

lmer for SAS PROC MIXED Users

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1 Introduction

The `lmer` function from the `lme4` package 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 `data.frame` objects used by `lmer`. To help users familiar with SAS PROC MIXED get up to speed with `lmer` more quickly, we provide transcripts of some `lmer` analyses paralleling the SAS PROC MIXED analyses in Littell et al. (1996).

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

2 Similarities between lmer and SAS PROC MIXED

Both SAS PROC MIXED and `lmer` 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 **lmer** the fixed effects and the random effects are both specified as terms in the **formula** argument to **lmer**.

Both **SAS PROC MIXED** and **lmer** 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** and in **lmer**. To get **ML** estimates use the optional argument **REML=FALSE** in the call to **lmer**.

3 Important differences

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 **lmer** also produces values of **AIC** and **BIC** but the definitions used in older versions of **PROC MIXED** are different from those used in more recent versions of **PROC MIXED** and in **lmer**. In **lmer** the definitions are such that “smaller is better”. In some older versions of **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.

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. Note that the `update` function provides a convenient way of refitting a model with changes to one or more arguments.

4 Data manipulation

Both PROC MIXED and `lmer` 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 R these data could be read from a file, say `animal.dat`, and converted to factors by

```
animal <- within(read.table("animal.dat", header = TRUE),
  {
```

```

        trait <- factor(trait)
        animal <- factor(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")=<environment: R_GlobalEnv>
 ..$ 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()

```

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 in the call to `lmer` object. The random effects term would be either

```
(1 | ET:Wafer)
```

or, equivalently

```
(1 | ET:Wafer) + (1 | ET)
```

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 <- within(Semiconductor, Grp <- factor(ET:Wafer))
```

after which we could specify a random effects term of `(1 | Grp)`. Alternatively, we can use the explicit term

```
(1 | ET:Wafer)
```

4.2 General approach

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

- Create a `data.frame` with one row per observation and one column per variable.
- Use `factor` or `as.factor` to explicitly convert any ordered factors to class `ordered`.
- Use `ordered` or `as.ordered` to explicitly convert any ordered factors to class `ordered`.
- If necessary, use interaction terms to create a factor with unique levels from inner nested factors.
- 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 `lmer` 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 may find it worthwhile to declare

```
> 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

```
> print(xyplot(adg ~ Treatment | Block, AvgDailyGain, type = c("g", "p", "r")
+       xlab = "Treatment (amount of feed additive)",
+       ylab = "Average daily weight gain (lb.)", aspect = "xy",
+       index.cond = function(x, y) coef(lm(y ~ x))[1]))

> ## compare with output 5.1, p. 178
> (fmlAdg <- lmer(adg ~ (Treatment - 1)*InitWt + (1 | Block), AvgDailyGain))
Linear mixed model fit by REML
Formula: adg ~ (Treatment - 1) * InitWt + (1 | Block)
Data: AvgDailyGain
```

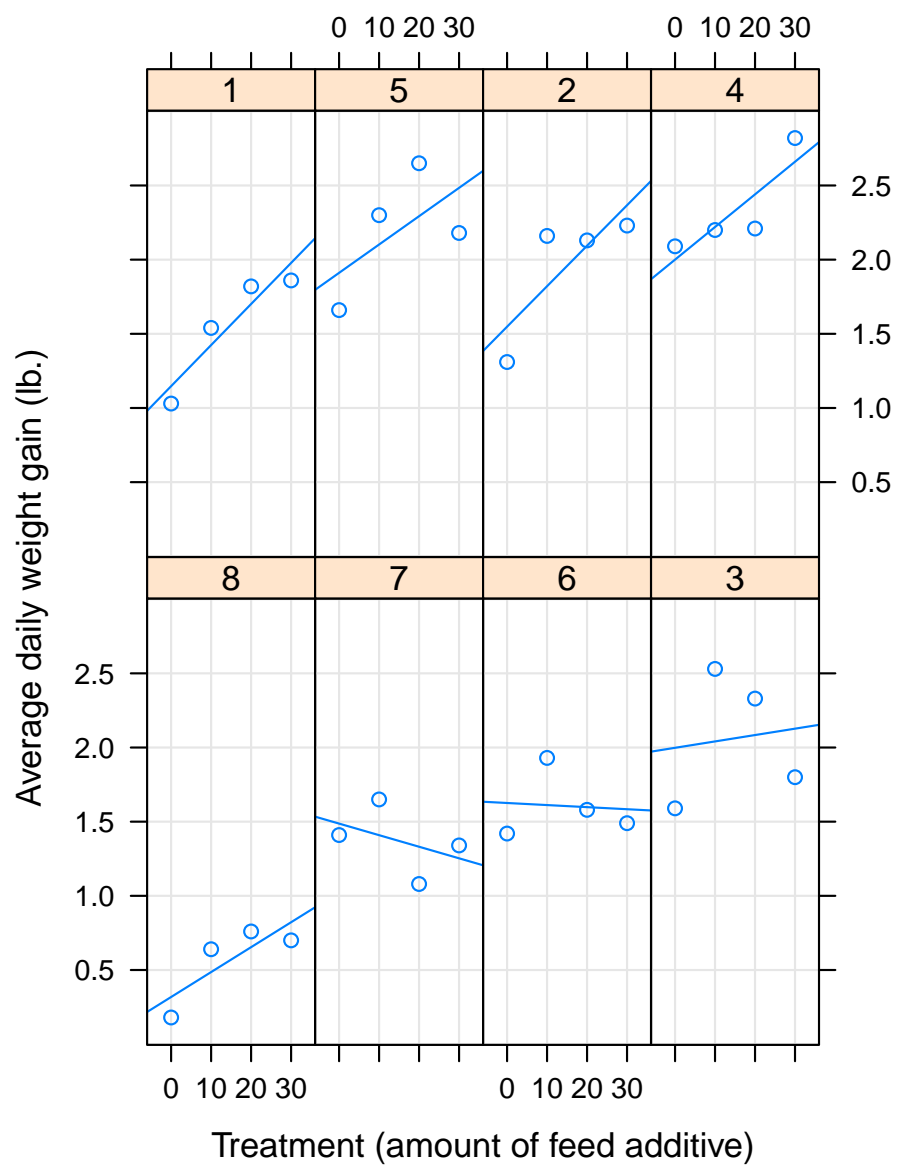


Figure 1: Average daily weight gain

```

      AIC   BIC logLik deviance REMLdev
85.33 99.98 -32.66   10.10   65.33

```

Random effects:

```

Groups   Name             Variance Std.Dev.
Block    (Intercept) 0.259312 0.50923
Residual                    0.049429 0.22233

```

Number of obs: 32, groups: Block, 8

Fixed effects:

```

              Estimate Std. Error t value
Treatment0      0.439126   0.711086   0.618
Treatment10     1.426112   0.637543   2.237
Treatment20     0.479620   0.548884   0.874
Treatment30     0.200117   0.775197   0.258
InitWt          0.004448   0.002082   2.137
Treatment0:InitWt -0.002154   0.002786  -0.773
Treatment10:InitWt -0.003365   0.002515  -1.338
Treatment20:InitWt -0.001082   0.002488  -0.435

```

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
Trtmnt0:InW -0.640  0.046 -0.024  0.754 -0.780
Trtmnt10:IW -0.021 -0.535 -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) # checking significance of terms
```

Analysis of Variance Table

```

              Df Sum Sq Mean Sq F value
Treatment      4  5.7185  1.42961 28.9225
InitWt         1  0.5495  0.54946 11.1160
Treatment:InitWt 3  0.1381  0.04603  0.9313

```

```
> ## common slope model
```

```
> (fm2Adg <- lmer(adg ~ InitWt + Treatment + (1 | Block), AvgDailyGain))
```

Linear mixed model fit by REML

Formula: adg ~ InitWt + Treatment + (1 | Block)

Data: AvgDailyGain

```

      AIC   BIC logLik deviance REMLdev

```


50.34 60.6 -18.17 13.62 36.34

Random effects:

Groups	Name	Variance	Std.Dev.
Block	(Intercept)	0.24084	0.49076
Residual		0.05008	0.22379

Number of obs: 32, groups: Block, 8

Fixed effects:

	Estimate	Std. Error	t value
(Intercept)	0.8011046	0.3556585	2.252
InitWt	0.0027797	0.0008334	3.336
Treatment0	-0.5520740	0.1148131	-4.808
Treatment10	-0.0685666	0.1189689	-0.576
Treatment20	-0.0881295	0.1162878	-0.758

Correlation of Fixed Effects:

	(Intr)	InitWt	Trtmn0	Trtm10
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	F value
InitWt	1	0.51451	0.51451	10.274
Treatment	3	1.52670	0.50890	10.162

> (fm3Adg <- lmer(adg ~ InitWt + Treatment - 1 + (1 | Block), AvgDailyGain))

Linear mixed model fit by REML

Formula: adg ~ InitWt + Treatment - 1 + (1 | Block)

Data: AvgDailyGain

AIC	BIC	logLik	deviance	REMLdev
50.34	60.6	-18.17	13.62	36.34

Random effects:

Groups	Name	Variance	Std.Dev.
Block	(Intercept)	0.24084	0.49076
Residual		0.05008	0.22379

Number of obs: 32, groups: Block, 8

Fixed effects:

Estimate	Std. Error	t value
----------	------------	---------

InitWt	0.0027797	0.0008334	3.336
Treatment0	0.2490307	0.3776294	0.659
Treatment10	0.7325380	0.3903774	1.876
Treatment20	0.7129751	0.3827661	1.863
Treatment30	0.8011046	0.3556585	2.252

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

```
> print(xyplot(y ~ x | Block, BIB, groups = Treatment, type = c("g", "p"),
+           aspect = "xy", auto.key = list(points = TRUE, space = "right",
+           lines = FALSE)))
```

```
> ## compare with Output 5.7, p. 188
```

```
> (fmlBIB <- lmer(y ~ Treatment * x + (1|Block), BIB))
```

Linear mixed model fit by REML

Formula: y ~ Treatment * x + (1 | Block)

Data: BIB

	AIC	BIC	logLik	deviance	REMLdev
	124.9	136.7	-52.45	93.5	104.9

Random effects:

Groups	Name	Variance	Std.Dev.
Block	(Intercept)	18.2499	4.2720
Residual		1.2004	1.0956

Number of obs: 24, groups: Block, 8

Fixed effects:

	Estimate	Std. Error	t value
(Intercept)	22.36787	3.10178	7.211
Treatment1	4.42948	3.36503	1.316
Treatment2	-0.43738	2.93319	-0.149
Treatment3	6.27861	3.28202	1.913
x	0.44255	0.08706	5.083
Treatment1:x	-0.22377	0.10608	-2.109

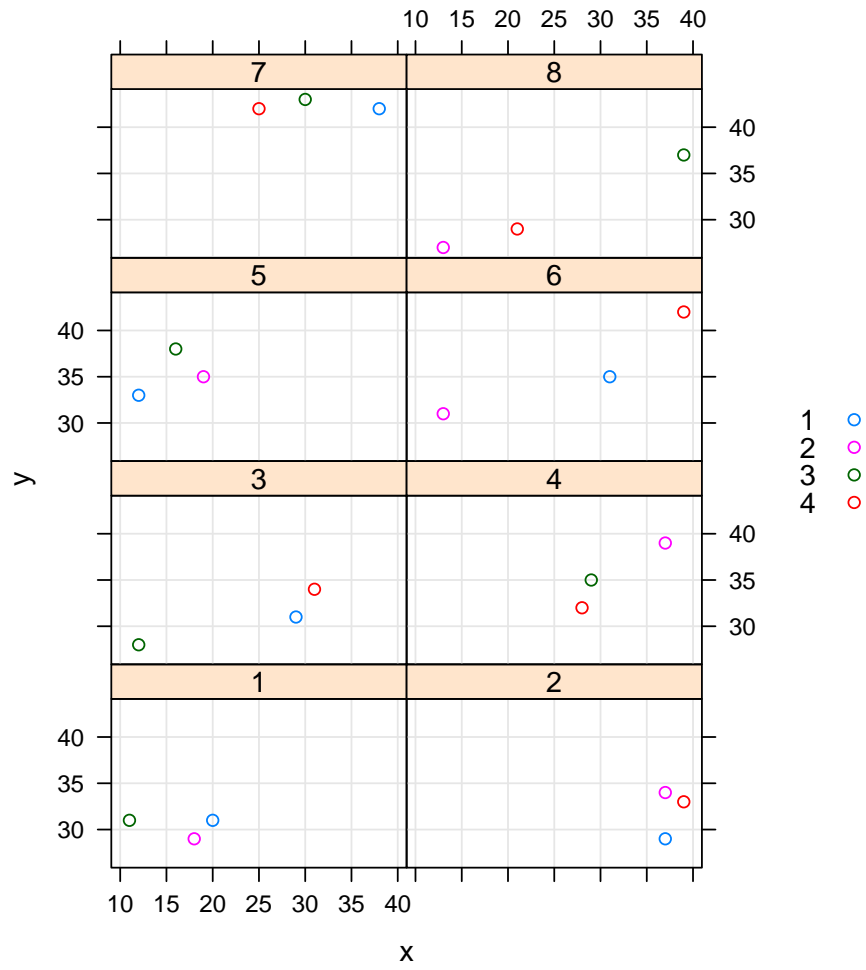


Figure 2: Balanced incomplete block design

```
Treatment2:x  0.05338    0.09714    0.550
Treatment3:x -0.17918    0.11571   -1.549
```

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(fm1BIB)      # strong evidence of different slopes
```

Analysis of Variance Table

```
          Df  Sum Sq Mean Sq  F value
Treatment    3  23.447   7.816    6.5108
x            1 136.803 136.803 113.9641
Treatment:x   3  18.429   6.143    5.1174
```

```
> ## compare with Output 5.9, p. 193
```

```
> (fm2BIB <- lmer(y ~ Treatment + x:Grp + (1|Block), BIB))
```

Linear mixed model fit by REML

Formula: y ~ Treatment + x:Grp + (1 | Block)

Data: BIB

```
      AIC      BIC logLik deviance REMLdev
115.2 124.6 -49.59   94.09   99.18
```

Random effects:

```
Groups   Name             Variance Std.Dev.
Block    (Intercept) 18.5257  4.3041
Residual                    1.0378  1.0187
```

Number of obs: 24, groups: Block, 8

Fixed effects:

```
          Estimate Std. Error t value
(Intercept) 20.94516    2.06230  10.156
Treatment1   5.34145    1.97570   2.704
Treatment2   1.13557    0.71399   1.590
Treatment3   8.18103    1.77010   4.622
x:Grp13      0.23952    0.04296   5.575
x:Grp24      0.48923    0.04412  11.088
```

```

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 F value
Treatment 3  23.424    7.808   7.5236
x:Grp     2 154.733   77.367  74.5471

```

C Bond

```

> ## compare with output 1.1 on p. 6
> (fm1Bond <- lmer(pressure ~ Metal + (1|Ingot), Bond))
Linear mixed model fit by REML
Formula: pressure ~ Metal + (1 | Ingot)
Data: Bond
      AIC      BIC logLik deviance REMLdev
117.8 123.0  -53.9   115.7   107.8
Random effects:
Groups      Name      Variance Std.Dev.
Ingot      (Intercept) 11.448    3.3835
Residual                    10.372    3.2205
Number of obs: 21, groups: Ingot, 7

```

```

Fixed effects:
      Estimate Std. Error t value
(Intercept)  71.1000    1.7655  40.27
Metalc       -0.9143    1.7214  -0.53
Metali        4.8000    1.7214   2.79

```

```

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 F value
Metal  2  131.9    65.95   6.3588

```

D Cultivation

```
> 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")=<environment: R_GlobalEnv>
 ..$ 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")=<environment: R_GlobalEnv>
 ..$ 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
> (fmlCult <- lmer(drywt ~ Inoc * Cult + (1|Block) + (1|Cult), Cultivation))
Linear mixed model fit by REML
Formula: drywt ~ Inoc * Cult + (1 | Block) + (1 | Cult)
Data: Cultivation
      AIC      BIC logLik deviance REMLdev
86.49 97.09 -34.24   74.94   68.49
Random effects:
Groups   Name      Variance Std.Dev.
Block    (Intercept) 1.20728  1.09876
Cult      (Intercept) 0.26578  0.51554
Residual                    1.19633  1.09377
Number of obs: 24, groups: Block, 4; Cult, 2
```

Fixed effects:

	Estimate	Std. Error	t value
(Intercept)	33.5250	0.9310	36.01
Inoccon	-5.5000	0.7734	-7.11
Inocdea	-2.8750	0.7734	-3.72
Culta	-0.3750	1.0629	-0.35
Inoccon:Culta	0.2500	1.0938	0.23
Inocdea:Culta	-1.0250	1.0938	-0.94

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	-0.515	
Inocdea:Clt	0.294	-0.354	-0.707	-0.515	0.500

> anova(fm1Cult)

Analysis of Variance Table

	Df	Sum Sq	Mean Sq	F value
Inoc	2	118.176	59.088	49.3908
Cult	1	0.656	0.656	0.5488
Inoc:Cult	2	1.826	0.913	0.7631

> (fm2Cult <- lmer(drywt ~ Inoc + Cult + (1|Block) + (1|Cult), Cultivation))

Linear mixed model fit by REML

Formula: drywt ~ Inoc + Cult + (1 | Block) + (1 | Cult)

Data: Cultivation

AIC BIC logLik deviance REMLdev

87.75 96 -36.88 76.9 73.75

Random effects:

Groups	Name	Variance	Std.Dev.
Block	(Intercept)	1.21283	1.1013
Cult	(Intercept)	0.25837	0.5083
Residual		1.16299	1.0784

Number of obs: 24, groups: Block, 4; Cult, 2

Fixed effects:

	Estimate	Std. Error	t value
(Intercept)	33.6542	0.8690	38.73
Inoccon	-5.3750	0.5392	-9.97

Inocdea	-3.3875	0.5392	-6.28
Culta	-0.6333	0.8427	-0.75

Correlation of Fixed Effects:

```

      (Intr) Inoccn Inocde
Inoccon -0.310
Inocdea -0.310  0.500
Culta   -0.485  0.000  0.000

```

> anova(fm2Cult)

Analysis of Variance Table

	Df	Sum Sq	Mean Sq	F value
Inoc	2	118.176	59.088	50.8069
Cult	1	0.656	0.656	0.5636

> (fm3Cult <- lmer(drywt ~ Inoc + (1|Block) + (1|Cult), Cultivation))

Linear mixed model fit by REML

Formula: drywt ~ Inoc + (1 | Block) + (1 | Cult)

Data: Cultivation

	AIC	BIC	logLik	deviance	REMLdev
	87.68	94.75	-37.84	77.32	75.68

Random effects:

Groups	Name	Variance	Std.Dev.
Block	(Intercept)	1.21283	1.10129
Cult	(Intercept)	0.10364	0.32193
Residual		1.16299	1.07842

Number of obs: 24, groups: Block, 4; Cult, 2

Fixed effects:

	Estimate	Std. Error	t value
(Intercept)	33.3375	0.7074	47.13
Inoccon	-5.3750	0.5392	-9.97
Inocdea	-3.3875	0.5392	-6.28

Correlation of Fixed Effects:

```

      (Intr) Inoccn
Inoccon -0.381
Inocdea -0.381  0.500

```

> anova(fm3Cult)

Analysis of Variance Table

	Df	Sum Sq	Mean Sq	F value
Inoc	2	118.18	59.088	50.807

E Demand

```
> ## compare to output 3.13, p. 132
> (fmlDemand <-
+ lmer(log(d) ~ log(y) + log(rd) + log(rt) + log(rs) + (1|State) + (1|Year),
+ Demand))
```

Linear mixed model fit by REML

Formula: $\log(d) \sim \log(y) + \log(rd) + \log(rt) + \log(rs) + (1 | \text{State}) +$

Data: Demand

	AIC	BIC	logLik	deviance	REMLdev
	-224.2	-205.4	120.1	-260.5	-240.2

Random effects:

Groups	Name	Variance	Std.Dev.
Year	(Intercept)	0.00026466	0.016268
State	(Intercept)	0.02950551	0.171772
Residual		0.00111698	0.033421

Number of obs: 77, groups: Year, 11; State, 7

Fixed effects:

	Estimate	Std. Error	t value
(Intercept)	-1.28382	0.72343	-1.775
log(y)	1.06978	0.10393	10.294
log(rd)	-0.29533	0.05246	-5.629
log(rt)	0.03988	0.02789	1.430
log(rs)	-0.32673	0.11438	-2.856

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 HR

```
> ## linear trend in time
> (fmlHR <- lmer(HR ~ Time * Drug + baseHR + (Time|Patient), HR))
```

Linear mixed model fit by REML

Formula: $\text{HR} \sim \text{Time} * \text{Drug} + \text{baseHR} + (\text{Time} | \text{Patient})$

Data: HR

	AIC	BIC	logLik	deviance	REMLdev
--	-----	-----	--------	----------	---------

```

789.6 820.3 -383.8    788.1    767.6
Random effects:
Groups   Name             Variance Std.Dev. Corr
Patient  (Intercept)  60.633    7.7867
          Time       37.784    6.1469  -0.563
Residual                24.361    4.9357
Number of obs: 120, groups: Patient, 24

Fixed effects:
              Estimate Std. Error t value
(Intercept)  33.9784    10.2826   3.304
Time         -3.1970     3.0850  -1.036
DrugA         3.5991     4.2314   0.851
DrugB         7.0912     4.2094   1.685
baseHR        0.5434     0.1161   4.679
Time:DrugA   -7.5013     4.3629  -1.719
Time:DrugB   -3.9894     4.3629  -0.914

Correlation of Fixed Effects:
              (Intr) Time   DrugA   DrugB   baseHR Tim:Drq
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 F value
Time          1 377.77   377.77 15.5072
Drug          2  92.83    46.42   1.9054
baseHR        1 533.01   533.01 21.8799
Time:Drug     2  72.12    36.06   1.4803
> ## remove interaction
> (fm3HR <- lmer(HR ~ Time + Drug + baseHR + (Time|Patient), HR))
Linear mixed model fit by REML
Formula: HR ~ Time + Drug + baseHR + (Time | Patient)
Data: HR
      AIC      BIC logLik deviance REMLdev
797.8 822.9 -389.9    791.2    779.8

```

Random effects:

Groups	Name	Variance	Std.Dev.	Corr
Patient	(Intercept)	61.560	7.8460	
	Time	40.963	6.4003	-0.571
Residual		24.361	4.9357	

Number of obs: 120, groups: Patient, 24

Fixed effects:

	Estimate	Std. Error	t value
(Intercept)	36.0471	10.1941	3.536
Time	-7.0273	1.8179	-3.866
Druga	-0.4526	3.5144	-0.129
Drugb	4.9364	3.4879	1.415
baseHR	0.5434	0.1161	4.679

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

> anova(fm3HR)

Analysis of Variance Table

	Df	Sum Sq	Mean Sq	F value
Time	1	362.71	362.71	14.8891
Drug	2	92.84	46.42	1.9055
baseHR	1	533.04	533.04	21.8811

> ## remove Drug term

> (fm4HR <- lmer(HR ~ Time + baseHR + (Time|Patient), HR))

Linear mixed model fit by REML

Formula: HR ~ Time + baseHR + (Time | Patient)

Data: HR

AIC	BIC	logLik	deviance	REMLdev
805.1	824.7	-395.6	794.3	791.1

Random effects:

Groups	Name	Variance	Std.Dev.	Corr
Patient	(Intercept)	63.026	7.9389	
	Time	40.963	6.4003	-0.553
Residual		24.361	4.9357	

Number of obs: 120, groups: Patient, 24

Fixed effects:

	Estimate	Std. Error	t value
(Intercept)	36.9321	9.9010	3.730
Time	-7.0273	1.8179	-3.866
baseHR	0.5508	0.1175	4.686

Correlation of Fixed Effects:

	(Intr)	Time
Time	-0.098	
baseHR	-0.984	0.000

> anova(fm4HR)

Analysis of Variance Table

	Df	Sum Sq	Mean Sq	F value
Time	1	362.58	362.58	14.884
baseHR	1	534.60	534.60	21.945

G Mississippi

```
> ## compare with output 4.1, p. 142
> (fmlMiss <- lmer(y ~ 1 + (1 | influent), Mississippi))
```

Linear mixed model fit by REML

Formula: y ~ 1 + (1 | influent)

Data: Mississippi

AIC	BIC	logLik	deviance	REMLdev
258.4	263.2	-126.2	256.6	252.4

Random effects:

Groups	Name	Variance	Std.Dev.
influ	(Intercept)	63.323	7.9576
Residual		42.658	6.5313

Number of obs: 37, groups: influent, 6

Fixed effects:

	Estimate	Std. Error	t value
(Intercept)	21.223	3.429	6.19

```
> ## compare with output 4.2, p. 143
```

```
> (fmlMLMiss <- lmer(y ~ 1 + (1 | influent), Mississippi, method = "ML"))
```

Linear mixed model fit by maximum likelihood

Formula: y ~ 1 + (1 | influent)

Data: Mississippi

```

      AIC    BIC logLik deviance REMLdev
262.6 267.4 -128.3    256.6    252.4
Random effects:
  Groups   Name      Variance Std.Dev.
influent (Intercept) 51.255    7.1592
Residual                42.697    6.5343
Number of obs: 37, groups: influent, 6

Fixed effects:
              Estimate Std. Error t value
(Intercept)   21.217      3.122    6.796
> ranef(fmlMLMiss)      # BLUP's of random effects on p. 144
$influent
  (Intercept)
1    0.3097985
2   -6.5774724
3   -3.7864007
4    2.8827777
5   -5.8437167
6   13.0150136
> ranef(fmlMiss)      # BLUP's of random effects on p. 142
$influent
  (Intercept)
1    0.3093146
2   -6.7198315
3   -3.8982115
4    2.9463224
5   -6.0133969
6   13.3758027
> VarCorr(fmlMiss)      # compare to output 4.7, p. 148
$influent
      (Intercept)
(Intercept)   63.32337
attr(,"stddev")
(Intercept)
      7.957598
attr(,"correlation")
      (Intercept)
(Intercept)      1

attr(,"sc")
[1] 6.531317

```

```

> ## compare to output 4.8 and 4.9, pp. 150-152
> (fm2Miss <- lmer(y ~ Type + (1 | influent), Mississippi))
Linear mixed model fit by REML
Formula: y ~ Type + (1 | influent)
Data: Mississippi
      AIC      BIC logLik deviance REMLdev
244.5 252.6 -117.3    247.5    234.5
Random effects:
Groups      Name      Variance Std.Dev.
influente (Intercept) 14.970    3.8691
Residual              42.514    6.5202
Number of obs: 37, groups: influente, 6

Fixed effects:
              Estimate Std. Error t value
(Intercept)   36.400      4.844    7.514
Type1         -20.800      5.933   -3.506
Type2         -16.462      5.516   -2.984

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 F value
Type  2 541.62  270.81    6.37

```

H Multilocation

```

> 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   7.1 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")=<environment: R_GlobalEnv>
..$ 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")=<environment: R_GlobalEnv>
..$ labels      :List of 1
.. ..$ Adj: chr "Adjusted yield"
..$ units       : list()
> ### Create a Block %in% Location factor
> Multilocation$Grp <- with(Multilocation, Block:Location)
> (fmlMult <- lmer(Adj ~ Location * Trt + (1|Grp), Multilocation))
Linear mixed model fit by REML
Formula: Adj ~ Location * Trt + (1 | Grp)
Data: Multilocation
AIC    BIC logLik deviance REMLdev
86.65 188.6 -5.323   -87.15    10.65
Random effects:
Groups   Name             Variance Std.Dev.
Grp      (Intercept) 0.0056193 0.074962
Residual                    0.0345787 0.185953
Number of obs: 108, groups: Grp, 27

Fixed effects:
              Estimate Std. Error t value
(Intercept)    2.35923    0.11575  20.381
LocationA       0.64930    0.16370   3.966
LocationB       0.06643    0.16370   0.406
LocationC       0.54533    0.16370   3.331
LocationD       0.37413    0.16370   2.285
LocationE       0.55000    0.16370   3.360
LocationF       0.99810    0.16370   6.097
LocationG       0.36057    0.16370   2.203
LocationH       1.01403    0.16370   6.194
Trt1            0.22720    0.15183   1.496
Trt2           -0.00140    0.15183  -0.009

```

Trt3	0.42323	0.15183	2.788
LocationA:Trt1	-0.18853	0.21472	-0.878
LocationB:Trt1	-0.27523	0.21472	-1.282
LocationC:Trt1	-0.04000	0.21472	-0.186
LocationD:Trt1	-0.53513	0.21472	-2.492
LocationE:Trt1	-0.26297	0.21472	-1.225
LocationF:Trt1	-0.27153	0.21472	-1.265
LocationG:Trt1	0.20323	0.21472	0.947
LocationH:Trt1	-0.14953	0.21472	-0.696
LocationA:Trt2	-0.09347	0.21472	-0.435
LocationB:Trt2	-0.32273	0.21472	-1.503
LocationC:Trt2	0.08960	0.21472	0.417
LocationD:Trt2	-0.29693	0.21472	-1.383
LocationE:Trt2	-0.30693	0.21472	-1.429
LocationF:Trt2	-0.30993	0.21472	-1.443
LocationG:Trt2	-0.10860	0.21472	-0.506
LocationH:Trt2	-0.33060	0.21472	-1.540
LocationA:Trt3	-0.40247	0.21472	-1.874
LocationB:Trt3	-0.56550	0.21472	-2.634
LocationC:Trt3	-0.12247	0.21472	-0.570
LocationD:Trt3	-0.54840	0.21472	-2.554
LocationE:Trt3	-0.32863	0.21472	-1.531
LocationF:Trt3	-0.46257	0.21472	-2.154
LocationG:Trt3	-0.25297	0.21472	-1.178
LocationH:Trt3	-0.37203	0.21472	-1.733

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 F value
Location      8  6.9474  0.86843  25.1145
Trt           3  1.2217  0.40725  11.7774
Location:Trt  24  0.9966  0.04152   1.2008
> (fm2Mult <- lmer(Adj ~ Location + Trt + (1|Grp), Multilocation))
Linear mixed model fit by REML
Formula: Adj ~ Location + Trt + (1 | Grp)
Data: Multilocation
   AIC   BIC logLik deviance REMLdev
  22 59.55  3.001   -51.22   -6.001
Random effects:
   Groups   Name      Variance Std.Dev.
Grp      (Intercept) 0.0050851 0.07131
Residual                0.0367154 0.19161
Number of obs: 108, groups: Grp, 27

Fixed effects:
              Estimate Std. Error t value
(Intercept)  2.53296    0.07599   33.33
LocationA     0.47818    0.09752    4.90
LocationB    -0.22443    0.09752   -2.30
LocationC     0.52712    0.09752    5.41
LocationD     0.02902    0.09752    0.30
LocationE     0.32537    0.09752    3.34
LocationF     0.73709    0.09752    7.56
LocationG     0.32098    0.09752    3.29
LocationH     0.80099    0.09752    8.21

```

Trt1	0.05834	0.05215	1.12
Trt2	-0.18802	0.05215	-3.61
Trt3	0.08379	0.05215	1.61

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
Trt3

```
> (fm3Mult <- lmer(Adj ~ Location + (1|Grp), Multilocation))
```

Linear mixed model fit by REML

Formula: Adj ~ Location + (1 | Grp)

Data: Multilocation

AIC	BIC	logLik	deviance	REMLdev
31.94	61.44	-4.968	-22.96	9.935

Random effects:

Groups	Name	Variance	Std.Dev.
Grp	(Intercept)	4.0504e-14	2.0125e-07
Residual		5.1642e-02	2.2725e-01

Number of obs: 108, groups: Grp, 27

Fixed effects:

	Estimate	Std. Error	t value
(Intercept)	2.52149	0.06560	38.44
LocationA	0.47818	0.09277	5.15
LocationB	-0.22443	0.09277	-2.42
LocationC	0.52712	0.09277	5.68
LocationD	0.02902	0.09277	0.31
LocationE	0.32537	0.09277	3.51
LocationF	0.73709	0.09277	7.95
LocationG	0.32098	0.09277	3.46
LocationH	0.80099	0.09277	8.63

Correlation of Fixed Effects:

	(Intr)	LoctnA	LoctnB	LoctnC	LoctnD	LoctnE	LoctnF	LoctnG
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

```
> (fm4Mult <- lmer(Adj ~ Trt + (1|Grp), Multilocation))
```

Linear mixed model fit by REML

Formula: Adj ~ Trt + (1 | Grp)

Data: Multilocation

AIC	BIC	logLik	deviance	REMLdev
43.51	59.6	-15.75	14.95	31.51

Random effects:

Groups	Name	Variance	Std.Dev.
Grp	(Intercept)	0.110922	0.33305
Residual		0.036715	0.19161

Number of obs: 108, groups: Grp, 27

Fixed effects:

	Estimate	Std. Error	t value
(Intercept)	2.86567	0.07395	38.75
Trt1	0.05834	0.05215	1.12
Trt2	-0.18802	0.05215	-3.61

```
Trt3          0.08379    0.05215    1.61
```

Correlation of Fixed Effects:

```
(Intr) Trt1    Trt2
```

```
Trt1 -0.353
```

```
Trt2 -0.353  0.500
```

```
Trt3 -0.353  0.500  0.500
```

```
> (fm5Mult <- lmer(Adj ~ 1 + (1/Grp), Multilocation))
```

Linear mixed model fit by REML

Formula: Adj ~ 1 + (1 | Grp)

Data: Multilocation

```
AIC    BIC logLik deviance REMLdev
53.33 61.37 -23.66   43.75   47.33
```

Random effects:

```
Groups   Name             Variance Std.Dev.
Grp      (Intercept) 0.107492 0.32786
Residual                    0.050439 0.22459
```

Number of obs: 108, groups: Grp, 27

Fixed effects:

```
Estimate Std. Error t value
(Intercept)  2.85419    0.06669   42.8
```

```
> anova(fm2Mult)
```

Analysis of Variance Table

```
Df Sum Sq Mean Sq F value
Location  8 7.3768 0.92210  25.115
Trt        3 1.2217 0.40725  11.092
```

```
> (fm2MultR <- lmer(Adj ~ Trt + (Trt - 1/Location) + (1/Block), Multilocation
+ verbose = TRUE))
```

```
0:    60.383823: 0.942809 0.942809 0.942809 0.942809 0.00000 0.00000 0.0
1:    26.054806: 1.19385  1.08439  1.12694  1.12035 0.375825 0.404184 0.3
2:    12.324367: 1.78879  1.10709 0.956708 0.957068 0.834630 0.796975 0.6
3:    10.066162: 1.94994 0.629725 0.327637 0.637437 0.573540 0.983609 1.
4:     3.4216352: 1.93818 0.623636 0.292366 0.642859 0.897798 0.874015 0.8
5:     2.9953154: 1.93884 0.572571 0.235852 0.620141 0.829278 0.973107 0.8
6:     2.2740843: 1.93432 0.497439 0.151063 0.590724 0.878755 0.899238 0.8
7:     2.0190177: 1.92976 0.409642 0.0603946 0.556743 0.837681 0.950455 0.
8:     1.8668385: 1.90947 0.320282  0.00000 0.527997 0.908733 0.926735 0.8
9:     1.7631814: 1.90871 0.315533  0.00000 0.528929 0.871513 0.937396 0.8
10:    1.7599466: 1.90782 0.312054  0.00000 0.529431 0.881514 0.923702 0.8
```

11:	1.7465121:	1.90773	0.307249	0.00000	0.530496	0.874590	0.929315	0.8
12:	1.7377057:	1.90400	0.294952	5.95711e-08	0.529562	0.885395	0.933792	0.8
13:	1.7201869:	1.90206	0.288071	0.00000	0.522782	0.878237	0.930513	0.8
14:	1.7119534:	1.90040	0.296097	0.00000	0.523872	0.872068	0.934761	0.8
15:	1.5977814:	1.87125	0.341599	0.00000	0.493695	0.869417	0.930239	0.8
16:	1.5833769:	1.88326	0.300545	0.103248	0.284199	0.874006	0.922977	0.8
17:	1.5334774:	1.86719	0.293568	0.0373396	0.210527	0.889551	0.955934	0.8
18:	1.4719386:	1.87013	0.232797	0.0266940	0.200586	0.876891	0.918091	0.8
19:	1.4381335:	1.88275	0.237861	0.00957824	0.188231	0.877069	0.940795	0.8
20:	1.4282918:	1.88290	0.248911	0.00700901	0.189067	0.882182	0.930061	0.8
21:	1.4244024:	1.88663	0.249068	0.000707448	0.181736	0.873614	0.935164	0.8
22:	1.4218921:	1.88698	0.245336	0.00000	0.173507	0.879458	0.933249	0.8
23:	1.4148803:	1.88148	0.235492	0.00000	0.101300	0.882306	0.940832	0.8
24:	1.4126660:	1.87973	0.234201	0.00000	0.0701867	0.883702	0.940938	0.8
25:	1.4116113:	1.88107	0.236379	6.72705e-05	0.0690894	0.883267	0.934181	0.8
26:	1.4101984:	1.88167	0.235259	4.30064e-05	0.0643339	0.879197	0.937180	0.8
27:	1.4098453:	1.88218	0.234638	2.03043e-05	0.0590238	0.880342	0.936066	0.8
28:	1.4097689:	1.88307	0.233645	0.00000	0.0483303	0.878317	0.937242	0.8
29:	1.4094043:	1.88363	0.233730	0.00000	0.0480684	0.879813	0.936005	0.8
30:	1.4088887:	1.89085	0.234194	1.34768e-07	0.0445718	0.878327	0.935968	0.8
31:	1.4087725:	1.89103	0.234150	1.25355e-07	0.0443828	0.879043	0.935543	0.8
32:	1.4087323:	1.89153	0.234145	9.78685e-08	0.0438396	0.879381	0.935308	0.8
33:	1.4087004:	1.89224	0.235076	0.000117165	0.0425805	0.878749	0.934978	0.8
34:	1.4086126:	1.89265	0.234066	0.000248911	0.0413392	0.878696	0.935601	0.8
35:	1.4085775:	1.89293	0.234559	0.000372552	0.0400229	0.879463	0.934762	0.8
36:	1.4084868:	1.89317	0.234734	0.000537872	0.0385422	0.878690	0.935219	0.8
37:	1.4084239:	1.89344	0.234487	0.000625295	0.0369563	0.879196	0.935135	0.8
38:	1.4082879:	1.89395	0.235669	0.00138217	0.0301548	0.879180	0.934486	0.8
39:	1.4080776:	1.89410	0.235512	0.00151417	0.0238666	0.878312	0.935624	0.8
40:	1.4079382:	1.89515	0.235882	0.00000	0.0216329	0.879022	0.934399	0.8
41:	1.4077780:	1.89549	0.236634	0.00000	0.0151077	0.878532	0.934954	0.8
42:	1.4076193:	1.89696	0.237940	0.00000	0.000324308	0.878399	0.934794	0.8
43:	1.4075996:	1.89717	0.237681	0.00000	0.000377330	0.878200	0.934771	0.8
44:	1.4075812:	1.89718	0.237534	0.00000	0.00000	0.878793	0.934675	0.8
45:	1.4075440:	1.89760	0.238582	0.00000	0.00000	0.878830	0.934525	0.8
46:	1.4074552:	1.89898	0.239976	0.00215515	0.00000	0.878179	0.934558	0.8
47:	1.4073284:	1.89844	0.243459	0.00000	0.00000	0.877005	0.934123	0.8
48:	1.4072091:	1.89669	0.243776	0.00000	0.00000	0.877846	0.934574	0.8
49:	1.4072050:	1.89673	0.243754	4.33982e-05	0.00000	0.877980	0.934484	0.8
50:	1.4072046:	1.89674	0.243785	3.29810e-05	0.000107187	0.877990	0.934444	0.8


```

51:      1.4072043:  1.89672 0.243865 9.41469e-06 0.000356118 0.877999 0.9345
52:      1.4072042:  1.89673 0.243838 1.14604e-05 0.000310929 0.877996 0.9345
53:      1.4072041:  1.89674 0.243810 1.23482e-05 0.000212064 0.877994 0.9345
54:      1.4072041:  1.89672 0.243778 7.76018e-06 7.28735e-05 0.877994 0.9344
55:      1.4072040:  1.89671 0.243747 2.02904e-06 0.000000 0.877994 0.934498
56:      1.4072040:  1.89671 0.243765 0.000000 0.000000 0.877998 0.934500 0.8
57:      1.4072040:  1.89671 0.243764 0.000000 0.000000 0.877996 0.934499 0.8
58:      1.4072040:  1.89671 0.243764 0.000000 0.000000 0.877996 0.934499 0.8

```

Linear mixed model fit by REML

Formula: Adj ~ Trt + (Trt - 1 | Location) + (1 | Block)

Data: Multilocation

	AIC	BIC	logLik	deviance	REMLdev
	33.41	76.32	-0.7036	-13.38	1.407

Random effects:

Groups	Name	Variance	Std.Dev.	Corr
Location	Trt1	0.135889	0.36863	
	Trt2	0.106998	0.32711	0.989
	Trt3	0.119086	0.34509	0.998 0.996
	Trt4	0.114108	0.33780	0.927 0.972 0.948
Block	(Intercept)	0.000000	0.00000	
Residual		0.037773	0.19435	

Number of obs: 108, groups: Location, 9; Block, 3

Fixed effects:

	Estimate	Std. Error	t value
(Intercept)	2.86567	0.11865	24.152
Trt1	0.05834	0.07012	0.832
Trt2	-0.18802	0.05921	-3.176
Trt3	0.08379	0.06447	1.300

Correlation of Fixed Effects:

	(Intr)	Trt1	Trt2
Trt1	-0.150		
Trt2	-0.306	0.620	
Trt3	-0.236	0.682	0.620

I PBIB

```

> 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")=<environment: R_GlobalEnv>
..$ order.groups: logi TRUE
..$ FUN           :function (x)
..$ outer         : NULL
..$ inner         : NULL
..$ labels        : list()
..$ units         : list()
> ## compare with output 1.7 pp. 24-25
> (fm1PBIB <- lmer(response ~ Treatment + (1 | Block), PBIB))
Linear mixed model fit by REML
Formula: response ~ Treatment + (1 | Block)
Data: PBIB
AIC    BIC logLik deviance REMLdev
85.98 121.6 -25.99    22.83    51.98
Random effects:
Groups   Name             Variance Std.Dev.
Block    (Intercept)  0.046522 0.21569
Residual                    0.085559 0.29250
Number of obs: 60, groups: Block, 15

Fixed effects:
              Estimate Std. Error t value
(Intercept)  2.891309    0.166412  17.374
Treatment1   -0.073788    0.222060  -0.332
Treatment10  -0.400249    0.222060  -1.802
Treatment11   0.007392    0.222060   0.033
Treatment12   0.161514    0.222060   0.727
Treatment13  -0.273542    0.222060  -1.232
Treatment14  -0.400000    0.227200  -1.761
Treatment15  -0.032076    0.222060  -0.144
Treatment2   -0.485995    0.222060  -2.189
Treatment3   -0.436366    0.222060  -1.965
Treatment4   -0.107474    0.227200  -0.473
Treatment5   -0.086411    0.222060  -0.389
Treatment6    0.019385    0.222060   0.087
Treatment7   -0.102323    0.222060  -0.461

```

```
Treatment8 -0.109705 0.222060 -0.494
```

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
```

J SIMS

```
> 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")=<environment: R_GlobalEnv>
..$ 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()
> ## compare to output 7.4, p. 262
> (fmlSIMS <- lmer(Gain ~ Pretot + (Pretot | Class), SIMS))
Linear mixed model fit by REML
Formula: Gain ~ Pretot + (Pretot | Class)
Data: SIMS
AIC    BIC logLik deviance REMLdev
22393 22430 -11190    22373    22381
Random effects:
Groups   Name             Variance Std.Dev. Corr
Class    (Intercept) 14.4894663 3.80650
          Pretot      0.0092027 0.09593 -0.641
Residual                22.2357583 4.71548
Number of obs: 3691, groups: Class, 190

Fixed effects:
              Estimate Std. Error t value
(Intercept)   7.0595     0.3659    19.29
Pretot        -0.1860     0.0161   -11.55

Correlation of Fixed Effects:
      (Intr)
Pretot -0.760

```