.0042  3.2948 0.070770 .
## as.factor(etype)   2  37.07 18.5375  6.1052 0.002599 **
## Residuals        236 716.58  3.0364
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Controlling for heterogeneity

What if observations within a subject are correlated?

```
anova(lm(score ~ as.factor(sub.ses) + as.factor(itype) + as.factor(etype) ,data=etest))

## Analysis of Variance Table
##
## Response: score
##                     Df Sum Sq Mean Sq F value    Pr(>F)
## as.factor(sub.ses)  79 531.66  6.7299   5.455 < 2.2e-16 ***
## as.factor(etype)     2  37.08 18.5375  15.026 1.062e-06 ***
## Residuals          158 194.92  1.2337
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
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Problem:

- Subjects assigned to only one itype.
- Accounting for all subject variation leaves none for itype to explain.

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Problem:

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What if observations within a session are correlated?

```
anova(lm(score ~ as.factor(session) + as.factor(itype) + as.factor(etype) ,data=etest))

## Analysis of Variance Table
##
## Response: score
##                     Df Sum Sq Mean Sq F value    Pr(>F)
## as.factor(session)   7 330.63  47.233  27.436 < 2.2e-16 ***
## as.factor(etype)     2  37.08  18.538  10.768 3.386e-05 ***
## Residuals          230 395.96   1.722
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
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- Each day has only one itype.
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```

Problem:

- Each day has only one `itype`.
- Accounting for all session variation leaves none for `itype` to explain .

A three-level model

Index the data as follows:

- $k = 1, \ldots, m_1 = 8$ indexes sessions;
- $j = 1, \ldots, m_2 = 10$ indexes subjects within a session;
- $i = 1, \ldots, n = 3$ indexes observations within a subject.

A simple multilevel model:

$$y_{i,j,k} = \mu + a_k + b_{j,k} + \texttt{itype}_k + \texttt{etype}_{i,j,k} + \epsilon_{i,j,k}$$
$$\{a_k\} \sim \text{i.i.d. normal}(0, \tau_1^2)$$
$$\{b_{j,k}\} \sim \text{i.i.d. normal}(0, \tau_2^2)$$
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- $\{a_k\}$ describes across-session heterogeneity;
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As you might guess, τ_1^2 and τ_2^2 relate to within-session and within-subject correlation, respectively.

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Nested models in lme4

```
fit1<-lmer(score ~ as.factor(itype) + as.factor(etype) + (1|session) + (1|sub.ses) , data=e
```

```
summary(fit1)

## Linear mixed model fit by maximum likelihood  ['lmerMod']
## Formula: score ~ as.factor(itype) + as.factor(etype) + (1 | session) +
##     (1 | sub.ses)
##    Data: etest
##
##      AIC      BIC   logLik deviance df.resid
##    830.1    854.5   -408.1    816.1      233
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.19164 -0.60931  0.04071  0.58343  2.73365
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  sub.ses  (Intercept) 0.5246   0.7243
##  session  (Intercept) 1.2429   1.1148
##  Residual             1.2183   1.1038
## Number of obs: 240, groups:  sub.ses, 80; session, 8
##
## Fixed effects:
##                   Estimate Std. Error t value
## (Intercept)        14.7542     0.5866  25.151
## as.factor(itype)2  -0.4083     0.8173  -0.500
## as.factor(etype)2  -0.5000     0.1745  -2.865
## as.factor(etype)3   0.4625     0.1745   2.650
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Alternative formulation

```
fit2<-lmer(score ~ as.factor(itype) + as.factor(etype) + (1|session/subject) , data=etest,R
```

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summary(fit2)

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##
```

Nested index sets

```
BIC(fit1)
## [1] 854.5021
BIC(fit2)
## [1] 854.5021
```

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Many datasets don't distinguish between (person 1,day 1) and (person 1,day 2).

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Nested index sets

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Beyond random intercepts

Do the effects of `itype`, `etype` vary across subjects or sessions?

Do we have enough data to detect such variance?

`itype`

- `itype` is a macro variable from the perspective of `session`
- `itype` is a macro variable from the perspective of `subject`

We do not have the data to detect variance in the effects of `itype` across either grouping factor.

`etype`

- `etype` is a micro variable from the perspective of `session`
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We can estimate variance in the effects of `etype` across sessions.

We only have one rep per `etype` per `subject` - can't estimate variance in the effects of `etype` across subjects.

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```
lmer(score ~ as.factor(itype) + as.factor(etype) + (1+etype |session) +
          (1 + etype|sub.ses) , data=etest,REML=FALSE)

## Error:  number of observations (=240) <= number of random effects (=240) for
term (1 + etype | sub.ses); the random-effects parameters and the residual
variance (or scale parameter) are probably unidentifiable
```

```
lmer(score ~ as.factor(itype) + as.factor(etype) + (1+etype |session) +
          (1|sub.ses) , data=etest,REML=FALSE)

## Linear mixed model fit by maximum likelihood  ['lmerMod']
## Formula: score ~ as.factor(itype) + as.factor(etype) + (1 + etype | session) +
##     (1 | sub.ses)
##    Data: etest
##       AIC       BIC    logLik  deviance  df.resid
##  837.4802  879.2479 -406.7401  813.4802       228
## Random effects:
##  Groups   Name        Std.Dev. Corr
##  sub.ses  (Intercept) 0.7326
##  session  (Intercept) 1.2743
##           etype2      0.2472   -1.00
##           etype3      0.3402   -0.70  0.70
##  Residual             1.0860
## Number of obs: 240, groups:  sub.ses, 80; session, 8
## Fixed Effects:
##       (Intercept)  as.factor(itype)2  as.factor(etype)2  as.factor(etype)3
##           14.7332            -0.3664            -0.5000             0.4625
## optimizer (nloptwrap) convergence code: 0 (OK) ; 0 optimizer warnings; 1 lme4 warnings
```

Some fits

```
fit<-lmer( score ~ as.factor(itype) + as.factor(etype) +
          ( as.factor(etype) | session )  +
          ( 1|sub.ses ) , data=etest,REML=FALSE )
```

```
drop1(fit,test="Chisq")

## Single term deletions
##
## Model:
## score ~ as.factor(itype) + as.factor(etype) + (as.factor(etype) |
##     session) + (1 | sub.ses)
##                  npar    AIC     LRT   Pr(Chi)
## <none>                837.48
## as.factor(itype)    1 835.73  0.2474 0.618910
## as.factor(etype)    2 846.71 13.2264 0.001343 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Some fits

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fit<-lmer( score ~ as.factor(itype) + as.factor(etype) +
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```

Do exam effects vary across sessions?

```
fit1<-lmer( score ~ as.factor(etype) +
          ( as.factor(etype) | session )  +
          ( 1|sub.ses ) , data=etest ,REML=FALSE)

fit0<-lmer( score ~ as.factor(etype) +
          ( 1| session )  +
          ( 1|sub.ses ) , data=etest,REML=FALSE )
```

```
BIC(fit1)

## [1] 874.0147

BIC(fit0)

## [1] 849.2673
```

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```

Is there excess group heterogeneity?

```
fit00<-lm( score ~ as.factor(etype) , data=etest)

fit10<-lmer( score ~ as.factor(etype) + ( 1| session ) , data=etest,REML=FALSE)

fit01<-lmer( score ~ as.factor(etype) + ( 1| sub.ses ) , data=etest,REML=FALSE)

fit11<-lmer( score ~ as.factor(etype) + ( 1| session ) +( 1| sub.ses ),data=etest,REML=FALS
```

```
BIC(fit00)

## [1] 968.8658

BIC(fit10)

## [1] 862.2868

BIC(fit01)

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BIC(fit11)

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Non nested grouping factors

Agricultural field trial:

Experimental material: $m_1 = 3$ plots of land for $m_2 = 6$ years.

Outcome: Crop yield

Treatments/explanatory variables:

- fertilizer type (`fert1`,`fert1`)
- seed variety (`seed1`,`seed2`)

Experimental design:

- `fert1` used in all plots in years 1-3, `fert2` used in all plots in years 4-6.
- each seed type assigned to two of four subplots, in each plot and year.

Exercise: Draw the design on the board.

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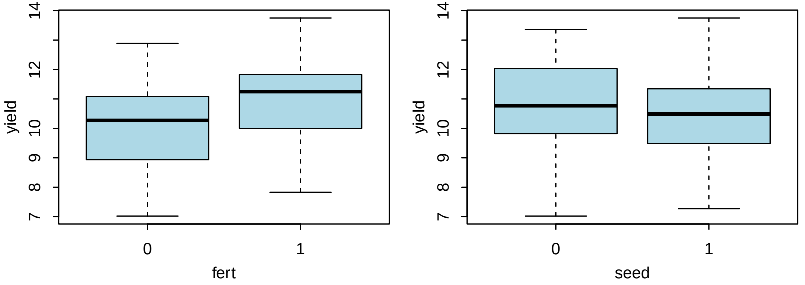
Data

```
crops[1:25,]

##    yield year plot fert seed
## 1  12.16    1    1    0    0
## 2  12.64    1    1    0    0
## 3  12.89    1    1    0    1
## 4  11.57    1    1    0    1
## 5  11.15    1    2    0    0
## 6  10.35    1    2    0    0
## 7  10.53    1    2    0    1
## 8  10.90    1    2    0    1
## 9  12.43    1    3    0    0
## 10 10.27    1    3    0    0
## 11  9.18    1    3    0    1
## 12 10.92    1    3    0    1
## 13 12.04    2    1    0    0
## 14 10.88    2    1    0    0
## 15 11.02    2    1    0    1
## 16 10.22    2    1    0    1
## 17  8.64    2    2    0    0
## 18 10.35    2    2    0    0
## 19 10.45    2    2    0    1
## 20  9.43    2    2    0    1
## 21  9.88    2    3    0    0
## 22  7.02    2    3    0    0
## 23 11.58    2    3    0    1
## 24 10.17    2    3    0    1
## 25 11.59    3    1    0    0
```

Exploratory analysis




```
summary(lm(yield~fert+seed,data=crops))

##
## Call:
## lm(formula = yield ~ fert + seed, data = crops)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -3.2589 -1.1164  0.1778  0.9261  2.9111
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  10.2789     0.2934  35.038  < 2e-16 ***
## fert          0.9067     0.3387   2.677  0.00929 **
## seed         -0.3000     0.3387  -0.886  0.37890
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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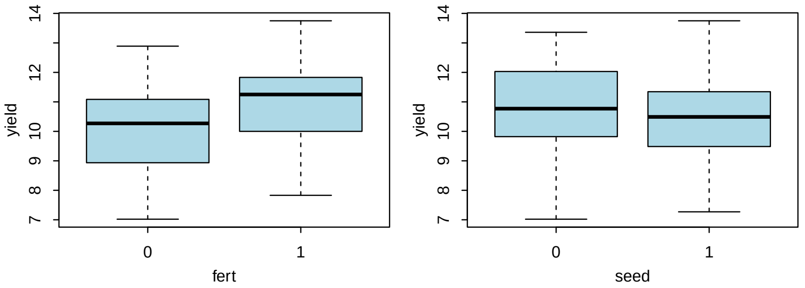


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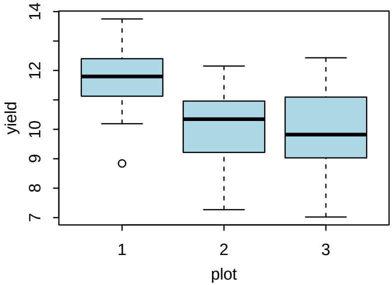


```
anova(lm(yield~as.factor(plot) ,data=crops))

## Analysis of Variance Table
##
## Response: yield
##                 Df Sum Sq Mean Sq F value    Pr(>F)
## as.factor(plot)  2  48.59 24.2951  15.192 3.411e-06 ***
## Residuals       69 110.34  1.5992
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Contolling for plot variaion

```
anova(lm(yield~ as.factor(plot) + fert + seed,data=crops))

## Analysis of Variance Table
##
## Response: yield
##                 Df Sum Sq Mean Sq F value    Pr(>F)
## as.factor(plot)  2 48.590 24.2951 17.3300 8.59e-07 ***
## fert             1 14.797 14.7968 10.5547 0.001813 **
## seed             1  1.620  1.6200  1.1556 0.286243
## Residuals       67 93.928  1.4019
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The `fert` p-value assumes we have $3 \times 3 \times 4 = 36$ independent observations for both levels of `fert`.

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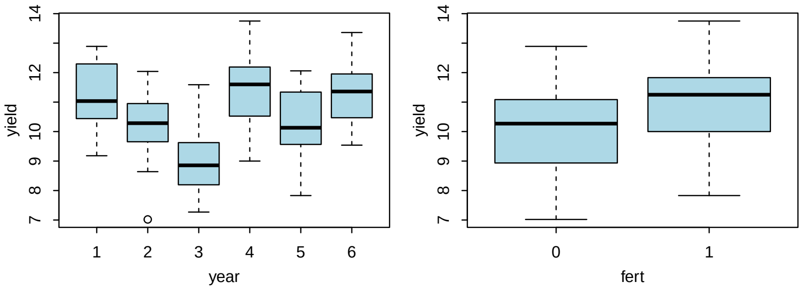
Replication at different levels

- How many times was the fertilizer type obtained and applied?
- Ignoring `plot` and `seed`, how confident are we in the effects of `fert`?
- Could anything else cause the effects we are attributing to `fert`?



The "sample size" for `fert` is more like $m_1 = 6$, with 3 obs per level.

This issue is common in multilevel experiments (e.g. *split-plot* designs). See the notes for more details.

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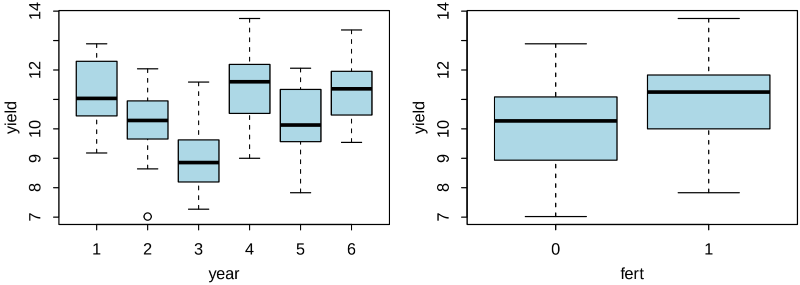

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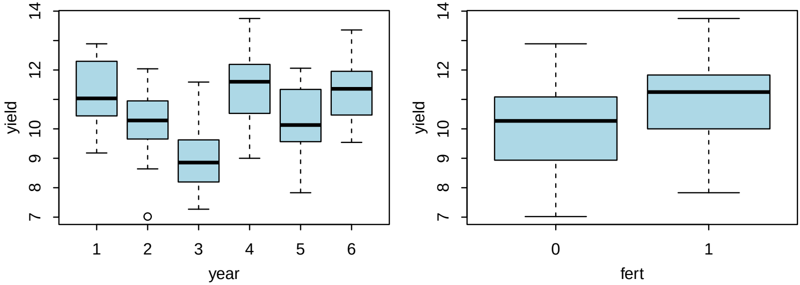

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Accounting for year effects

```
anova(lm(yield~ as.factor(year) + as.factor(plot) + fert + seed,data=crops))

## Analysis of Variance Table
##
## Response: yield
##                 Df Sum Sq Mean Sq F value    Pr(>F)
## as.factor(year)  5 56.471 11.2942 13.6169 5.214e-09 ***
## as.factor(plot)  2 48.590 24.2951 29.2915 1.013e-09 ***
## seed             1  1.620  1.6200  1.9532    0.1671
## Residuals       63 52.254  0.8294
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Accounting for all year-to-year variability leaves none for `fert`.

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Multilevel approach

$$\begin{aligned}\texttt{yield}_{i,j,k} &= \mu + a_j + b_k + \beta_1 \times \texttt{fert}_k + \beta_2 \times \texttt{seed}_{i,j,k} + \epsilon_{i,j,k} \\ \{a_j\} &\sim \ iid \ N(0, \tau_a^2) \\ \{b_k\} &\sim \ iid \ N(0, \tau_b^2) \\ \{\epsilon_{i,j,k}\} &\sim \ iid \ N(0, \sigma^2)\end{aligned}$$

- $\{a_j\}$ represents heterogeneity across plots;
- $\{b_k\}$ represents heterogeneity across years;
- $\{\epsilon_{i,j,k}\}$ represents heterogeneity within years and plots.

Fitting with lmer

```
fit<-lmer( yield ~ fert + seed + (1|year) + (1|plot),  data=crops,REML=FALSE)
BIC(fit)

## [1] 236.3216

summary(fit)$coef

##               Estimate Std. Error   t value
## (Intercept) 10.2788889  0.6827214 15.055759
## fert         0.9066667  0.6600107  1.373715
## seed        -0.3000000  0.2130316 -1.408242
```

Other things to investigate:

- heterogeneity of seed effects across plots and years: `(seed|plots) + (seed|years)`
- heterogeneity of fert effects across plots, but not years. `(fert|plots)`

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