

# **lme for SAS PROC MIXED Users**

Douglas Bates  
Department of Statistics  
University of Wisconsin – Madison  
Bates@wisc.edu

## **1 Introduction**

The `lme` function from the `lme4` library for R is used to fit linear mixed-effects models. It is similar in scope to the SAS procedure PROC MIXED described in Littell et al. (1996).

A file on the SAS Institute web site (<http://www.sas.com>) contains all the data sets in the book and all the SAS programs used in Littell et al. (1996). We have converted the data sets from the tabular representation used for SAS PROC MIXED to the `groupedData` objects used by `lme`. To help users familiar with SAS PROC MIXED get up to speed with `lme` more quickly, we provide transcripts of some `lme` analyses paralleling the SAS PROC MIXED analyses in Littell et al. (1996).

In this paper we highlight some of the similarities and differences of `lme` analysis and SAS PROC MIXED analysis.

## **2 Similarities between lme and SAS PROC MIXED**

Both SAS PROC MIXED and `lme` can fit linear mixed-effects models expressed in the Laird-Ware formulation. For a single level of grouping Laird and Ware (1982) write the  $n_i$ -dimensional response vector  $\mathbf{y}_i$  for the  $i$ th experimental

unit as

$$\begin{aligned} \mathbf{y}_i &= \mathbf{X}_i\boldsymbol{\beta} + \mathbf{Z}_i\mathbf{b}_i + \boldsymbol{\epsilon}_i, \quad i = 1, \dots, M \\ \mathbf{b}_i &\sim \mathcal{N}(\mathbf{0}, \boldsymbol{\Sigma}), \quad \boldsymbol{\epsilon}_i \sim \mathcal{N}(\mathbf{0}, \sigma^2 \mathbf{I}) \end{aligned} \tag{1}$$

where  $\boldsymbol{\beta}$  is the  $p$ -dimensional vector of *fixed effects*,  $\mathbf{b}_i$  is the  $q$ -dimensional vector of *random effects*,  $\mathbf{X}_i$  (of size  $n_i \times p$ ) and  $\mathbf{Z}_i$  (of size  $n_i \times q$ ) are known fixed-effects and random-effects regressor matrices, and  $\boldsymbol{\epsilon}_i$  is the  $n_i$ -dimensional *within-group error* vector with a spherical Gaussian distribution. The assumption  $\text{Var}(\boldsymbol{\epsilon}_i) = \sigma^2 \mathbf{I}$  can be relaxed using additional arguments in the model fitting.

The basic specification of the model requires a linear model expression for the fixed effects and a linear model expression for the random effects. In SAS PROC MIXED the fixed-effects part is specified in the `model` statement and the random-effects part in the `random` statement. In `lme` the arguments are called `fixed` and `random`.

Both SAS PROC MIXED and `lme` allow a mixed-effects model to be fit by maximum likelihood (`method = ml` in SAS) or by maximum residual likelihood, sometimes also called restricted maximum likelihood or REML. This is the default criterion in SAS PROC MIXED. The default criterion in `lme` is maximum likelihood. To get REML estimates in `lme`, set the optional argument `REML=TRUE`.

### 3 Important differences

One of the most important differences has just been stated but is worth repeating. SAS defaults to REML fits; `lme` defaults to maximum likelihood fits.

The output from PROC MIXED typically includes values of the Akaike Information Criterion (AIC) and Schwartz’s Bayesian Criterion (SBC). These are used to compare different models fit to the same data. The output of the `summary` function applied to the object created by `lme` also produces values of AIC and BIC but the definitions used in PROC MIXED and in `lme` are different. In `lme` the definitions are such that “smaller is better”. In PROC MIXED the definitions are such that “bigger is better”.

When models are fit by REML, the values of AIC, SBC (or BIC) and the log-likelihood can only be compared between models with exactly the same fixed-effects structure. When models are fit by maximum likelihood these

criteria can be compared between any models fit to the same data. That is, these quality-of-fit criteria can be used to evaluate different fixed-effects specifications or different random-effects specifications or different specifications of both fixed effects and random effects. The greater flexibility of model comparisons when using maximum likelihood is the reason that this is the default criterion in `lme`.

We encourage developing and testing the model using likelihood ratio tests or the AIC and BIC criteria. Once a form for both the random effects and the fixed effects has been determined, the model can be refit with `REML = TRUE` if the restricted estimates of the variance components are desired.

## 4 Data manipulation

Both `PROC MIXED` and `lme` work with data in a tabular form with one row per observation. There are, however, important differences in the internal representations of variables in the data.

In `SAS` a qualitative factor can be stored either as numerical values or alphanumeric labels. When a factor stored as numerical values is used in `PROC MIXED` it is listed in the `class` statement to indicate that it is a factor. In `S` this information is stored with the data itself by converting the variable to a factor when it is first stored. If the factor represents an ordered set of levels, it should be converted to an `ordered` factor.

For example the `SAS` code

```
data animal;
  input trait animal y;
  datalines;
1 1 6
1 2 8
1 3 7
2 1 9
2 2 5
2 3 .
;
```

would require that the `trait` and `animal` variables be specified in a `class` statement in any model that is fit.

In `S` these data could be read from a file, say `animal.dat`, and converted to factors by

```

animal <- read.table("animal.dat", header = TRUE)
animal$trait <- as.factor(animal$trait)
animal$animal <- as.factor(animal$animal)

```

In general it is a good idea to check the types of variables in a data frame before working with it. One way of doing this is to apply the function `data.class` to each variable in turn using the `sapply` function.

```

> sapply(Animal, data.class)
      Sire      Dam AvgDailyGain
"factor" "factor" "numeric"
> str(Animal)
`data.frame`:      20 obs. of  3 variables:
 $ Sire      : Factor w/ 5 levels "1","2","3","4",...: 1 1 1 1 2 2 2 2 3 3 ...
 $ Dam       : Factor w/ 2 levels "1","2": 1 1 2 2 1 1 2 2 1 1 ...
 $ AvgDailyGain: num  2.24 1.85 2.05 2.41 1.99 1.93 2.72 2.32 2.33 2.68 ...
- attr(*, "ginfo")=List of 7
 ..$ formula      :Class 'formula' length 3 AvgDailyGain ~ 1 | Sire/Dam
 .. .. ..- attr(*, ".Environment")=length 0 <environment>
 ..$ order.groups:List of 2
 .. ..$ Sire: logi TRUE
 .. ..$ Dam : logi TRUE
 ..$ FUN        :function (x)
 ..$ outer      : NULL
 ..$ inner      : NULL
 ..$ labels     :List of 1
 .. ..$ AvgDailyGain: chr "Average Daily Weight Gain"
 ..$ units      : list()

```

To make specification of models in `lme` easier and to make graphic presentations more informative, we recommend converting from a `data.frame` object to a `groupedData` object. This class of objects contains a formula specifying the response, the primary covariate (if there is one) and the grouping factor or factors. The data sets from Littell et al. (1996) have been converted to `groupedData` objects in this directory.

## 4.1 Unique levels of factors

Designs with nested grouping factors are indicated differently in the two languages. An example of such an experimental design is the semiconductor experiment described in section 2.2 of Littell et al. (1996) where twelve wafers

are assigned to four experimental treatments with three wafers per treatment. The levels for the wafer factor are 1, 2, and 3 but the wafer factor is only meaningful within the same level of the treatment factor, **et**. There is nothing associating wafer 1 of the third treatment group with wafer 1 of the first treatment group.

In **SAS** this nesting of factors is denoted by **wafer(et)**. In **S** the nesting is written with **ET/Wafer** and read “wafer within ET”. If both levels of nested factors are to be associated with random effects then this is all you need to know. You would use an expression with a **"/"** in the grouping factor part of the formula for the **groupedData** object. Then the random effects could be specified as

```
random = list( ET = ~ 1, Wafer = ~ 1 )
```

or, equivalently

```
random = ~ 1 | ET/Wafer
```

In this case, however, there would not usually be any random effects associated with the “experimental treatment” or **ET** factor. The only random effects are at the **Wafer** level. It is necessary to create a factor that will have unique levels for each **Wafer** within each level of **ET**. One way to do this is to assign

```
> Semiconductor$Grp <- with(Semiconductor, ET:Wafer)
```

after which we could specify **random = 1 | Grp**.

## 4.2 General approach

As a general approach to importing data into **S** for mixed-effects analysis you should:

- Create a **data.frame** with one row per observation and one column per variable.
- Use **ordered** or **as.ordered** to convert any ordered factors to class **ordered**.
- Use **factor** or **as.factor** to convert any ordered factors to class **factor**.
- If necessary, use **interaction** or **:** to create a factor with unique levels from inner nested factors.

- Specify the formula for the response, the primary covariate and the grouping structure to create a `groupedData` object from the data frame. Labels and units for the response and the primary covariate can also be specified at this time as can `outer` and `inner` factor expressions.
- Plot the data. Plot it several ways. The use of lattice graphics is closely integrated with the `lme4` library. Lattice plots can provide invaluable insight into the structure of the data. Use them.

## 5 Contrasts

When comparing estimates produced by SAS PROC MIXED and by `lme` one must be careful to consider the contrasts that are used to define the effects of factors. In SAS a model with an intercept and a qualitative factor is defined in terms of the intercept and the indicator variables for all but the last level of the factor. The default behaviour in S is to use the Helmert contrasts for the factor. On a balanced factor these provide a set of orthogonal contrasts. In R the default is the “treatment” contrasts which are almost the same as the SAS parameterization except that they drop the indicator of the first level, not the last level.

When in doubt, check which contrasts are being used with the `contrasts` function.

To make comparisons easier, you want to use

```
> options(contrasts = c(factor = "contr.SAS", ordered = "contr.poly"))
```

at the beginning of your session.

## References

- Nan M. Laird and James H. Ware. Random-effects models for longitudinal data. *Biometrics*, 38:963–974, 1982.
- Ramon C. Littell, George A. Milliken, Walter W. Stroup, and Russell D. Wolfinger. *SAS System for Mixed Models*. SAS Institute, Inc., 1996.

## A AvgDailyGain

Analysis of average daily weight gain data given as data set 5.3. Compare these results with output 5.1 (p. 178).

```
> print(gplot(AvgDailyGain))

> fmlAdg <- lme(adg ~ (Treatment - 1) * InitWt, data = AvgDailyGain,
+      random = ~1 | Block)
> summary(fmlAdg)
Linear mixed-effects model fit by REML
Fixed: adg ~ (Treatment - 1) * InitWt
Data: AvgDailyGain
      AIC      BIC    logLik
85.32685 99.9842 -32.66342

Random effects:
  Groups   Name      Variance Std.Dev.
Block     (Intercept) 0.259311 0.50923
Residual                0.049429 0.22233
# of obs: 32, groups: Block, 8

Fixed effects:
              Estimate Std. Error DF t value Pr(>|t|)
Treatment0      0.4391368   0.7110882 24  0.6176  0.54268
Treatment10     1.4261185   0.6375459 24  2.2369  0.03485 *
Treatment20     0.4796283   0.5488868 24  0.8738  0.39088
Treatment30     0.2001073   0.7751990 24  0.2581  0.79850
InitWt          0.0044480   0.0020816 24  2.1368  0.04301 *
Treatment0:InitWt -0.0021543   0.0027863 24 -0.7732  0.44695
Treatment10:InitWt -0.0033651   0.0025148 24 -1.3381  0.19340
Treatment20:InitWt -0.0010823   0.0024875 24 -0.4351  0.66737
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:
              Trtmn0 Trtm10 Trtm20 Trtm30 InitWt Tr0:IW T10:IW
Treatment10    0.039
Treatment20    0.080  0.334
Treatment30    0.011  0.097  0.043
InitWt         0.050 -0.032  0.035 -0.967
```

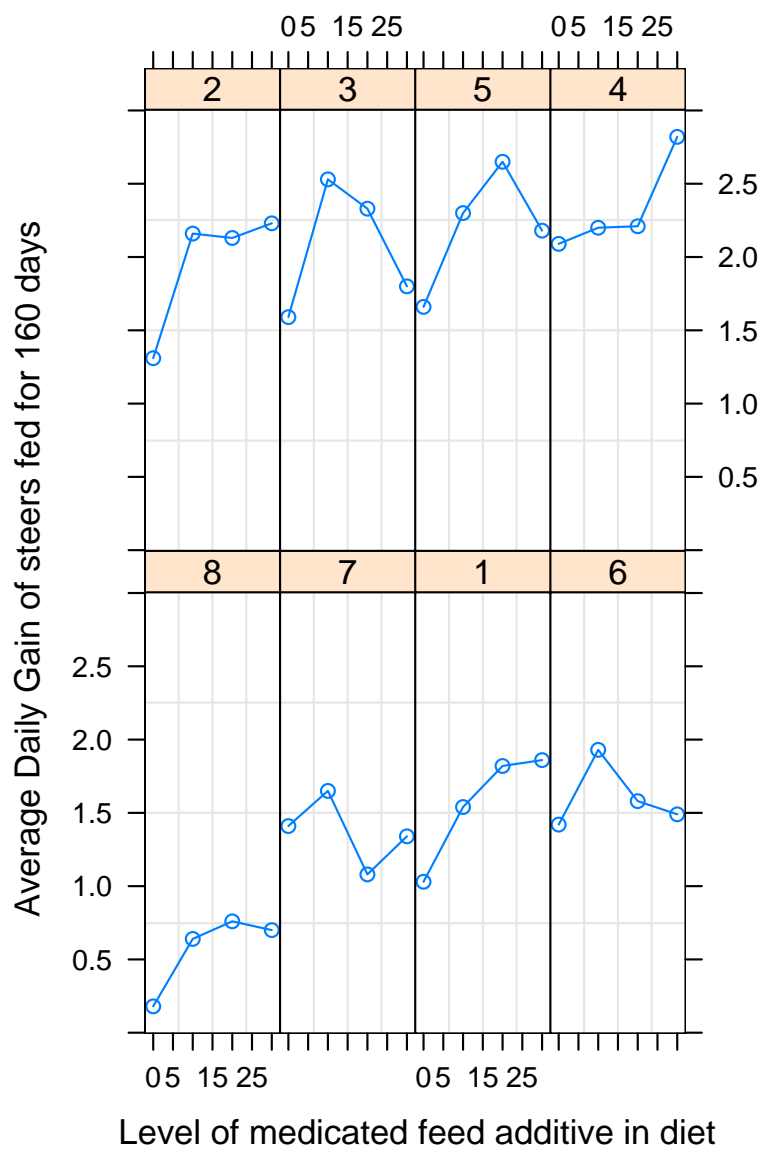


Figure 1: Average daily weight gain



```

Trtmnt0:InW -0.640  0.046 -0.024  0.754 -0.780
Trtmnt10:IW -0.021 -0.534 -0.178  0.781 -0.808  0.617
Trtmnt20:IW -0.040 -0.106 -0.512  0.828 -0.856  0.666  0.775
> anova(fm1Adg)
Analysis of Variance Table

            Df Sum Sq Mean Sq  Denom F value    Pr(>F)
Treatment      4  5.7248  1.4312 24.0000 28.9543 7.159e-09 ***
InitWt          1  0.5495  0.5495 24.0000 11.1175  0.00277 **
Treatment:InitWt 3  0.1381  0.0460 24.0000  0.9312  0.44088
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
> fm2Adg <- update(fm1Adg, adg ~ InitWt + Treatment)
> summary(fm2Adg)
Linear mixed-effects model fit by REML
Fixed: adg ~ InitWt + Treatment
Data: AvgDailyGain
      AIC      BIC    logLik
50.33733 60.59748 -18.16866

Random effects:
Groups   Name      Variance Std.Dev.
Block    (Intercept) 0.24084  0.49076
Residual                0.05008  0.22379
# of obs: 32, groups: Block, 8

Fixed effects:
            Estimate Std. Error DF t value Pr(>|t|)
(Intercept)  0.80110842  0.35566103 27  2.2524  0.032628 *
InitWt        0.00277971  0.00083335 27  3.3356  0.002486 **
Treatment0   -0.55207364  0.11481306 27 -4.8085 5.096e-05 ***
Treatment10  -0.06856608  0.11896892 27 -0.5763  0.569162
Treatment20  -0.08812909  0.11628776 27 -0.7579  0.455103
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:
            (Intr) InitWt Trtmn0 Trtml0
InitWt      -0.844
Treatment0   0.036 -0.224
Treatment10  0.139 -0.340  0.534
Treatment20  0.079 -0.272  0.530  0.545

```

```

> anova(fm2Adg)
Analysis of Variance Table

            Df Sum Sq Mean Sq  Denom F value    Pr(>F)
InitWt       1  0.5146   0.5146  27.0000   10.275 0.0034525 **
Treatment    3  1.5267   0.5089  27.0000   10.162 0.0001185 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
> summary(update(fmlAdg, adg ~ InitWt + Treatment - 1))
Linear mixed-effects model fit by REML
Fixed: adg ~ InitWt + Treatment - 1
Data: AvgDailyGain
      AIC      BIC    logLik
50.33733 60.59748 -18.16866

Random effects:
Groups   Name             Variance Std.Dev.
Block    (Intercept) 0.24084   0.49076
Residual                        0.05008   0.22379
# of obs: 32, groups: Block, 8

Fixed effects:
              Estimate Std. Error DF t value Pr(>|t|)
InitWt       2.7797e-03 8.3335e-04 27   3.3356 0.002486 **
Treatment0   2.4903e-01 3.7763e-01 27   0.6595 0.515183
Treatment10  7.3254e-01 3.9038e-01 27   1.8765 0.071437 .
Treatment20  7.1298e-01 3.8277e-01 27   1.8627 0.073420 .
Treatment30  8.0111e-01 3.5566e-01 27   2.2524 0.032628 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:
              InitWt Trtmn0 Trtm10 Trtm20
Treatment0   -0.863
Treatment10  -0.873   0.957
Treatment20  -0.867   0.957   0.958
Treatment30  -0.844   0.953   0.953   0.953

```

## B BIB

A balanced incomplete, blocked design. Compare with output 5.7 (p. 188) and output 5.9 (p. 193).

```

> print(gplot(BIB))

> fmlBIB <- lme(y ~ Treatment * x, data = BIB, random = ~1 /
+      Block)
> summary(fmlBIB)
Linear mixed-effects model fit by REML
Fixed: y ~ Treatment * x
Data: BIB
      AIC      BIC    logLik
124.8945 136.675 -52.44723

Random effects:
Groups   Name      Variance Std.Dev.
Block    (Intercept) 18.2494  4.2719
Residual                1.2004  1.0956
# of obs: 24, groups: Block, 8

Fixed effects:
              Estimate Std. Error DF t value Pr(>|t|)
(Intercept)  22.367853   3.101833 16  7.2112 2.075e-06 ***
Treatment1    4.429485   3.365069 16  1.3163 0.2066152
Treatment2   -0.437371   2.933224 16 -0.1491 0.8833305
Treatment3    6.278627   3.282059 16  1.9130 0.0738148 .
x              0.442547   0.087063 16  5.0831 0.0001107 ***
Treatment1:x  -0.223765   0.106083 16 -2.1093 0.0510220 .
Treatment2:x   0.053384   0.097143 16  0.5495 0.5902247
Treatment3:x  -0.179177   0.115710 16 -1.5485 0.1410542
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:
              (Intr) Trtmn1 Trtmn2 Trtmn3 x      Trtm1: Trtm2:
Treatment1   -0.728
Treatment2   -0.778  0.797
Treatment3   -0.796  0.827  0.826
x            -0.859  0.797  0.865  0.886
Treatment1:x  0.709 -0.979 -0.774 -0.797 -0.799
Treatment2:x  0.722 -0.731 -0.965 -0.763 -0.829  0.729
Treatment3:x  0.769 -0.789 -0.790 -0.976 -0.879  0.777  0.748
> anova(fmlBIB)

```

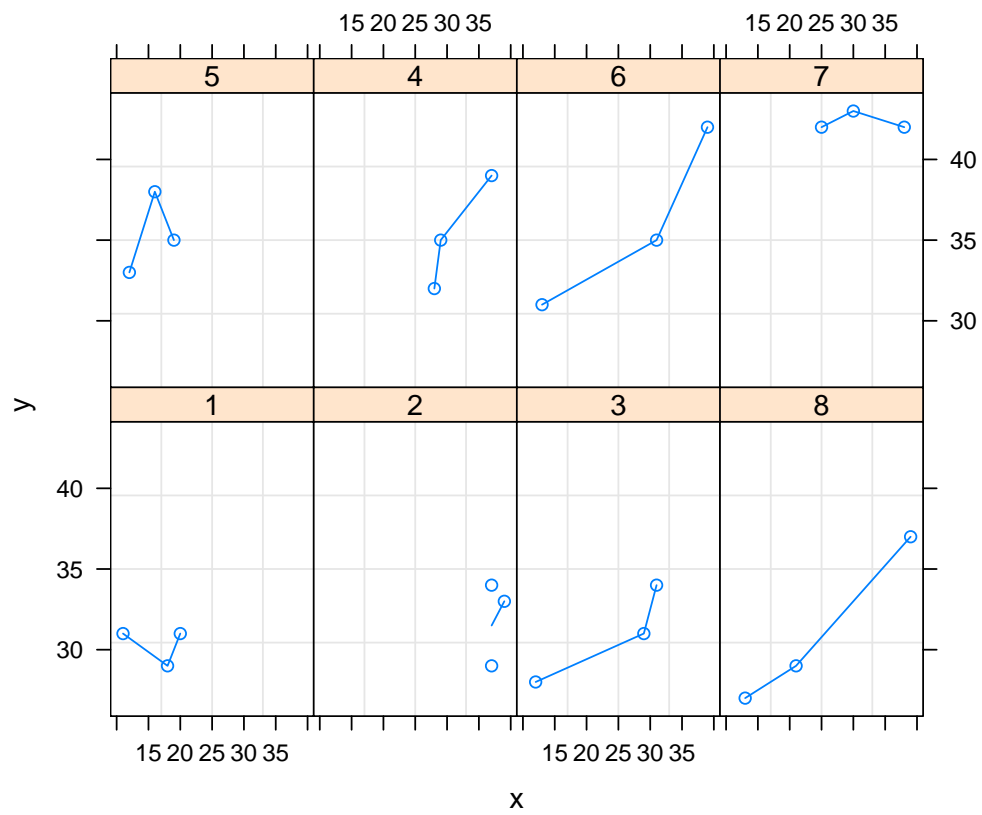


Figure 2: Balanced incomplete block design

# Analysis of Variance Table

	Df	Sum Sq	Mean Sq	Denom	F value	Pr(>F)	
Treatment	3	23.447	7.816	16.000	6.5108	0.004367	**
x	1	136.809	136.809	16.000	113.9669	1.098e-08	***
Treatment:x	3	18.427	6.142	16.000	5.1167	0.011347	*

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

```
> fm2BIB <- lme(y ~ Treatment + x:Grp, data = BIB, random = ~1 /
+ Block)
> summary(fm2BIB)
```

Linear mixed-effects model fit by REML

Fixed: y ~ Treatment + x:Grp

Data: BIB

	AIC	BIC	logLik
	115.1770	124.6015	-49.58851

Random effects:

Groups	Name	Variance	Std.Dev.
Block	(Intercept)	18.5255	4.3041
Residual		1.0378	1.0187

# of obs: 24, groups: Block, 8

Fixed effects:

	Estimate	Std. Error	DF	t value	Pr(> t )	
(Intercept)	20.945165	2.062297	18	10.1562	7.032e-09	***
Treatment1	5.341445	1.975705	18	2.7036	0.0145412	*
Treatment2	1.135569	0.713988	18	1.5905	0.1291410	
Treatment3	8.181034	1.770100	18	4.6218	0.0002119	***
x:Grp13	0.239520	0.042964	18	5.5750	2.722e-05	***
x:Grp24	0.489230	0.044122	18	11.0882	1.781e-09	***

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:

	(Intr)	Trtmn1	Trtmn2	Trtmn3	x:Gr13
Treatment1	-0.501				
Treatment2	-0.431	0.559			
Treatment3	-0.527	0.942	0.581		
x:Grp13	0.027	-0.663	-0.165	-0.605	
x:Grp24	-0.639	0.651	0.452	0.688	0.042

```
> anova(fm2BIB)
Analysis of Variance Table

      Df Sum Sq Mean Sq    Denom F value    Pr(>F)
Treatment  3  23.424   7.808    18.000  7.5235 0.001818 **
x:Grp      2 154.733  77.367    18.000 74.5468 1.954e-09 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

## C Bond

Compare with output 1.1 (p. 6).

```
> fm1Bond <- lme(pressure ~ Metal, data = Bond, random = ~1 |
+               Ingot)
```

```
> summary(fm1Bond)
```

Linear mixed-effects model fit by REML

Fixed: pressure ~ Metal

Data: Bond

	AIC	BIC	logLik
	117.7902	123.0128	-53.8951

Random effects:

Groups	Name	Variance	Std.Dev.
Ingot	(Intercept)	11.448	3.3835
Residual		10.372	3.2205

# of obs: 21, groups: Ingot, 7

Fixed effects:

	Estimate	Std. Error	DF	t value	Pr(> t )
(Intercept)	71.10000	1.76552	18	40.2715	< 2e-16 ***
Metalc	-0.91429	1.72143	18	-0.5311	0.60183
Metali	4.80000	1.72143	18	2.7884	0.01213 *

---

```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Correlation of Fixed Effects:

	(Intr) Metalc
Metalc	-0.488
Metali	-0.488 0.500

```
> anova(fm1Bond)
```

## Analysis of Variance Table

	Df	Sum Sq	Mean Sq	Denom	F value	Pr(>F)
Metal	2	131.90	65.95	18.00	6.3588	0.008147 **

---

signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

## D Cultivation

```
> print(bwplot(Cult ~ drywt / Block, Cultivation, layout = c(1,
+ 4)))
```

A blocked split-plot design. Compare these results with output 2.10 (p. 58).

```
> str(Cultivation)
`data.frame`:      24 obs. of  4 variables:
 $ Block: Factor w/ 4 levels "1","2","3","4": 1 1 1 1 1 1 2 2 2 2 ...
 $ Cult : Factor w/ 2 levels "a","b": 1 1 1 2 2 2 1 1 1 2 ...
 $ Inoc : Factor w/ 3 levels "con","dea","liv": 1 2 3 1 2 3 1 2 3 1 ...
 $ drywt: num  27.4 29.7 34.5 29.4 32.5 34.4 28.9 28.7 33.4 28.7 ...
 - attr(*, "ginfo")=List of 7
 ..$ formula      :Class 'formula' length 3 drywt ~ 1 | Block/Cult
 .. .. ..- attr(*, ".Environment")=length 6 <environment>
 ..$ order.groups:List of 2
 .. ..$ Block: logi TRUE
 .. ..$ Cult : logi TRUE
 ..$ FUN        :function (x)
 ..$ outer      : NULL
 ..$ inner      :List of 1
 .. ..$ Cult:Class 'formula' length 2 ~Inoc
 .. .. ..- attr(*, ".Environment")=length 6 <environment>
 ..$ labels     :List of 1
 .. ..$ drywt: chr "Yield"
 ..$ units      : list()
> xtabs(~Block + Cult, Cultivation)
      Cult
Block a b
  1 3 3
  2 3 3
  3 3 3
  4 3 3
```

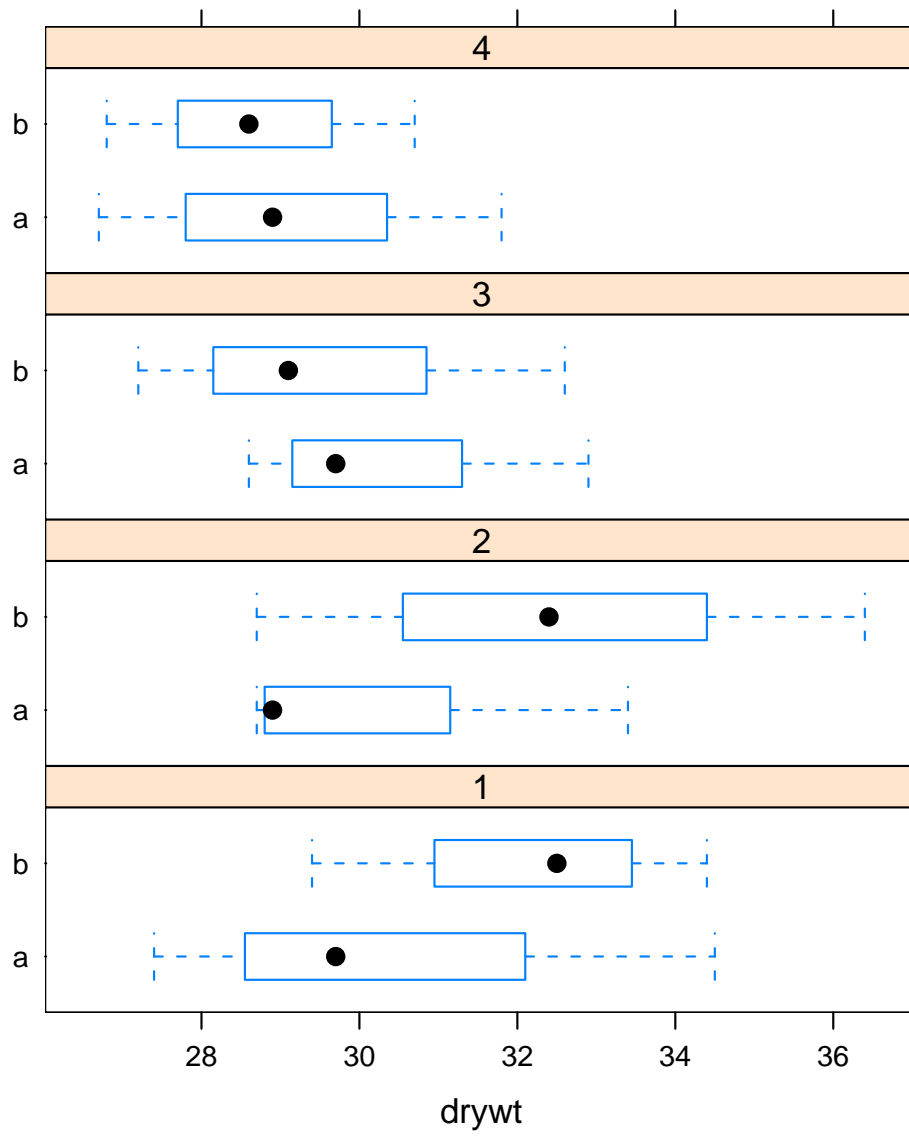


Figure 3: Cultivation data



```

> fmlCult <- lme(drywt ~ Inoc * Cult, data = Cultivation, random = list(Block
+     Cult = ~1))
> summary(fmlCult)
Linear mixed-effects model fit by REML
Fixed: drywt ~ Inoc * Cult
Data: Cultivation
      AIC      BIC    logLik
86.48742 97.0899 -34.24371

Random effects:
Groups   Name             Variance Std.Dev.
Block    (Intercept) 1.20728   1.09876
Cult      (Intercept) 0.26585   0.51561
Residual                  1.19633   1.09377
# of obs: 24, groups: Block, 4; Cult, 2

Fixed effects:
              Estimate Std. Error DF t value Pr(>|t|)
(Intercept)   33.52500    0.93100 18 36.0098 < 2.2e-16 ***
Inoccon       -5.50000    0.77341 18 -7.1113 1.256e-06 ***
Inocdea       -2.87500    0.77341 18 -3.7173 0.001577 **
Culta         -0.37500    1.06295 18 -0.3528 0.728343
Inoccon:Culta  0.25000    1.09377 18  0.2286 0.821782
Inocdea:Culta -1.02500    1.09377 18 -0.9371 0.361098
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:
              (Intr) Inoccn Inocde Culta  Incc:C
Inoccon      -0.415
Inocdea      -0.415  0.500
Culta        -0.571  0.364  0.364
Inoccon:Clt  0.294 -0.707 -0.354 -0.514
Inocdea:Clt  0.294 -0.354 -0.707 -0.514  0.500
> anova(fmlCult)
Analysis of Variance Table

      Df Sum Sq Mean Sq  Denom F value    Pr(>F)
Inoc    2 118.176   59.088   18.000 49.3909 4.91e-08 ***
Cult    1   0.656    0.656   18.000  0.5486  0.4684
Inoc:Cult 2   1.826    0.913   18.000  0.7631  0.4807

```

```

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
> fm2Cult <- update(fm1Cult, drywt ~ Inoc + Cult)
> anova(fm2Cult)
Analysis of Variance Table

      Df Sum Sq Mean Sq    Denom F value    Pr(>F)
Inoc   2 118.176   59.088   20.000 50.8069 1.447e-08 ***
Cult   1   0.656    0.656   20.000  0.5644   0.4613
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
> fm3Cult <- update(fm1Cult, drywt ~ Inoc)
> anova(fm3Cult)
Analysis of Variance Table

      Df Sum Sq Mean Sq    Denom F value    Pr(>F)
Inoc   2 118.176   59.088   21.000  50.807 8.988e-09 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
> summary(fm3Cult)
Linear mixed-effects model fit by REML
Fixed: drywt ~ Inoc
Data: Cultivation
      AIC      BIC    logLik
87.67784 94.74616 -37.83892

Random effects:
Groups   Name             Variance Std.Dev.
Block    (Intercept)  1.21283   1.10129
Cult     (Intercept)  0.10364   0.32193
Residual                    1.16299   1.07842
# of obs: 24, groups: Block, 4; Cult, 2

Fixed effects:
              Estimate Std. Error DF t value Pr(>|t|)
(Intercept) 33.33750    0.70739 21 47.1275 < 2.2e-16 ***
Inoccon     -5.37500    0.53921 21 -9.9683 2.048e-09 ***
Inocdea     -3.38750    0.53921 21 -6.2823 3.134e-06 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:

```

```

      (Intr) Inoccn
Inoccon -0.381
Inocdea -0.381  0.500

```

A blocked split-plot with missing data (sec 2.7, pp. 68-75). The data in Block 1 and Cultivar 'a' are removed from the data set

```

> CultMiss <- Cultivation[Cultivation$Block != 1 | Cultivation$Cult !=
+   "a", ]
> dim(CultMiss)
[1] 21  4
> print(bwplot(Cult ~ drywt | Block, CultMiss, layout = c(1,
+   4)))

```

```

> fmlCultM <- lme(drywt ~ Cult * Inoc, CultMiss, list(Block = ~1,
+   Cult = ~1), method = "ML")
> summary(fmlCultM)

```

Linear mixed-effects model fit by maximum likelihood

Fixed: drywt ~ Cult \* Inoc

Data: CultMiss

	AIC	BIC	logLik
	81.96929	91.36999	-31.98464

Random effects:

Groups	Name	Variance	Std.Dev.
Block	(Intercept)	1.1906e+00	1.0911e+00
Cult	(Intercept)	8.2202e-11	9.0666e-06
Residual		8.2202e-01	9.0666e-01

# of obs: 21, groups: Block, 4; Cult, 2

Fixed effects:

	Estimate	Std. Error	DF	t value	Pr(> t )
(Intercept)	33.52500	0.70934	15	47.2625	< 2.2e-16 ***
Culta	-0.45467	0.70575	15	-0.6442	0.5291462
Inoccon	-5.50000	0.64110	15	-8.5790	3.604e-07 ***
Inocdea	-2.87500	0.64110	15	-4.4845	0.0004366 ***
Culta:Inoccon	0.86667	0.97930	15	0.8850	0.3901303
Culta:Inocdea	-0.72500	0.97930	15	-0.7403	0.4705331

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

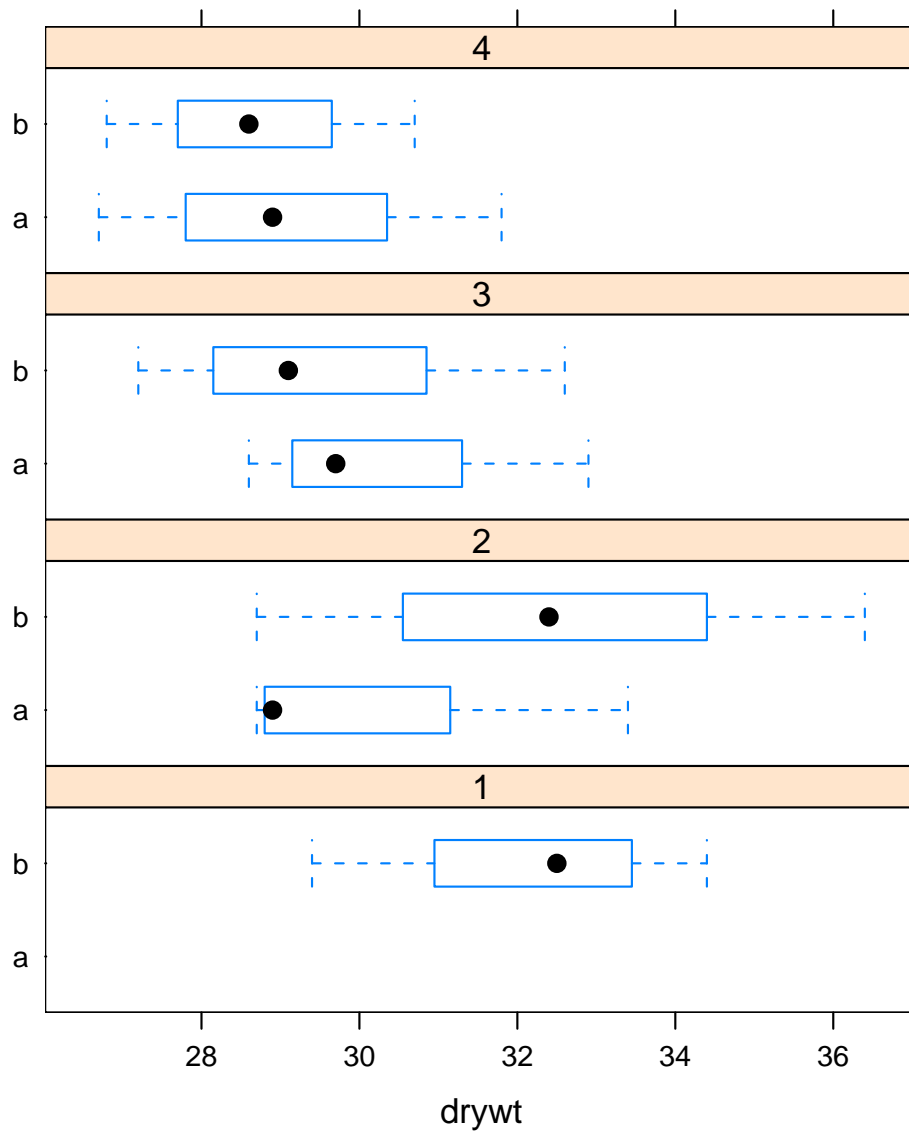


Figure 4: Cultivation data with missing cell

Correlation of Fixed Effects:

```

              (Intr) Cultra  Inoccn Inocde Clt:Incc
Cultra        -0.411
Inoccon       -0.452  0.454
Inocdea       -0.452  0.454  0.500
Cultra:Inccn  0.296 -0.694 -0.655 -0.327
Cultra:Inocd  0.296 -0.694 -0.327 -0.655  0.500

```

```

> fm2CultM <- update(fm1CultM, drywt ~ Cult + Inoc)
> fm3CultM <- update(fm1CultM, drywt ~ Inoc)
> fm4CultM <- update(fm1CultM, drywt ~ 1)
> anova(fm1CultM, fm2CultM, fm3CultM, fm4CultM)

```

Data: CultMiss

Models: <fixed>: <random>

```

fm4CultM: drywt ~ 1: list(Block = ~1, Cult = ~1)
fm3CultM: drywt ~ Inoc: list(Block = ~1, Cult = ~1)
fm2CultM: drywt ~ Cult + Inoc: list(Block = ~1, Cult = ~1)
fm1CultM: drywt ~ Cult * Inoc: list(Block = ~1, Cult = ~1)

```

	Df	AIC	BIC	logLik	Chisq	Chi	Df	Pr(>Chisq)
fm4CultM	4	107.333	111.511	-49.667				
fm3CultM	6	79.263	85.531	-33.632	32.0696		2	1.087e-07 ***
fm2CultM	7	80.430	87.741	-33.215	0.8340		1	0.3611
fm1CultM	9	81.969	91.370	-31.985	2.4602		2	0.2923

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

```

> fm3RCultM <- update(fm3CultM, method = "REML")
> summary(fm3RCultM)

```

Linear mixed-effects model fit by REML

Fixed: drywt ~ Inoc

Data: CultMiss

	AIC	BIC	logLik
	77.31883	83.58596	-32.65941

Random effects:

Groups	Name	Variance	Std.Dev.
Block	(Intercept)	1.7626e+00	1.3276e+00
Cult	(Intercept)	1.1064e-10	1.0518e-05
Residual		1.1064e+00	1.0518e+00

# of obs: 21, groups: Block, 4; Cult, 2

Fixed effects:

	Estimate	Std. Error	DF	t value	Pr(> t )
(Intercept)	33.35105	0.77645	18	42.9532	< 2.2e-16 ***
Inoccon	-5.12857	0.56223	18	-9.1218	3.604e-08 ***
Inocdea	-3.18571	0.56223	18	-5.6662	2.249e-05 ***

---  
Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:

	(Intr)	Inoccn
Inoccon	-0.362	
Inocdea	-0.362	0.500

## E Demand

```
> print(gplot(Demand, scales = list(y = list(log = 2))))
```

Analysis of the per capita demand deposits data given as data set 3.6. Compare these results with output 3.13 (p. 132).

Notice that although Year is stored numerically, it is converted to a factor when used as a grouping factor.

```
> str(Demand)
'data.frame':      77 obs. of  7 variables:
 $ State: Factor w/ 7 levels "CA","DC","FL",...: 1 1 1 1 1 1 1 1 1 1 1 ...
 $ Year : num  1949 1950 1951 1952 1953 ...
 $ d     : num  533 603 669 651 609 634 665 676 642 678 ...
 $ y     : num  1347 1464 1608 1636 1669 ...
 $ rd    : num  0.343 0.364 0.367 0.369 0.41 0.499 0.496 0.533 0.63 0.667 ...
 $ rt    : num  1.11 1.16 1.49 1.57 1.59 ...
 $ rs    : num  2.90 2.94 3.09 3.07 3.36 ...
- attr(*, "ginfo")=List of 7
 ..$ formula      :Class 'formula' length 3 d ~ Year | State
 .. .. - attr(*, ".Environment")=length 15 <environment>
 ..$ order.groups: logi TRUE
 ..$ FUN          :function (x)
 ..$ outer        : NULL
 ..$ inner        : NULL
 ..$ labels       :List of 1
 .. ..$ d: chr "per capita demand deposits"
 ..$ units        : list()
```

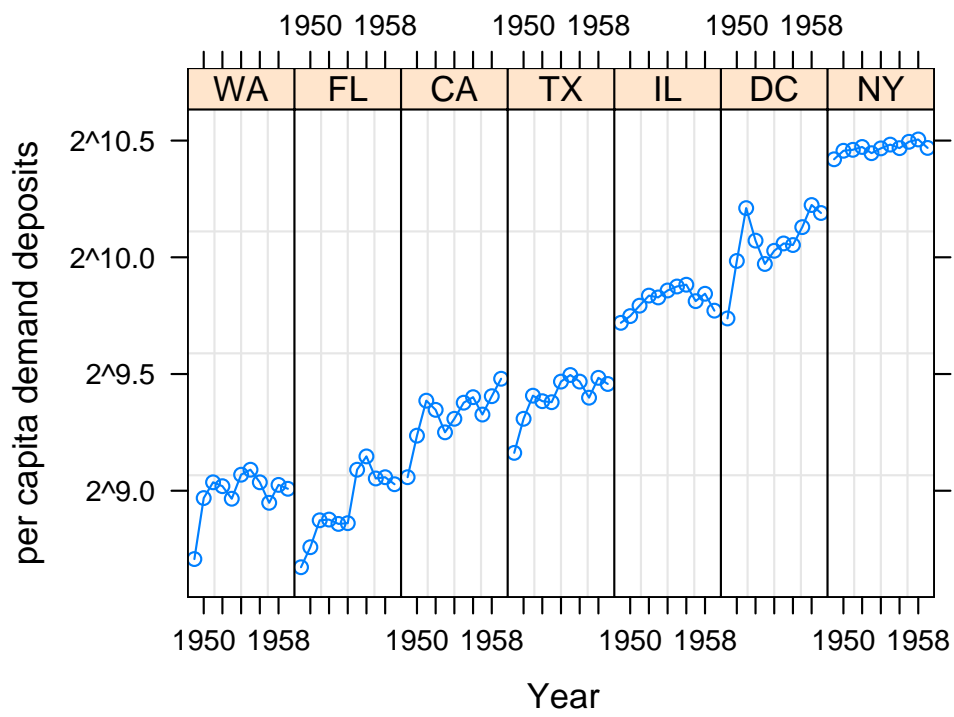


Figure 5: Per-capita demand deposits versus year by state. The vertical axis is on a logarithmic scale.

```

> fmlDemand <- lme(log(d) ~ log(y) + log(rd) + log(rt) + log(rs),
+   Demand, ~1 | State + Year)
> summary(fmlDemand)
Linear mixed-effects model fit by REML
Fixed: log(d) ~ log(y) + log(rd) + log(rt) + log(rs)
Data: Demand
      AIC      BIC    logLik
-224.1653 -205.4148 120.0826

Random effects:
Groups   Name      Variance  Std.Dev.
Year     (Intercept) 0.00026465 0.016268
State    (Intercept) 0.02948900 0.171724
Residual                0.00111705 0.033422
# of obs: 77, groups: Year, 11; State, 7

Fixed effects:
              Estimate Std. Error DF t value Pr(>|t|)
(Intercept) -1.284043    0.723423 72 -1.7750  0.080132 .
log(y)       1.069806    0.103925 72 10.2941 8.553e-16 ***
log(rd)      -0.295342    0.052463 72 -5.6296 3.265e-07 ***
log(rt)       0.039882    0.027889 72  1.4300  0.157034
log(rs)      -0.326739    0.114385 72 -2.8565  0.005595 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:
      (Intr) log(y) lg(rd) lg(rt)
log(y)  -0.976
log(rd)  0.383 -0.227
log(rt)  0.077 -0.062 -0.337
log(rs)  0.444 -0.600 -0.270 -0.323

```

## F Genetics

Analysis of the heritability data given as data set 4.5. To obtain a term for the location/family interaction we must create a separate grouping factor. Similarly for the Block within Location.

```

> Genetics$LocFam <- with(Genetics, Location:Family)
> Genetics$LocBloc <- with(Genetics, Location:Block)

```



```

> fmlGen <- lme(Yield ~ 1, Genetics, ~1 | LocFam + LocBloc +
+   Family + Location)
> summary(fmlGen)
Linear mixed-effects model fit by REML
Fixed: Yield ~ 1
Data: Genetics
      AIC      BIC    logLik
485.9865 498.5525 -236.9932

Random effects:
Groups   Name             Variance Std.Dev.
LocFam   (Intercept)    74.861    8.6523
LocBloc  (Intercept)    89.325    9.4512
Family   (Intercept)   187.857   13.7061
Location (Intercept)   612.945   24.7577
Residual                    51.854    7.2010
# of obs: 60, groups: LocFam, 20; LocBloc, 12; Family, 5; Location, 4

Fixed effects:
              Estimate Std. Error DF t value Pr(>|t|)
(Intercept)  209.133      14.243  59  14.683 < 2.2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> summary(fm2Gen <- lme(Yield ~ Family, Genetics, ~1 | LocFam +
+   LocBloc + Location))
Linear mixed-effects model fit by REML
Fixed: Yield ~ Family
Data: Genetics
      AIC      BIC    logLik
457.6174 476.4665 -219.8087

Random effects:
Groups   Name             Variance Std.Dev.
LocFam   (Intercept)    74.861    8.6522
LocBloc  (Intercept)    89.322    9.4510
Location (Intercept)   613.082   24.7605
Residual                    51.850    7.2007
# of obs: 60, groups: LocFam, 20; LocBloc, 12; Location, 4

Fixed effects:

```

	Estimate	Std. Error	DF	t value	Pr(> t )	
(Intercept)	207.4167	13.5554	55	15.3014	< 2.2e-16	***
Family1	22.1667	6.7876	55	3.2657	0.001882	**
Family2	9.0833	6.7876	55	1.3382	0.186332	
Family3	-15.0833	6.7876	55	-2.2222	0.030403	*
Family4	-7.5833	6.7876	55	-1.1172	0.268754	

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

#### Correlation of Fixed Effects:

	(Intr)	Famly1	Famly2	Famly3
Family1	-0.250			
Family2	-0.250	0.500		
Family3	-0.250	0.500	0.500	
Family4	-0.250	0.500	0.500	0.500

```
> summary(fm3Gen <- lme(Yield ~ Family, Genetics, ~1 | LocBloc +
+ Location))
```

Linear mixed-effects model fit by REML

Fixed: Yield ~ Family

Data: Genetics

	AIC	BIC	logLik
	469.8516	486.6063	-226.9258

#### Random effects:

Groups	Name	Variance	Std.Dev.
LocBloc	(Intercept)	77.07	8.779
Location	(Intercept)	628.64	25.073
Residual		113.10	10.635

# of obs: 60, groups: LocBloc, 12; Location, 4

#### Fixed effects:

	Estimate	Std. Error	DF	t value	Pr(> t )	
(Intercept)	207.4167	13.1532	55	15.7692	< 2.2e-16	***
Family1	22.1667	4.3416	55	5.1057	4.246e-06	***
Family2	9.0833	4.3416	55	2.0922	0.041052	*
Family3	-15.0833	4.3416	55	-3.4742	0.001007	**
Family4	-7.5833	4.3416	55	-1.7467	0.086276	.

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

```

Correlation of Fixed Effects:
      (Intr) Famly1 Famly2 Famly3
Family1 -0.165
Family2 -0.165  0.500
Family3 -0.165  0.500  0.500
Family4 -0.165  0.500  0.500  0.500
> anova(fm2Gen, fm3Gen)
Data: Genetics

Models: <fixed>: <random>
fm3Gen: Yield ~ Family: ~1 | LocBloc + Location
fm2Gen: Yield ~ Family: ~1 | LocFam + LocBloc + Location

      Df      AIC      BIC  logLik  Chisq Chi Df Pr(>Chisq)
fm3Gen  8  494.51  511.27 -239.26
fm2Gen  9  485.85  504.70 -233.93 10.660      1  0.001095 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

## G HR

```
> print(gplot(HR))
```

Analysis of the Heart rate data given as data set 3.5. Compare with output

3.12 (pp. 128–129)

```

> fm1HR <- lme(HR ~ Time * Drug + baseHR, data = HR, random = ~Time /
+ Patient)
> summary(fm1HR)

```

Linear mixed-effects model fit by REML

Fixed: HR ~ Time \* Drug + baseHR

Data: HR

	AIC	BIC	logLik
	789.607	820.2694	-383.8035

Random effects:

Groups	Name	Variance	Std.Dev.	Corr
Patient	(Intercept)	60.630	7.7866	
	Time	37.786	6.1470	-0.563
Residual		24.361	4.9357	

# of obs: 120, groups: Patient, 24

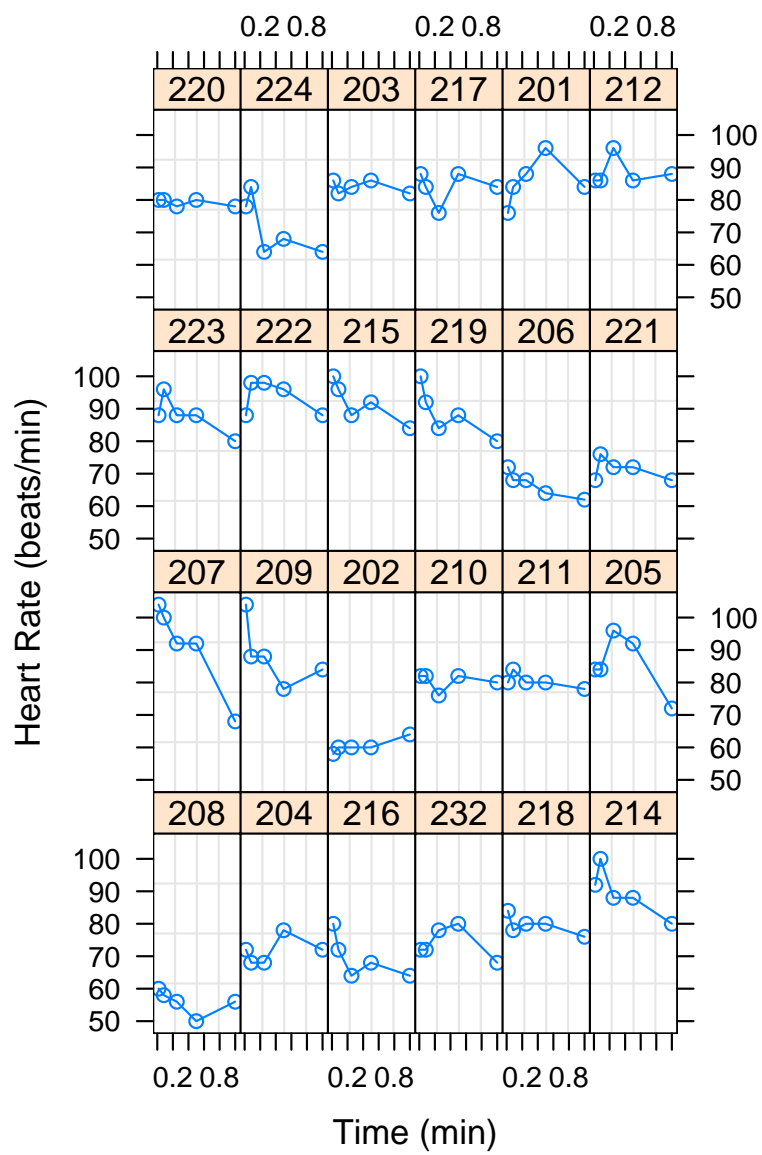


Figure 6: Heart rate data

Fixed effects:

	Estimate	Std. Error	DF	t value	Pr(> t )
(Intercept)	33.97835	10.28243	113	3.3045	0.001275 **
Time	-3.19704	3.08498	113	-1.0363	0.302263
Druga	3.59915	4.23132	113	0.8506	0.396791
Drugb	7.09121	4.20934	113	1.6846	0.094819 .
baseHR	0.54342	0.11614	113	4.6789	8.058e-06 ***
Time:Druga	-7.50131	4.36282	113	-1.7194	0.088285 .
Time:Drugb	-3.98942	4.36282	113	-0.9144	0.362447

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:

	(Intr)	Time	Druga	Drugb	baseHR	Tim:Drg
Time	-0.162					
Druga	-0.308	0.394				
Drugb	-0.244	0.396	0.501			
baseHR	-0.957	0.000	0.110	0.041		
Time:Druga	0.115	-0.707	-0.557	-0.280	0.000	
Time:Drugb	0.115	-0.707	-0.278	-0.560	0.000	0.500

> anova(fm1HR)

Analysis of Variance Table

	Df	Sum Sq	Mean Sq	Denom	F value	Pr(>F)
Time	1	379.22	379.22	113.00	15.5665	0.0001387 ***
Drug	2	92.90	46.45	113.00	1.9067	0.1533252
baseHR	1	533.32	533.32	113.00	21.8923	8.058e-06 ***
Time:Drug	2	72.11	36.06	113.00	1.4801	0.2319904

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

> fm3HR <- update(fm1HR, HR ~ Time + Drug + baseHR)

> anova(fm3HR)

Analysis of Variance Table

	Df	Sum Sq	Mean Sq	Denom	F value	Pr(>F)
Time	1	364.03	364.03	115.00	14.9431	0.0001839 ***
Drug	2	92.88	46.44	115.00	1.9064	0.1532830
baseHR	1	533.27	533.27	115.00	21.8905	7.937e-06 ***

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

> summary(fm3HR)

Linear mixed-effects model fit by REML

Fixed: HR ~ Time + Drug + baseHR

Data: HR

	AIC	BIC	logLik
	797.8283	822.9158	-389.9142

Random effects:

Groups	Name	Variance	Std.Dev.	Corr
Patient	(Intercept)	61.560	7.8460	
	Time	40.963	6.4002	-0.571
Residual		24.361	4.9357	

# of obs: 120, groups: Patient, 24

Fixed effects:

	Estimate	Std. Error	DF	t value	Pr(> t )
(Intercept)	36.04640	10.19449	115	3.5359	0.0005868 ***
Time	-7.02729	1.81789	115	-3.8656	0.0001839 ***
Druga	-0.45237	3.51456	115	-0.1287	0.8978087
Drugb	4.93648	3.48807	115	1.4152	0.1596980
baseHR	0.54342	0.11615	115	4.6787	7.937e-06 ***

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:

	(Intr) Time	Druga	Drugb
Time	-0.096		
Druga	-0.297	0.000	
Drugb	-0.219	0.000	0.502
baseHR	-0.966	0.000	0.132

> fm4HR <- update(fm3HR, HR ~ Time + baseHR)

> anova(fm4HR)

Analysis of Variance Table

	Df	Sum Sq	Mean Sq	Denom	F value	Pr(>F)
Time	1	364.03	364.03	117.00	14.943	0.0001825 ***
baseHR	1	534.87	534.87	117.00	21.956	7.593e-06 ***

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

> summary(fm4HR)

Linear mixed-effects model fit by REML

Fixed: HR ~ Time + baseHR

```

Data: HR
      AIC      BIC    logLik
805.1481 824.6605 -395.5740

Random effects:
Groups   Name             Variance Std.Dev. Corr
Patient (Intercept) 63.026    7.9389
          Time      40.963    6.4002  -0.553
Residual                24.361    4.9357
# of obs: 120, groups: Patient, 24

Fixed effects:
              Estimate Std. Error  DF t value Pr(>|t|)
(Intercept)  36.93141    9.90143 117  3.7299 0.0002969 ***
Time         -7.02729    1.81789 117 -3.8656 0.0001825 ***
baseHR        0.55078    0.11754 117  4.6857 7.593e-06 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:
          (Intr) Time
Time      -0.098
baseHR    -0.984  0.000

```

## H Mississippi

```
> print(gplot(Mississippi))
```

Analysis of the Mississippi nitrogen concentrations given as data set 4.2. Compare with output 4.1 (p. 142), 4.2 (p. 143) up to output 4.9 (pp. 150–152).

```
> fmlMiss <- lme(y ~ 1, data = Mississippi, random = ~1 | influent)
> summary(fmlMiss)
```

Linear mixed-effects model fit by REML

Fixed: y ~ 1

Data: Mississippi

```

      AIC      BIC    logLik
258.3511 263.1839 -126.1756

```

Random effects:

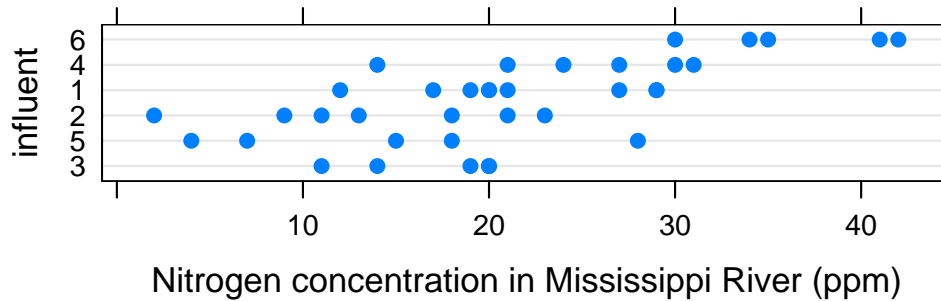


Figure 7: Heart rate data

```

Groups      Name          Variance Std.Dev.
influent (Intercept) 63.323    7.9576
Residual              42.658    6.5313
# of obs: 37, groups: influent, 6

Fixed effects:
              Estimate Std. Error DF t value Pr(>|t|)
(Intercept)   21.223      3.429 36  6.1892 3.885e-07 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
> fmlMLMiss <- update(fmlMiss, method = "ML")
> summary(fmlMLMiss)
Linear mixed-effects model fit by maximum likelihood
Fixed: y ~ 1
Data: Mississippi
      AIC      BIC    logLik
262.557 267.3898 -128.2785

Random effects:
Groups      Name          Variance Std.Dev.
influent (Intercept) 51.255    7.1592
Residual              42.697    6.5343
# of obs: 37, groups: influent, 6

Fixed effects:

```



```

              Estimate Std. Error DF t value Pr(>|t|)
(Intercept)  21.217      3.122 36   6.796 6.089e-08 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
> ranef(fm1MLMiss)
$influent
  (Intercept)
1    0.3097833
2   -6.5772278
3   -3.7862748
4    2.8826711
5   -5.8435210
6   13.0145691
> ranef(fm1Miss)
$influent
  (Intercept)
1    0.309286
2   -6.719332
3   -3.897945
4    2.946104
5   -6.012984
6   13.374871
> VarCorr(fm1Miss)
Groups   Name             Variance Std.Dev.
influent (Intercept)  63.323     7.9576
Residual                42.658     6.5313
> fm2Miss <- lme(y ~ Type, data = Mississippi, random = ~1 |
+   influent, method = "REML")
> summary(fm2Miss)
Linear mixed-effects model fit by REML
Fixed: y ~ Type
Data: Mississippi
      AIC      BIC    logLik
244.5246 252.5792 -117.2623

Random effects:
Groups   Name             Variance Std.Dev.
influent (Intercept)  14.970     3.8691
Residual                42.514     6.5202
# of obs: 37, groups: influent, 6

```

```

Fixed effects:
              Estimate Std. Error DF t value  Pr(>|t|)
(Intercept)  36.4000      4.8449 34   7.5131 1.011e-08 ***
Type1        -20.8000      5.9338 34  -3.5054 0.001302 **
Type2        -16.4619      5.5168 34  -2.9840 0.005238 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:
      (Intr) Type1
Type1 -0.816
Type2 -0.878  0.717
> anova(fm2Miss)
Analysis of Variance Table

      Df Sum Sq Mean Sq  Denom F value    Pr(>F)
Type   2  541.76   270.88   34.00   6.3716 0.004466 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

## I Multilocation

Analysis of the Multilocation data with fixed effects for the locations. We create a grouping factor for Block within Location and for the Location/Treatment interaction.

```

> str(Multilocation)
`data.frame`:      108 obs. of  7 variables:
 $ obs      : num   3 4 6 7 9 10 12 16 19 20 ...
 $ Location: Factor w/ 9 levels "A","B","C","D",...: 1 1 1 1 1 1 1 1 1 1 ...
 $ Block    : Factor w/ 3 levels "1","2","3": 1 1 1 1 2 2 2 2 3 3 ...
 $ Trt      : Factor w/ 4 levels "1","2","3","4": 3 4 2 1 2 1 3 4 1 2 ...
 $ Adj      : num   3.16 3.12 3.16 3.25 2.71 ...
 $ Fe       : num   7.10 6.68 6.83 6.53 8.25 ...
 $ Grp      : Factor w/ 27 levels "A/1","A/2","A/3",...: 1 1 1 1 2 2 2 2 3 3 ..
 - attr(*, "ginfo")=List of 7
 ..$ formula      :Class 'formula' length 3 Adj ~ 1 | Location/Block
 .. .. - attr(*, ".Environment")=length 26 <environment>
 ..$ order.groups:List of 2
 .. ..$ Location: logi TRUE

```

```

.. ..$ Block      : logi TRUE
..$ FUN           :function (x)
..$ outer         : NULL
..$ inner         :List of 1
.. ..$ Block:Class 'formula' length 2 ~Trt
.. .. ..- attr(*, ".Environment")=length 26 <environment>
..$ labels        :List of 1
.. ..$ Adj: chr "Adjusted yield"
..$ units         : list()
> Multilocation$Grp <- with(Multilocation, Block:Location)[drop = TRUE]
> Multilocation$Int <- with(Multilocation, Location:Trt)[drop = TRUE]
> fmlMult <- lme(Adj ~ Location * Trt, data = Multilocation,
+ ~1 / Grp)
> summary(fmlMult)
Linear mixed-effects model fit by REML
Fixed: Adj ~ Location * Trt
Data: Multilocation
      AIC      BIC    logLik
86.64621 188.5672 -5.323106

Random effects:
Groups      Name      Variance Std.Dev.
Grp      (Intercept) 0.0056193 0.074962
Residual              0.0345787 0.185953
# of obs: 108, groups: Grp, 27

Fixed effects:
      Estimate Std. Error DF t value Pr(>|t|)
(Intercept)  2.359233   0.115755 72 20.3812 < 2.2e-16 ***
LocationA    0.649300   0.163703 72  3.9663 0.0001705 ***
LocationB    0.066433   0.163703 72  0.4058 0.6860811
LocationC    0.545333   0.163703 72  3.3312 0.0013667 **
LocationD    0.374133   0.163703 72  2.2854 0.0252337 *
LocationE    0.550000   0.163703 72  3.3597 0.0012505 **
LocationF    0.998100   0.163703 72  6.0970 4.861e-08 ***
LocationG    0.360567   0.163703 72  2.2026 0.0308276 *
LocationH    1.014033   0.163703 72  6.1943 3.252e-08 ***
Trt1         0.227200   0.151830 72  1.4964 0.1389186
Trt2        -0.001400   0.151830 72 -0.0092 0.9926685
Trt3         0.423233   0.151830 72  2.7875 0.0067874 **

```

LocationA:Trt1	-0.188533	0.214721	72	-0.8780	0.3828425	
LocationB:Trt1	-0.275233	0.214721	72	-1.2818	0.2040178	
LocationC:Trt1	-0.040000	0.214721	72	-0.1863	0.8527423	
LocationD:Trt1	-0.535133	0.214721	72	-2.4922	0.0149969	*
LocationE:Trt1	-0.262967	0.214721	72	-1.2247	0.2246830	
LocationF:Trt1	-0.271533	0.214721	72	-1.2646	0.2100968	
LocationG:Trt1	0.203233	0.214721	72	0.9465	0.3470587	
LocationH:Trt1	-0.149533	0.214721	72	-0.6964	0.4884150	
LocationA:Trt2	-0.093467	0.214721	72	-0.4353	0.6646509	
LocationB:Trt2	-0.322733	0.214721	72	-1.5030	0.1372028	
LocationC:Trt2	0.089600	0.214721	72	0.4173	0.6777105	
LocationD:Trt2	-0.296933	0.214721	72	-1.3829	0.1709748	
LocationE:Trt2	-0.306933	0.214721	72	-1.4295	0.1571983	
LocationF:Trt2	-0.309933	0.214721	72	-1.4434	0.1532374	
LocationG:Trt2	-0.108600	0.214721	72	-0.5058	0.6145606	
LocationH:Trt2	-0.330600	0.214721	72	-1.5397	0.1280231	
LocationA:Trt3	-0.402467	0.214721	72	-1.8744	0.0649358	.
LocationB:Trt3	-0.565500	0.214721	72	-2.6337	0.0103329	*
LocationC:Trt3	-0.122467	0.214721	72	-0.5704	0.5702135	
LocationD:Trt3	-0.548400	0.214721	72	-2.5540	0.0127654	*
LocationE:Trt3	-0.328633	0.214721	72	-1.5305	0.1302711	
LocationF:Trt3	-0.462567	0.214721	72	-2.1543	0.0345659	*
LocationG:Trt3	-0.252967	0.214721	72	-1.1781	0.2426279	
LocationH:Trt3	-0.372033	0.214721	72	-1.7326	0.0874414	.
---						
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1						

Correlation of Fixed Effects:

	(Intr)	LoctnA	LoctnB	LoctnC	LoctnD	LoctnE	LoctnF	LoctnG	LoctnH
LocationA	-0.707								
LocationB	-0.707	0.500							
LocationC	-0.707	0.500	0.500						
LocationD	-0.707	0.500	0.500	0.500					
LocationE	-0.707	0.500	0.500	0.500	0.500				
LocationF	-0.707	0.500	0.500	0.500	0.500	0.500			
LocationG	-0.707	0.500	0.500	0.500	0.500	0.500	0.500		
LocationH	-0.707	0.500	0.500	0.500	0.500	0.500	0.500	0.500	
Trt1	-0.656	0.464	0.464	0.464	0.464	0.464	0.464	0.464	0.464
Trt2	-0.656	0.464	0.464	0.464	0.464	0.464	0.464	0.464	0.464
Trt3	-0.656	0.464	0.464	0.464	0.464	0.464	0.464	0.464	0.464

LoctnA:Trt1	0.464	-0.656	-0.328	-0.328	-0.328	-0.328	-0.328	-0.328	-0.328
LoctnB:Trt1	0.464	-0.328	-0.656	-0.328	-0.328	-0.328	-0.328	-0.328	-0.328
LoctnC:Trt1	0.464	-0.328	-0.328	-0.656	-0.328	-0.328	-0.328	-0.328	-0.328
LoctnD:Trt1	0.464	-0.328	-0.328	-0.328	-0.656	-0.328	-0.328	-0.328	-0.328
LoctnE:Trt1	0.464	-0.328	-0.328	-0.328	-0.328	-0.656	-0.328	-0.328	-0.328
LoctnF:Trt1	0.464	-0.328	-0.328	-0.328	-0.328	-0.328	-0.656	-0.328	-0.328
LoctnG:Trt1	0.464	-0.328	-0.328	-0.328	-0.328	-0.328	-0.328	-0.656	-0.328
LoctnH:Trt1	0.464	-0.328	-0.328	-0.328	-0.328	-0.328	-0.328	-0.328	-0.656
LoctnA:Trt2	0.464	-0.656	-0.328	-0.328	-0.328	-0.328	-0.328	-0.328	-0.328
LoctnB:Trt2	0.464	-0.328	-0.656	-0.328	-0.328	-0.328	-0.328	-0.328	-0.328
LoctnC:Trt2	0.464	-0.328	-0.328	-0.656	-0.328	-0.328	-0.328	-0.328	-0.328
LoctnD:Trt2	0.464	-0.328	-0.328	-0.328	-0.656	-0.328	-0.328	-0.328	-0.328
LoctnE:Trt2	0.464	-0.328	-0.328	-0.328	-0.328	-0.656	-0.328	-0.328	-0.328
LoctnF:Trt2	0.464	-0.328	-0.328	-0.328	-0.328	-0.328	-0.656	-0.328	-0.328
LoctnG:Trt2	0.464	-0.328	-0.328	-0.328	-0.328	-0.328	-0.328	-0.656	-0.328
LoctnH:Trt2	0.464	-0.328	-0.328	-0.328	-0.328	-0.328	-0.328	-0.328	-0.656
LoctnA:Trt3	0.464	-0.656	-0.328	-0.328	-0.328	-0.328	-0.328	-0.328	-0.328
LoctnB:Trt3	0.464	-0.328	-0.656	-0.328	-0.328	-0.328	-0.328	-0.328	-0.328
LoctnC:Trt3	0.464	-0.328	-0.328	-0.656	-0.328	-0.328	-0.328	-0.328	-0.328
LoctnD:Trt3	0.464	-0.328	-0.328	-0.328	-0.656	-0.328	-0.328	-0.328	-0.328
LoctnE:Trt3	0.464	-0.328	-0.328	-0.328	-0.328	-0.656	-0.328	-0.328	-0.328
LoctnF:Trt3	0.464	-0.328	-0.328	-0.328	-0.328	-0.328	-0.656	-0.328	-0.328
LoctnG:Trt3	0.464	-0.328	-0.328	-0.328	-0.328	-0.328	-0.328	-0.656	-0.328
LoctnH:Trt3	0.464	-0.328	-0.328	-0.328	-0.328	-0.328	-0.328	-0.328	-0.656
	Trt1	Trt2	Trt3	LcA:T1	LcB:T1	LcC:T1	LcD:T1	LcE:T1	LcF:T1
LocationA									
LocationB									
LocationC									
LocationD									
LocationE									
LocationF									
LocationG									
LocationH									
Trt1									
Trt2	0.500								
Trt3	0.500	0.500							
LoctnA:Trt1	-0.707	-0.354	-0.354						
LoctnB:Trt1	-0.707	-0.354	-0.354	0.500					
LoctnC:Trt1	-0.707	-0.354	-0.354	0.500	0.500				
LoctnD:Trt1	-0.707	-0.354	-0.354	0.500	0.500	0.500			

LoctnE:Trt1	-0.707	-0.354	-0.354	0.500	0.500	0.500	0.500		
LoctnF:Trt1	-0.707	-0.354	-0.354	0.500	0.500	0.500	0.500	0.500	
LoctnG:Trt1	-0.707	-0.354	-0.354	0.500	0.500	0.500	0.500	0.500	0.500
LoctnH:Trt1	-0.707	-0.354	-0.354	0.500	0.500	0.500	0.500	0.500	0.500
LoctnA:Trt2	-0.354	-0.707	-0.354	0.500	0.250	0.250	0.250	0.250	0.250
LoctnB:Trt2	-0.354	-0.707	-0.354	0.250	0.500	0.250	0.250	0.250	0.250
LoctnC:Trt2	-0.354	-0.707	-0.354	0.250	0.250	0.500	0.250	0.250	0.250
LoctnD:Trt2	-0.354	-0.707	-0.354	0.250	0.250	0.250	0.500	0.250	0.250
LoctnE:Trt2	-0.354	-0.707	-0.354	0.250	0.250	0.250	0.250	0.500	0.250
LoctnF:Trt2	-0.354	-0.707	-0.354	0.250	0.250	0.250	0.250	0.250	0.500
LoctnG:Trt2	-0.354	-0.707	-0.354	0.250	0.250	0.250	0.250	0.250	0.250
LoctnH:Trt2	-0.354	-0.707	-0.354	0.250	0.250	0.250	0.250	0.250	0.250
LoctnA:Trt3	-0.354	-0.354	-0.707	0.500	0.250	0.250	0.250	0.250	0.250
LoctnB:Trt3	-0.354	-0.354	-0.707	0.250	0.500	0.250	0.250	0.250	0.250
LoctnC:Trt3	-0.354	-0.354	-0.707	0.250	0.250	0.500	0.250	0.250	0.250
LoctnD:Trt3	-0.354	-0.354	-0.707	0.250	0.250	0.250	0.500	0.250	0.250
LoctnE:Trt3	-0.354	-0.354	-0.707	0.250	0.250	0.250	0.250	0.500	0.250
LoctnF:Trt3	-0.354	-0.354	-0.707	0.250	0.250	0.250	0.250	0.250	0.500
LoctnG:Trt3	-0.354	-0.354	-0.707	0.250	0.250	0.250	0.250	0.250	0.250
LoctnH:Trt3	-0.354	-0.354	-0.707	0.250	0.250	0.250	0.250	0.250	0.250
	LcG:T1	LcH:T1	LcA:T2	LcB:T2	LcC:T2	LcD:T2	LcE:T2	LcF:T2	LcG:T2
LocationA									
LocationB									
LocationC									
LocationD									
LocationE									
LocationF									
LocationG									
LocationH									
Trt1									
Trt2									
Trt3									
LoctnA:Trt1									
LoctnB:Trt1									
LoctnC:Trt1									
LoctnD:Trt1									
LoctnE:Trt1									
LoctnF:Trt1									
LoctnG:Trt1									
LoctnH:Trt1	0.500								

LoctnA:Trt2	0.250	0.250							
LoctnB:Trt2	0.250	0.250	0.500						
LoctnC:Trt2	0.250	0.250	0.500	0.500					
LoctnD:Trt2	0.250	0.250	0.500	0.500	0.500				
LoctnE:Trt2	0.250	0.250	0.500	0.500	0.500	0.500			
LoctnF:Trt2	0.250	0.250	0.500	0.500	0.500	0.500	0.500		
LoctnG:Trt2	0.500	0.250	0.500	0.500	0.500	0.500	0.500	0.500	
LoctnH:Trt2	0.250	0.500	0.500	0.500	0.500	0.500	0.500	0.500	0.500
LoctnA:Trt3	0.250	0.250	0.500	0.250	0.250	0.250	0.250	0.250	0.250
LoctnB:Trt3	0.250	0.250	0.250	0.500	0.250	0.250	0.250	0.250	0.250
LoctnC:Trt3	0.250	0.250	0.250	0.250	0.500	0.250	0.250	0.250	0.250
LoctnD:Trt3	0.250	0.250	0.250	0.250	0.250	0.500	0.250	0.250	0.250
LoctnE:Trt3	0.250	0.250	0.250	0.250	0.250	0.250	0.500	0.250	0.250
LoctnF:Trt3	0.250	0.250	0.250	0.250	0.250	0.250	0.250	0.500	0.250
LoctnG:Trt3	0.500	0.250	0.250	0.250	0.250	0.250	0.250	0.250	0.500
LoctnH:Trt3	0.250	0.500	0.250	0.250	0.250	0.250	0.250	0.250	0.250

LcH:T2	LcA:T3	LcB:T3	LcC:T3	LcD:T3	LcE:T3	LcF:T3	LcG:T3
--------	--------	--------	--------	--------	--------	--------	--------

LocationA

LocationB

LocationC

LocationD

LocationE

LocationF

LocationG

LocationH

Trt1

Trt2

Trt3

LoctnA:Trt1

LoctnB:Trt1

LoctnC:Trt1

LoctnD:Trt1

LoctnE:Trt1

LoctnF:Trt1

LoctnG:Trt1

LoctnH:Trt1

LoctnA:Trt2

LoctnB:Trt2

LoctnC:Trt2

LoctnD:Trt2

```

LoctnE:Trt2
LoctnF:Trt2
LoctnG:Trt2
LoctnH:Trt2
LoctnA:Trt3  0.250
LoctnB:Trt3  0.250  0.500
LoctnC:Trt3  0.250  0.500  0.500
LoctnD:Trt3  0.250  0.500  0.500  0.500
LoctnE:Trt3  0.250  0.500  0.500  0.500  0.500
LoctnF:Trt3  0.250  0.500  0.500  0.500  0.500  0.500
LoctnG:Trt3  0.250  0.500  0.500  0.500  0.500  0.500  0.500
LoctnH:Trt3  0.500  0.500  0.500  0.500  0.500  0.500  0.500  0.500

```

```
> anova(fm1Mult)
```

Analysis of Variance Table

	Df	Sum Sq	Mean Sq	Denom	F value	Pr(>F)
Location	8	6.947	0.868	72.000	25.1147	< 2.2e-16 ***
Trt	3	1.222	0.407	72.000	11.7774	2.307e-06 ***
Location:Trt	24	0.997	0.042	72.000	1.2008	0.2710

```
---
```

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

```
> fm2Mult <- update(fm1Mult, Adj ~ Location + Trt)
```

```
> fm3Mult <- update(fm1Mult, Adj ~ Location)
```

```
> fm4Mult <- update(fm1Mult, Adj ~ Trt)
```

```
> fm5Mult <- update(fm1Mult, Adj ~ 1)
```

```
> summary(fm2Mult)
```

Linear mixed-effects model fit by REML

Fixed: Adj ~ Location + Trt

Data: Multilocation

	AIC	BIC	logLik
	21.99894	59.54877	3.000531

Random effects:

Groups	Name	Variance	Std.Dev.
Grp	(Intercept)	0.0050851	0.07131
Residual		0.0367154	0.19161

# of obs: 108, groups: Grp, 27

Fixed effects:

	Estimate	Std. Error	DF	t value	Pr(> t )
(Intercept)	2.532965	0.075990	96	33.3327	< 2.2e-16 ***



```

LocationA      0.478183      0.097516 96      4.9037 3.828e-06 ***
LocationB     -0.224433      0.097516 96     -2.3015 0.0235251 *
LocationC      0.527117      0.097516 96      5.4055 4.710e-07 ***
LocationD      0.029017      0.097516 96      0.2976 0.7666828
LocationE      0.325367      0.097516 96      3.3366 0.0012075 **
LocationF      0.737092      0.097516 96      7.5587 2.411e-11 ***
LocationG      0.320983      0.097516 96      3.2916 0.0013947 **
LocationH      0.800992      0.097516 96      8.2140 9.996e-13 ***
Trt1           0.058344      0.052150 96      1.1188 0.2660283
Trt2          -0.188022      0.052150 96     -3.6054 0.0004966 ***
Trt3           0.083785      0.052150 96      1.6066 0.1114247
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

# Correlation of Fixed Effects:

```

              (Intr) LoctnA LoctnB LoctnC LoctnD LoctnE LoctnF LoctnG LoctnH
LocationA -0.642
LocationB -0.642      0.500
LocationC -0.642      0.500      0.500
LocationD -0.642      0.500      0.500      0.500
LocationE -0.642      0.500      0.500      0.500      0.500
LocationF -0.642      0.500      0.500      0.500      0.500      0.500
LocationG -0.642      0.500      0.500      0.500      0.500      0.500      0.500
LocationH -0.642      0.500      0.500      0.500      0.500      0.500      0.500      0.500
Trt1       -0.343      0.000      0.000      0.000      0.000      0.000      0.000      0.000      0.000
Trt2       -0.343      0.000      0.000      0.000      0.000      0.000      0.000      0.000      0.000
Trt3       -0.343      0.000      0.000      0.000      0.000      0.000      0.000      0.000      0.000
Trt1      Trt2

```

```

LocationA
LocationB
LocationC
LocationD
LocationE
LocationF
LocationG
LocationH
Trt1
Trt2      0.500
Trt3      0.500      0.500
> anova(fm2Mult)

```

# Analysis of Variance Table

	Df	Sum Sq	Mean Sq	Denom	F value	Pr(>F)
Location	8	7.377	0.922	96.000	25.115	< 2.2e-16 ***
Trt	3	1.222	0.407	96.000	11.092	2.571e-06 ***

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

```
> anova(fm1Mult, fm2Mult, fm3Mult, fm4Mult, fm5Mult)
```

Data: Multilocation

Models: <fixed>: <random>

fm5Mult: Adj ~ 1: ~1 | Grp

fm4Mult: Adj ~ Trt: ~1 | Grp

fm3Mult: Adj ~ Location: ~1 | Grp

fm2Mult: Adj ~ Location + Trt: ~1 | Grp

fm1Mult: Adj ~ Location \* Trt: ~1 | Grp

	Df	AIC	BIC	logLik	Chisq	Chi	Df	Pr(>Chisq)
fm5Mult	3	49.745	57.792	-21.873				
fm4Mult	6	26.951	43.044	-7.476	28.794		3	2.474e-06 ***
fm3Mult	11	-0.174	29.330	11.087	37.125		5	5.655e-07 ***
fm2Mult	14	-23.220	14.330	25.610	29.046		3	2.190e-06 ***
fm1Mult	38	-11.146	90.775	43.573	35.926		24	0.0558 .

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

```
> fm2MultR <- lme(Adj ~ Trt - 1, Multilocation, ~1 | Int +
+ Location + Grp)
```

```
> summary(fm2MultR)
```

Linear mixed-effects model fit by REML

Fixed: Adj ~ Trt - 1

Data: Multilocation

	AIC	BIC	logLik
	17.61322	39.07027	-0.8066104

Random effects:

Groups	Name	Variance	Std.Dev.
Int	(Intercept)	0.0023148	0.048112
Grp	(Intercept)	0.0056193	0.074962
Location	(Intercept)	0.1140784	0.337755
Residual		0.0345787	0.185953

# of obs: 108, groups: Int, 36; Grp, 27; Location, 9

Fixed effects:

	Estimate	Std. Error	DF	t value	Pr(> t )
Trt1	2.92401	0.12009	104	24.349	< 2.2e-16 ***
Trt2	2.67764	0.12009	104	22.297	< 2.2e-16 ***
Trt3	2.94945	0.12009	104	24.561	< 2.2e-16 ***
Trt4	2.86567	0.12009	104	23.863	< 2.2e-16 ***

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:

	Trt1	Trt2	Trt3
Trt2	0.893		
Trt3	0.893	0.893	
Trt4	0.893	0.893	0.893

## J PBIB

A partially balanced incomplete block design. Compare with output 1.7 (pp. 24-25).

```
> str(PBIB)
```

```
`data.frame':      60 obs. of  3 variables:
 $ response : num  2.4 2.5 2.6 2 2.7 2.8 2.4 2.7 2.6 2.8 ...
 $ Treatment: Factor w/ 15 levels "1","10","11",...: 7 15 1 5 11 13 14 1 2 1 .
 $ Block     : Factor w/ 15 levels "1","10","11",...: 1 1 1 1 8 8 8 8 9 9 ...
- attr(*, "ginfo")=List of 7
 ..$ formula      :Class 'formula' length 3 response ~ Treatment | Block
 .. .. ..- attr(*, ".Environment")=length 33 <environment>
 ..$ order.groups: logi TRUE
 ..$ FUN          :function (x)
 ..$ outer        : NULL
 ..$ inner        : NULL
 ..$ labels       : list()
 ..$ units        : list()
```

```
> fmlPBIB <- lme(response ~ Treatment, PBIB, ~1 | Block)
```

```
> summary(fmlPBIB)
```

Linear mixed-effects model fit by REML

Fixed: response ~ Treatment

Data: PBIB

AIC	BIC	logLik
85.9849	121.5888	-25.99245

Random effects:

Groups	Name	Variance	Std.Dev.
Block	(Intercept)	0.046522	0.21569
Residual		0.085559	0.29250

# of obs: 60, groups: Block, 15

Fixed effects:

	Estimate	Std. Error	DF	t value	Pr(> t )
(Intercept)	2.8913111	0.1664127	45	17.3743	< 2e-16 ***
Treatment1	-0.0737886	0.2220608	45	-0.3323	0.74121
Treatment10	-0.4002495	0.2220608	45	-1.8024	0.07818 .
Treatment11	0.0073879	0.2220608	45	0.0333	0.97361
Treatment12	0.1615103	0.2220608	45	0.7273	0.47079
Treatment13	-0.2735419	0.2220608	45	-1.2318	0.22441
Treatment14	-0.4000000	0.2272003	45	-1.7606	0.08511 .
Treatment15	-0.0320781	0.2220608	45	-0.1445	0.88579
Treatment2	-0.4859962	0.2220608	45	-2.1886	0.03386 *
Treatment3	-0.4363680	0.2220608	45	-1.9651	0.05560 .
Treatment4	-0.1074807	0.2272003	45	-0.4731	0.63845
Treatment5	-0.0864131	0.2220608	45	-0.3891	0.69901
Treatment6	0.0193828	0.2220608	45	0.0873	0.93083
Treatment7	-0.1023261	0.2220608	45	-0.4608	0.64716
Treatment8	-0.1097056	0.2220608	45	-0.4940	0.62369

---  
 Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:

	(Intr)	Trtmn1	Trtm10	Trtm11	Trtm12	Trtm13	Trtm14	Trtm15	Trtmn2
Treatment1	-0.667								
Treatment10	-0.667	0.500							
Treatment11	-0.667	0.477	0.500						
Treatment12	-0.667	0.500	0.500	0.500					
Treatment13	-0.667	0.500	0.500	0.500	0.500				
Treatment14	-0.683	0.512	0.512	0.512	0.512	0.512			
Treatment15	-0.667	0.500	0.477	0.500	0.500	0.500	0.512		
Treatment2	-0.667	0.500	0.500	0.500	0.477	0.500	0.512	0.500	
Treatment3	-0.667	0.500	0.500	0.500	0.500	0.477	0.512	0.500	0.500

Treatment4	-0.683	0.512	0.512	0.512	0.512	0.512	0.500	0.512	0.512
Treatment5	-0.667	0.500	0.477	0.500	0.500	0.500	0.512	0.477	0.500
Treatment6	-0.667	0.477	0.500	0.477	0.500	0.500	0.512	0.500	0.500
Treatment7	-0.667	0.500	0.500	0.500	0.477	0.500	0.512	0.500	0.477
Treatment8	-0.667	0.500	0.500	0.500	0.500	0.477	0.512	0.500	0.500
	Trtmn3	Trtmn4	Trtmn5	Trtmn6	Trtmn7				
Treatment1									
Treatment10									
Treatment11									
Treatment12									
Treatment13									
Treatment14									
Treatment15									
Treatment2									
Treatment3									
Treatment4	0.512								
Treatment5	0.500	0.512							
Treatment6	0.500	0.512	0.500						
Treatment7	0.500	0.512	0.500	0.500					
Treatment8	0.477	0.512	0.500	0.500	0.500				

## K SIMS

Analysis of the data from the Second International Mathematics Study. Compare to output 7.4 (p. 262).

```
> str(SIMS)
`data.frame':      3691 obs. of  3 variables:
 $ Pretot: num  29 38 31 31 29 23 23 33 30 32 ...
 $ Gain   : num   2 0 6 6 5 9 7 2 1 3 ...
 $ Class  : Factor w/ 190 levels "1","10","100",...: 1 1 1 1 1 1 1 1 1 1 ...
- attr(*, "ginfo")=List of 7
 ..$ formula      :Class 'formula' length 3 Gain ~ Pretot | Class
 .. .. ..- attr(*, ".Environment")=length 34 <environment>
 ..$ order.groups: logi TRUE
 ..$ FUN          :function (x)
 ..$ outer        : NULL
 ..$ inner        : NULL
 ..$ labels       :List of 2
 .. ..$ Pretot: chr "Sum of pre-test core item scores"
```

```

.. ..$ Gain : chr "Gain in mathematics achievement score"
..$ units : list()
> fmlSIMS <- lme(Gain ~ Pretot, SIMS, ~Pretot | Class)
> summary(fmlSIMS)
Linear mixed-effects model fit by REML
Fixed: Gain ~ Pretot
Data: SIMS
      AIC      BIC    logLik
22393.16 22430.45 -11190.58

Random effects:
Groups   Name      Variance Std.Dev. Corr
Class    (Intercept) 13.568605 3.68356
          Pretot      0.010648 0.10319  -0.551
Residual                22.172141 4.70873
# of obs: 3691, groups: Class, 190

Fixed effects:
      Estimate Std. Error  DF t value Pr(>|t|)
(Intercept)   7.068137   0.359603 3689  19.655 < 2.2e-16 ***
Pretot        -0.188670   0.016511 3689 -11.427 < 2.2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:
      (Intr)
Pretot -0.740

```