

Nested and nonnested grouping factors

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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.

It is fairly straightforward to do this with random effects models, although some care has to be used in coding the group labels and fitting group-specific regression parameters.

Nested groups - ET example

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

- $\text{itype} \in \{1, 2\}$, instruction type, an unordered categorical factor.
- $\text{etype} \in \{1, 2, 3\}$, 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);
- $\text{itype}=1$ was given on odd days, $\text{itype}=2$ was on even;
- Each subject given one of two instruction types; took all three exams.

Exercise: Draw the design on the board.

Nested groups

```
etest[1:25,]

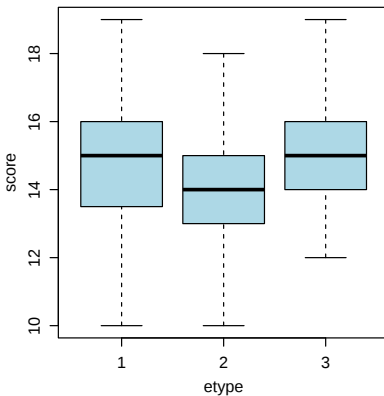
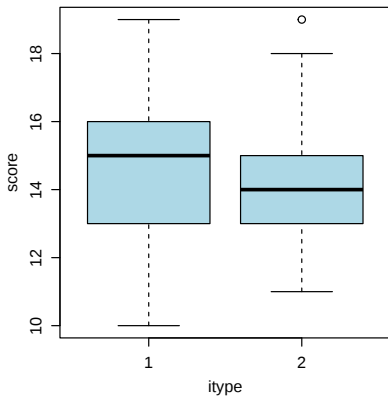
##      session itype subject sub.ses etype score
## 1          1      1        1         1      1     17
## 2          1      1        1         1      2     16
## 3          1      1        1         1      3     17
## 4          1      1        2         2      1     17
## 5          1      1        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
```

Problem:

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

Controlling for heterogeneity

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
```

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:

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

A simple multilevel model:

$$y_{i,j,k} = \mu + a_k + b_{j,k} + \text{itype}_k + \text{etype}_{i,j,k} + \epsilon_{i,j,k}$$

$$\{a_k\} \sim \text{i.i.d. normal}(0, \tau_1^2)$$

$$\{b_{j,k}\} \sim \text{i.i.d. normal}(0, \tau_2^2)$$

$$\{\epsilon_{i,j,k}\} \sim \text{i.i.d. normal}(0, \sigma^2)$$

- $\{a_k\}$ describes across-session heterogeneity;
- $\{b_{j,k}\}$ describes across-subject heterogeneity;
- $\{\epsilon_{i,j,k}\}$ describes within-subject heterogeneity.

As you might guess, τ_1^2 and τ_2^2 relate to within-session and within-subject correlation, respectively.

Nested models in lme4

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

```
summary(fit1)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: score ~ as.factor(itype) + as.factor(etype) + (1 | session) +
##      (1 | sub.ses)
##      Data: etest
##
## REML criterion at convergence: 818
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.16205 -0.60066  0.04381  0.57415  2.73733
##
## Random effects:
##   Groups   Name                Variance Std.Dev.
## sub.ses   (Intercept)  0.5195     0.7207
## session   (Intercept)  1.6882     1.2993
## Residual                   1.2337     1.1107
## Number of obs: 240, groups:  sub.ses, 80; session, 8
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)    14.7542    0.6750  21.859
## as.factor(itype)2  -0.4083    0.9437  -0.433
## as.factor(etype)2  -0.5000    0.1756  -2.847
## as.factor(etype)3   0.4625    0.1756   2.634
##
```

Alternative formulation

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

```
summary(fit2)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: score ~ as.factor(itype) + as.factor(etype) + (1 | session/subject)
## Data: etest
##
## REML criterion at convergence: 818
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.16205 -0.60066  0.04381  0.57415  2.73733
##
## Random effects:
## Groups           Name                Variance Std.Dev.
## subject:session (Intercept) 0.5195   0.7207
## session          (Intercept) 1.6882   1.2993
## Residual                    1.2337   1.1107
## Number of obs: 240, groups:  subject:session, 80; session, 8
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)   14.7542    0.6750  21.859
## as.factor(itype)2  -0.4083    0.9437  -0.433
## as.factor(etype)2  -0.5000    0.1756  -2.847
## as.factor(etype)3   0.4625    0.1756   2.634
##
## Correlation of Fixed Effects:
```

Nested index sets

```
BIC(fit1)
## [1] 856.328

BIC(fit2)
## [1] 856.328
```

The term (1|session/subject) here is a convenience feature.

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

If these people are different, you need to tell the software somehow:

- code them manually to be different;

- use the nesting feature in `lmer`

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
- `etype` is a micro variable from the perspective of subject

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.

Some fits

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

```
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)      1 835.61  0.1277 0.720837
## as.factor(etype)      2 846.71 13.2264 0.001343 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Do exam effects vary across sessions?

```
fit1<-lmer( score ~ as.factor(etype) +  
            ( as.factor(etype) | session ) +  
            ( 1|sub.ses ) , data=etest )  
  
fit0<-lmer( score ~ as.factor(etype) +  
            ( 1| session ) +  
            ( 1|sub.ses ) , data=etest )
```

```
BIC(fit1)
```

```
## [1] 876.9898
```

```
BIC(fit0)
```

```
## [1] 852.7055
```

Is there excess group heterogeneity?

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

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

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

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

```
BIC(fit00)
## [1] 968.8658

BIC(fit10)
## [1] 865.0546

BIC(fit01)
## [1] 896.9276

BIC(fit11)
## [1] 852.7055
```

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.

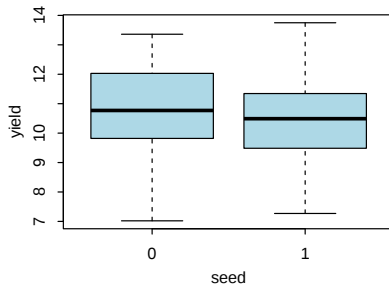
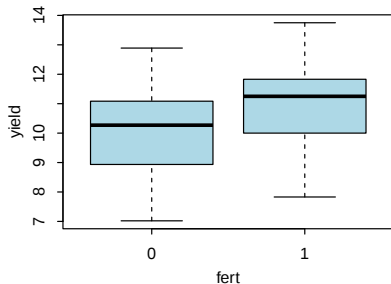
Exercise: Draw the design on the board.

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

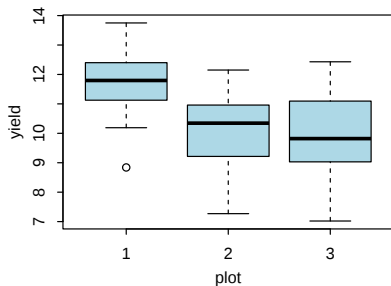


```
summary(lm(yield~fert+seed,data=crops))
```

```
##
## 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
```

Exploratory analysis



```
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
```

Controlling for plot variation

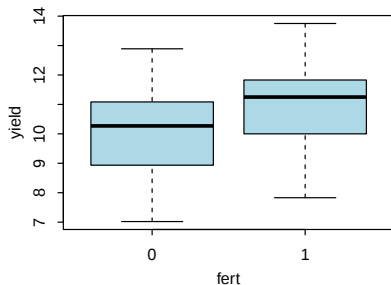
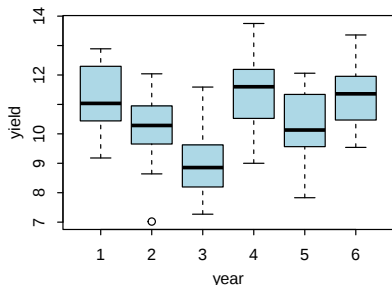
```
anova(lm(yield~ as.factor(plot) + fert + seed,data=crops))

## 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.

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.

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.

Multilevel approach

$$\text{yield}_{i,j,k} = \mu + a_j + b_k + \beta_1 \times \text{fert}_k + \beta_2 \times \text{seed}_{i,j,k} + \epsilon_{i,j,k}$$

$$\{a_j\} \sim \text{iid } N(0, \tau_a^2)$$

$$\{b_k\} \sim \text{iid } N(0, \tau_b^2)$$

$$\{\epsilon_{i,j,k}\} \sim \text{iid } N(0, \sigma^2)$$

- $\{a_j\}$ 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) 10.278889   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)