lmer for SAS PROC MIXED Users

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1 Introduction

The `lmer` function from the `Matrix` 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 to the `groupedData` 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 $\boldsymbol{y}_i$ for the ith experimental

unit as

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

where $\boldsymbol{\beta}$ is the p-dimensional vector of *fixed effects*, $\boldsymbol{b}_i$ is the q-dimensional vector of *random effects*, $\boldsymbol{X}_i$ (of size $n_i \times p$) and $\boldsymbol{Z}_i$ (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 $\mathrm{Var}(\boldsymbol{\epsilon}_i) = \sigma^2\boldsymbol{I}$ 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 arguments are called `fixed` and `random`.

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 in `lmer`, set the optional argument `method="REML"`.

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 `PROC MIXED` and in `lmer` are different. In `lmer` 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 `lmer`.

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 `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 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 `lmer` 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 a random effects term of `(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 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 `getGroups` 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 trellis graphics is closely integrated with the `nlme` library. The trellis 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]))
```

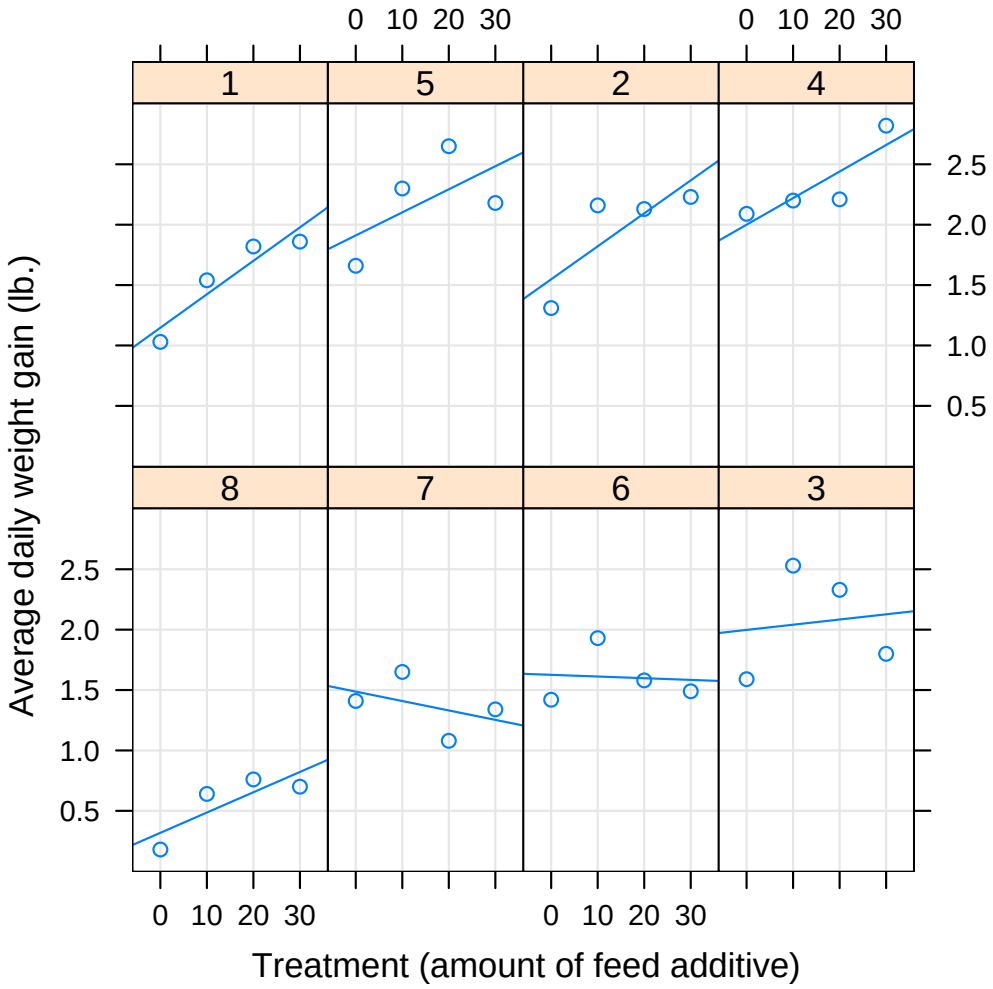

Figure 1: Average daily weight gain

```
> (fm1Adg <- lmer(adg ~ (Treatment - 1) * InitWt + (1 | Block),
+     AvgDailyGain))
Linear mixed-effects model fit by REML
Formula: adg ~ (Treatment - 1) * InitWt + (1 | Block)
   Data: AvgDailyGain
      AIC      BIC    logLik MLdeviance REMLdeviance
 83.32685 96.51847 -32.66342   10.09817     65.32685
Random effects:
 Groups   Name        Variance Std.Dev.
 Block    (Intercept) 0.25930  0.50922
 Residual             0.04943  0.22233
# of obs: 32, groups: Block, 8

Fixed effects:
                     Estimate Std. Error  t value
Treatment0          0.4391279  0.7110925  0.61754
Treatment10         1.4261132  0.6375493  2.23687
Treatment20         0.4796212  0.5488892  0.87380
Treatment30         0.2001150  0.7752039  0.25814
InitWt              0.0044480  0.0020816  2.13680
Treatment0:InitWt  -0.0021543  0.0027863 -0.77318
Treatment10:InitWt -0.0033651  0.0025148 -1.33809
Treatment20:InitWt -0.0010823  0.0024876 -0.43509

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)
Analysis of Variance Table
                Df Sum Sq Mean Sq
Treatment        4 5.7250  1.4313
InitWt           1 0.5495  0.5495
Treatment:InitWt 3 0.1381  0.0460
> (fm2Adg <- lmer(adg ~ InitWt + Treatment + (1 | Block), AvgDailyGain))
```

```
Linear mixed-effects model fit by REML
Formula: adg ~ InitWt + Treatment + (1 | Block)
   Data: AvgDailyGain
      AIC      BIC    logLik MLdeviance REMLdeviance
 48.33733 57.13174 -18.16866   13.62304     36.33733
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 t value
(Intercept)  0.80110753  0.35566101  2.2524
InitWt       0.00277972  0.00083335  3.3356
Treatment0  -0.55207371  0.11481324 -4.8084
Treatment10 -0.06856620  0.11896910 -0.5763
Treatment20 -0.08812918  0.11628794 -0.7579

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
InitWt     1 0.51456 0.51456
Treatment  3 1.52670 0.50890
> (fm3Adg <- lmer(adg ~ InitWt + Treatment - 1 + (1 | Block),
+     AvgDailyGain))
Linear mixed-effects model fit by REML
Formula: adg ~ InitWt + Treatment - 1 + (1 | Block)
   Data: AvgDailyGain
      AIC      BIC    logLik MLdeviance REMLdeviance
 48.33733 57.13174 -18.16866   13.62304     36.33733
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 t value
InitWt      0.00277972 0.00083335  3.3356
Treatment0  0.24903382 0.37763180  0.6595
Treatment10 0.73254134 0.39037982  1.8765
Treatment20 0.71297835 0.38276851  1.8627
Treatment30 0.80110753 0.35566101  2.2524

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)))

> (fm1BIB <- lmer(y ~ Treatment * x + (1 | Block), BIB))
Linear mixed-effects model fit by REML
Formula: y ~ Treatment * x + (1 | Block)
   Data: BIB
      AIC      BIC    logLik MLdeviance REMLdeviance
 122.8945 133.4969 -52.44723    93.4961     104.8945
Random effects:
 Groups   Name        Variance Std.Dev.
 Block    (Intercept) 18.2499  4.2720
 Residual              1.2004  1.0956
# of obs: 24, groups: Block, 8

Fixed effects:
              Estimate Std. Error t value
(Intercept)  22.367841   3.101821  7.2112
Treatment1    4.429491   3.365036  1.3163
```

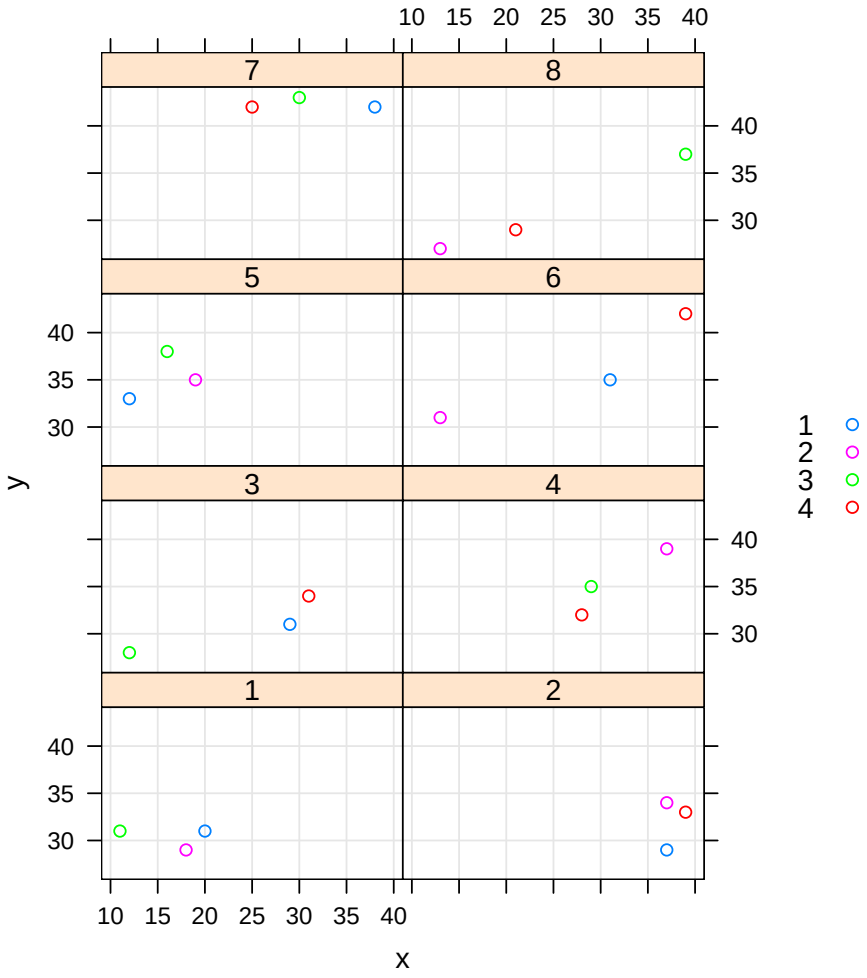

Figure 2: Balanced incomplete block design

```
Treatment2   -0.437367   2.933196 -0.1491
Treatment3    6.278639   3.282027  1.9130
x             0.442548   0.087062  5.0831
Treatment1:x -0.223766   0.106082 -2.1094
Treatment2:x  0.053384   0.097142  0.5495
Treatment3:x -0.179177   0.115709 -1.5485

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
Treatmnt1:x  0.709 -0.979 -0.774 -0.797 -0.799
Treatmnt2:x  0.722 -0.731 -0.965 -0.763 -0.829  0.729
Treatmnt3:x  0.769 -0.789 -0.790 -0.976 -0.879  0.777  0.748
> anova(fm1BIB)
Analysis of Variance Table
            Df  Sum Sq Mean Sq
Treatment    3  23.447   7.816
x            1 136.809 136.809
Treatment:x  3  18.427   6.142
> (fm2BIB <- lmer(y ~ Treatment + x:Grp + (1 | Block), BIB))
Linear mixed-effects model fit by REML
Formula: y ~ Treatment + x:Grp + (1 | Block)
   Data: BIB
      AIC      BIC    logLik MLdeviance REMLdeviance
 113.1770 121.4234 -49.58851   94.08929     99.17702
Random effects:
 Groups   Name        Variance Std.Dev.
 Block    (Intercept) 18.5214  4.3036
 Residual              1.0380  1.0188
# of obs: 24, groups: Block, 8

Fixed effects:
             Estimate Std. Error t value
(Intercept) 20.945232   2.062233 10.1566
Treatment1   5.341392   1.975836  2.7034
Treatment2   1.135550   0.714037  1.5903
Treatment3   8.180984   1.770218  4.6215
```

```
x:Grp13      0.239519   0.042966  5.5746
x:Grp24      0.489228   0.044125 11.0874

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
Treatment  3  23.424   7.808
x:Grp      2 154.733  77.366
```

C Bond

```
> (fm1Bond <- lmer(pressure ~ Metal + (1 | Ingot), Bond))
Linear mixed-effects model fit by REML
Formula: pressure ~ Metal + (1 | Ingot)
   Data: Bond
      AIC      BIC   logLik MLdeviance REMLdeviance
 115.7902 119.9683 -53.8951   115.7074     107.7902
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 t value
(Intercept) 71.10000    1.76552  40.271
Metalc      -0.91429    1.72143  -0.531
Metali       4.80000    1.72143   2.788

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
Metal  2 131.90   65.95
```

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")=length 7 <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 7 <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
> (fm1Cult <- lmer(drywt ~ Inoc * Cult + (1 | Block) + (1 |
+     Cult), Cultivation))
Linear mixed-effects model fit by REML
Formula: drywt ~ Inoc * Cult + (1 | Block) + (1 | Cult)
   Data: Cultivation
      AIC      BIC    logLik MLdeviance REMLdeviance
```

```
 84.48742 93.91185 -34.24371   76.69963     68.48742
Random effects:
 Groups   Name        Variance Std.Dev.
 Block    (Intercept) 1.2073   1.0988
 Cult     (Intercept) 1.0634   1.0312
 Residual             1.1963   1.0938
# of obs: 24, groups: Block, 4; Cult, 2

Fixed effects:
             Estimate Std. Error t value
(Intercept)   33.52500    1.29008 25.9867
Inoccon       -5.50000    0.77341 -7.1113
Inocdea       -2.87500    0.77341 -3.7173
Culta         -0.37500    1.65075 -0.2272
Inoccon:Culta  0.25000    1.09377  0.2286
Inocdea:Culta -1.02500    1.09377 -0.9371

Correlation of Fixed Effects:
            (Intr) Inoccn Inocde Culta  Incc:C
Inoccon     -0.300
Inocdea     -0.300  0.500
Culta       -0.640  0.234  0.234
Inoccon:Clt  0.212 -0.707 -0.354 -0.331
Inocdea:Clt  0.212 -0.354 -0.707 -0.331  0.500
> anova(fm1Cult)
Analysis of Variance Table
          Df  Sum Sq Mean Sq
Inoc       2 118.176  59.088
Cult       1   0.206   0.206
Inoc:Cult  2   1.826   0.913
> (fm2Cult <- lmer(drywt ~ Inoc + Cult + (1 | Block) + (1 |
+     Cult), Cultivation))
Linear mixed-effects model fit by REML
Formula: drywt ~ Inoc + Cult + (1 | Block) + (1 | Cult)
   Data: Cultivation
      AIC     BIC    logLik MLdeviance REMLdeviance
 85.75348 92.8218 -36.87674   78.64603     73.75348
Random effects:
 Groups   Name        Variance Std.Dev.
 Block    (Intercept) 1.2128   1.1013
```

```
 Cult     (Intercept) 1.0338   1.0167
 Residual             1.1630   1.0784
# of obs: 24, groups: Block, 4; Cult, 2

Fixed effects:
            Estimate Std. Error t value
(Intercept) 33.65417    1.23726 27.2006
Inoccon     -5.37500    0.53921 -9.9683
Inocdea     -3.38750    0.53921 -6.2823
Culta       -0.63333    1.50379 -0.4212

Correlation of Fixed Effects:
        (Intr) Inoccn Inocde
Inoccon -0.218
Inocdea -0.218  0.500
Culta   -0.608  0.000  0.000
> anova(fm2Cult)
Analysis of Variance Table
     Df  Sum Sq Mean Sq
Inoc  2 118.176  59.088
Cult  1   0.206   0.206
> (fm3Cult <- lmer(drywt ~ Inoc + (1 | Block) + (1 | Cult),
+     Cultivation))
Linear mixed-effects model fit by REML
Formula: drywt ~ Inoc + (1 | Block) + (1 | Cult)
   Data: Cultivation
      AIC     BIC    logLik MLdeviance REMLdeviance
 85.67784 91.5681 -37.83892   77.32082     75.67784
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 t value
(Intercept) 33.33750    0.70739  47.127
Inoccon     -5.37500    0.53921  -9.968
Inocdea     -3.38750    0.53921  -6.282
```

```
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
Inoc  2 118.176  59.088
```

E Demand

```
> (fm1Demand <- lmer(log(d) ~ log(y) + log(rd) + log(rt) +
+     log(rs) + (1 | State) + (1 | Year), Demand))
Linear mixed-effects model fit by REML
Formula: log(d) ~ log(y) + log(rd) + log(rt) + log(rs) + (1 | State) +      (
   Data: Demand
       AIC       BIC   logLik MLdeviance REMLdeviance
 -226.1653 -209.7586 120.0826  -260.5211    -240.1653
Random effects:
 Groups   Name        Variance   Std.Dev.
 Year     (Intercept) 0.00026466 0.016268
 State    (Intercept) 0.02950854 0.171781
 Residual             0.00111697 0.033421
# of obs: 77, groups: Year, 11; State, 7

Fixed effects:
             Estimate Std. Error t value
(Intercept) -1.283775   0.723437 -1.7745
log(y)       1.069773   0.103926 10.2936
log(rd)     -0.295322   0.052464 -5.6291
log(rt)      0.039880   0.027888  1.4300
log(rs)     -0.326733   0.114383 -2.8565

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

```
> (fm1HR <- lmer(HR ~ Time * Drug + baseHR + (Time | Patient),
+     HR))
Linear mixed-effects model fit by REML
Formula: HR ~ Time * Drug + baseHR + (Time | Patient)
   Data: HR
     AIC     BIC    logLik MLdeviance REMLdeviance
 787.607 815.482 -383.8035   788.1223      767.607
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
# of obs: 120, groups: Patient, 24

Fixed effects:
            Estimate Std. Error t value
(Intercept) 33.97762   10.28298  3.3043
Time        -3.19704    3.08493 -1.0363
Druga        3.59919    4.23138  0.8506
Drugb        7.09122    4.20941  1.6846
baseHR       0.54343    0.11615  4.6787
Time:Druga  -7.50131    4.36275 -1.7194
Time:Drugb  -3.98942    4.36275 -0.9144

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
Time       1 379.22  379.22
Drug       2  92.88   46.44
baseHR     1 533.27  533.27
Time:Drug  2  72.12   36.06
```

```
> (fm3HR <- lmer(HR ~ Time + Drug + baseHR + (Time | Patient),
+     HR))
Linear mixed-effects model fit by REML
Formula: HR ~ Time + Drug + baseHR + (Time | Patient)
   Data: HR
      AIC      BIC    logLik MLdeviance REMLdeviance
 795.8283 818.1283 -389.9142   791.2093     779.8283
Random effects:
 Groups   Name        Variance Std.Dev. Corr
 Patient  (Intercept) 61.560   7.8460
          Time        40.964   6.4003   -0.571
 Residual             24.361   4.9357
# of obs: 120, groups: Patient, 24

Fixed effects:
            Estimate Std. Error t value
(Intercept) 36.04657   10.19444  3.5359
Time        -7.02729    1.81789 -3.8656
Druga       -0.45243    3.51454 -0.1287
Drugb        4.93646    3.48805  1.4152
baseHR       0.54342    0.11615  4.6787

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  0.050
> anova(fm3HR)
Analysis of Variance Table
       Df Sum Sq Mean Sq
Time    1 364.02  364.02
Drug    2  92.88   46.44
baseHR  1 533.27  533.27
> (fm4HR <- lmer(HR ~ Time + baseHR + (Time | Patient), HR))
Linear mixed-effects model fit by REML
Formula: HR ~ Time + baseHR + (Time | Patient)
   Data: HR
      AIC     BIC    logLik MLdeviance REMLdeviance
 803.1481 819.873 -395.5740   794.2834     791.1481
```

```
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
# of obs: 120, groups: Patient, 24

Fixed effects:
            Estimate Std. Error t value
(Intercept) 36.93139    9.90143  3.7299
Time        -7.02729    1.81789 -3.8656
baseHR       0.55078    0.11754  4.6857

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
Time    1 364.02  364.02
baseHR  1 534.87  534.87
```

G Mississippi

```
> (fm1Miss <- lmer(y ~ 1 + (1 | influent), Mississippi))
Linear mixed-effects model fit by REML
Formula: y ~ 1 + (1 | influent)
   Data: Mississippi
      AIC     BIC    logLik MLdeviance REMLdeviance
 256.3511 259.573 -126.1756   256.6398     252.3511
Random effects:
 Groups   Name        Variance Std.Dev.
 influent (Intercept) 63.324   7.9576
 Residual             42.658   6.5313
# of obs: 37, groups: influent, 6

Fixed effects:
            Estimate Std. Error t value
(Intercept)   21.223      3.429  6.1892
```

```
> (fm1MLMiss <- lmer(y ~ 1 + (1 | influent), Mississippi, method = "ML"))
Linear mixed-effects model fit by maximum likelihood
Formula: y ~ 1 + (1 | influent)
   Data: Mississippi
     AIC      BIC    logLik MLdeviance REMLdeviance
 260.557 263.7788 -128.2785    256.557     252.4286
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 t value
(Intercept)   21.217      3.122   6.796
> ranef(fm1MLMiss)
An object of class "lmer.ranef"
[[1]]
  (Intercept)
1   0.3097833
2  -6.5772271
3  -3.7862742
4   2.8826708
5  -5.8435201
6  13.0145672
> ranef(fm1Miss)
An object of class "lmer.ranef"
[[1]]
  (Intercept)
1    0.309286
2   -6.719335
3   -3.897948
4    2.946106
5   -6.012988
6   13.374879
> VarCorr(fm1Miss)
$influent
1 x 1 Matrix of class "dpoMatrix"
            (Intercept)
(Intercept)    63.32364

attr(,"sc")
[1] 6.531315
```

```
> (fm2Miss <- lmer(y ~ Type + (1 | influent), Mississippi))
Linear mixed-effects model fit by REML
Formula: y ~ Type + (1 | influent)
   Data: Mississippi
      AIC      BIC    logLik MLdeviance REMLdeviance
 242.5246 248.9683 -117.2623   247.4686     234.5246
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 t value
(Intercept)  36.4000     4.8449  7.5131
Type1       -20.8000     5.9338 -3.5054
Type2       -16.4619     5.5168 -2.9840

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
Type  2 541.76  270.88
```

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  7.10 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 17 <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 17 <environment>
  ..$ labels      :List of 1
  .. ..$ Adj: chr "Adjusted yield"
  ..$ units       : list()
> Multilocation$Grp <- with(Multilocation, Block:Location)
> (fm1Mult <- lmer(Adj ~ Location * Trt + (1 | Grp), Multilocation))
Linear mixed-effects model fit by REML
Formula: Adj ~ Location * Trt + (1 | Grp)
   Data: Multilocation
      AIC      BIC    logLik MLdeviance REMLdeviance
 84.64621 183.8851 -5.323106  -87.14598     10.64621
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 t value
(Intercept)     2.359233   0.115755 20.3812
LocationA       0.649300   0.163703  3.9663
LocationB       0.066433   0.163703  0.4058
LocationC       0.545333   0.163703  3.3312
LocationD       0.374133   0.163703  2.2854
LocationE       0.550000   0.163703  3.3597
LocationF       0.998100   0.163703  6.0970
LocationG       0.360567   0.163703  2.2026
LocationH       1.014033   0.163703  6.1943
Trt1            0.227200   0.151830  1.4964
Trt2           -0.001400   0.151830 -0.0092
Trt3            0.423233   0.151830  2.7875
LocationA:Trt1 -0.188533   0.214721 -0.8780
```

```
LocationB:Trt1 -0.275233   0.214721 -1.2818
LocationC:Trt1 -0.040000   0.214721 -0.1863
LocationD:Trt1 -0.535133   0.214721 -2.4922
LocationE:Trt1 -0.262967   0.214721 -1.2247
LocationF:Trt1 -0.271533   0.214721 -1.2646
LocationG:Trt1  0.203233   0.214721  0.9465
LocationH:Trt1 -0.149533   0.214721 -0.6964
LocationA:Trt2 -0.093467   0.214721 -0.4353
LocationB:Trt2 -0.322733   0.214721 -1.5030
LocationC:Trt2  0.089600   0.214721  0.4173
LocationD:Trt2 -0.296933   0.214721 -1.3829
LocationE:Trt2 -0.306933   0.214721 -1.4295
LocationF:Trt2 -0.309933   0.214721 -1.4434
LocationG:Trt2 -0.108600   0.214721 -0.5058
LocationH:Trt2 -0.330600   0.214721 -1.5397
LocationA:Trt3 -0.402467   0.214721 -1.8744
LocationB:Trt3 -0.565500   0.214721 -2.6337
LocationC:Trt3 -0.122467   0.214721 -0.5704
LocationD:Trt3 -0.548400   0.214721 -2.5540
LocationE:Trt3 -0.328633   0.214721 -1.5305
LocationF:Trt3 -0.462567   0.214721 -2.1543
LocationG:Trt3 -0.252967   0.214721 -1.1781
LocationH:Trt3 -0.372033   0.214721 -1.7326

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
Location      8 6.9475  0.8684
Trt           3 1.2217  0.4072
Location:Trt 24 0.9966  0.0415
> (fm2Mult <- lmer(Adj ~ Location + Trt + (1 | Grp), Multilocation))
Linear mixed-effects model fit by REML
Formula: Adj ~ Location + Trt + (1 | Grp)
   Data: Multilocation
      AIC      BIC   logLik MLdeviance REMLdeviance
 19.99894 54.86664 3.000531  -51.21968    -6.001063
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 t value
(Intercept)  2.532965   0.075990  33.333
LocationA    0.478183   0.097516   4.904
LocationB   -0.224433   0.097516  -2.302
LocationC    0.527117   0.097516   5.405
LocationD    0.029017   0.097516   0.298
LocationE    0.325367   0.097516   3.337
LocationF    0.737092   0.097516   7.559
LocationG    0.320983   0.097516   3.292
LocationH    0.800992   0.097516   8.214
Trt1         0.058344   0.052150   1.119
Trt2        -0.188022   0.052150  -3.605
```

```
Trt3         0.083785   0.052150   1.607

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
> (fm3Mult <- lmer(Adj ~ Location + (1 | Grp), Multilocation))
Linear mixed-effects model fit by REML
Formula: Adj ~ Location + (1 | Grp)
   Data: Multilocation
      AIC     BIC    logLik MLdeviance REMLdeviance
 29.82048 56.6418 -4.910242  -22.17353     9.820484
Random effects:
 Groups   Name        Variance  Std.Dev.
 Grp      (Intercept) 0.0016543 0.040673
 Residual             0.0504389 0.224586
# of obs: 108, groups: Grp, 27

Fixed effects:
```

```
             Estimate Std. Error t value
(Intercept)  2.521492   0.068954  36.568
LocationA    0.478183   0.097516   4.904
LocationB   -0.224433   0.097516  -2.302
LocationC    0.527117   0.097516   5.405
LocationD    0.029017   0.097516   0.298
LocationE    0.325367   0.097516   3.337
LocationF    0.737092   0.097516   7.559
LocationG    0.320983   0.097516   3.292
LocationH    0.800992   0.097516   8.214

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-effects model fit by REML
Formula: Adj ~ Trt + (1 | Grp)
   Data: Multilocation
      AIC      BIC    logLik MLdeviance REMLdeviance
 41.50571 54.91636 -15.75285   14.95111     31.50571
Random effects:
 Groups   Name        Variance Std.Dev.
 Grp      (Intercept) 0.110923 0.33305
 Residual             0.036715 0.19161
# of obs: 108, groups: Grp, 27

Fixed effects:
             Estimate Std. Error t value
(Intercept)  2.865667   0.073946  38.753
Trt1         0.058344   0.052150   1.119
Trt2        -0.188022   0.052150  -3.605
Trt3         0.083785   0.052150   1.607
```

```
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-effects model fit by REML
Formula: Adj ~ 1 + (1 | Grp)
   Data: Multilocation
      AIC      BIC    logLik MLdeviance REMLdeviance
 51.32725 56.69152 -23.66363   43.74521     47.32725
Random effects:
 Groups   Name        Variance Std.Dev.
 Grp      (Intercept) 0.107491 0.32786
 Residual             0.050439 0.22459
# of obs: 108, groups: Grp, 27

Fixed effects:
            Estimate Std. Error t value
(Intercept) 2.854194   0.066695  42.795
> anova(fm2Mult)
Analysis of Variance Table
         Df Sum Sq Mean Sq
Location  8 7.3768  0.9221
Trt       3 1.2217  0.4072
> (fm2MultR <- lmer(Adj ~ Trt + (Trt - 1 | Location) + (1 |
+     Block), Multilocation, control = list(msV = 1, niterEM = 200)))
  0      1.47880: 0.0372320 0.00596830 0.337426  3.04245 0.459977 -1.51310 0.
  1      1.41586: 0.0199035 5.00000e-10 0.337337  3.04245 0.459785 -1.51364 0
  2      1.41586: 0.0199035 5.00000e-10 0.337337  3.04245 0.459785 -1.51364 0
Linear mixed-effects model fit by REML
Formula: Adj ~ Trt + (Trt - 1 | Location) + (1 | Block)
   Data: Multilocation
      AIC      BIC    logLik MLdeviance REMLdeviance
 31.41586 71.64783 -0.707931  -13.34759     1.415862
Random effects:
 Groups   Name        Variance   Std.Dev.   Corr
 Location Trt1        1.3633e-01 3.6923e-01
          Trt2        1.0750e-01 3.2787e-01 0.989
          Trt3        1.1977e-01 3.4608e-01 0.996 0.996
```

```
          Trt4        1.1464e-01 3.3858e-01 0.929 0.970 0.945
 Block    (Intercept) 1.8840e-11 4.3405e-06
 Residual             3.7680e-02 1.9411e-01
# of obs: 108, groups: Location, 9; Block, 3

Fixed effects:
             Estimate Std. Error t value
(Intercept)  2.865667   0.118883 24.1049
Trt1         0.058344   0.069802  0.8359
Trt2        -0.188022   0.059525 -3.1587
Trt3         0.083785   0.064945  1.2901

Correlation of Fixed Effects:
     (Intr) Trt1   Trt2
Trt1 -0.148
Trt2 -0.306  0.619
Trt3 -0.236  0.677  0.626
```

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")=length 24 <environment>
  ..$ order.groups: logi TRUE
  ..$ FUN         :function (x)
  ..$ outer       : NULL
  ..$ inner       : NULL
  ..$ labels      : list()
  ..$ units       : list()
> (fm1PBIB <- lmer(response ~ Treatment + (1 | Block), PBIB))
Linear mixed-effects model fit by REML
Formula: response ~ Treatment + (1 | Block)
   Data: PBIB
     AIC      BIC    logLik MLdeviance REMLdeviance
 83.9849 117.4944 -25.99245   22.82831     51.98489
```

```
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 t value
(Intercept)  2.8913111  0.1664127 17.3743
Treatment1  -0.0737886  0.2220608 -0.3323
Treatment10 -0.4002495  0.2220608 -1.8024
Treatment11  0.0073879  0.2220608  0.0333
Treatment12  0.1615103  0.2220608  0.7273
Treatment13 -0.2735419  0.2220608 -1.2318
Treatment14 -0.4000000  0.2272003 -1.7606
Treatment15 -0.0320781  0.2220608 -0.1445
Treatment2  -0.4859962  0.2220608 -2.1886
Treatment3  -0.4363680  0.2220608 -1.9651
Treatment4  -0.1074807  0.2272003 -0.4731
Treatment5  -0.0864131  0.2220608 -0.3891
Treatment6   0.0193828  0.2220608  0.0873
Treatment7  -0.1023261  0.2220608 -0.4608
Treatment8  -0.1097056  0.2220608 -0.4940

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")=length 25 <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()
> (fm1SIMS <- lmer(Gain ~ Pretot + (Pretot | Class), SIMS))
Linear mixed-effects model fit by REML
Formula: Gain ~ Pretot + (Pretot | Class)
   Data: SIMS
      AIC      BIC    logLik MLdeviance REMLdeviance
 22390.57 22421.64 -11190.29   22373.12     22380.57
```

```
Random effects:
 Groups   Name        Variance   Std.Dev. Corr
 Class    (Intercept) 14.4895421 3.806513
          Pretot       0.0092029 0.095932 -0.641
 Residual             22.2357533 4.715480
# of obs: 3691, groups: Class, 190

Fixed effects:
             Estimate Std. Error t value
(Intercept)  7.059609   0.365898  19.294
Pretot      -0.186032   0.016098 -11.556

Correlation of Fixed Effects:
       (Intr)
Pretot -0.760
```