

# **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  $\mathbf{y}_i$  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 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]))
```

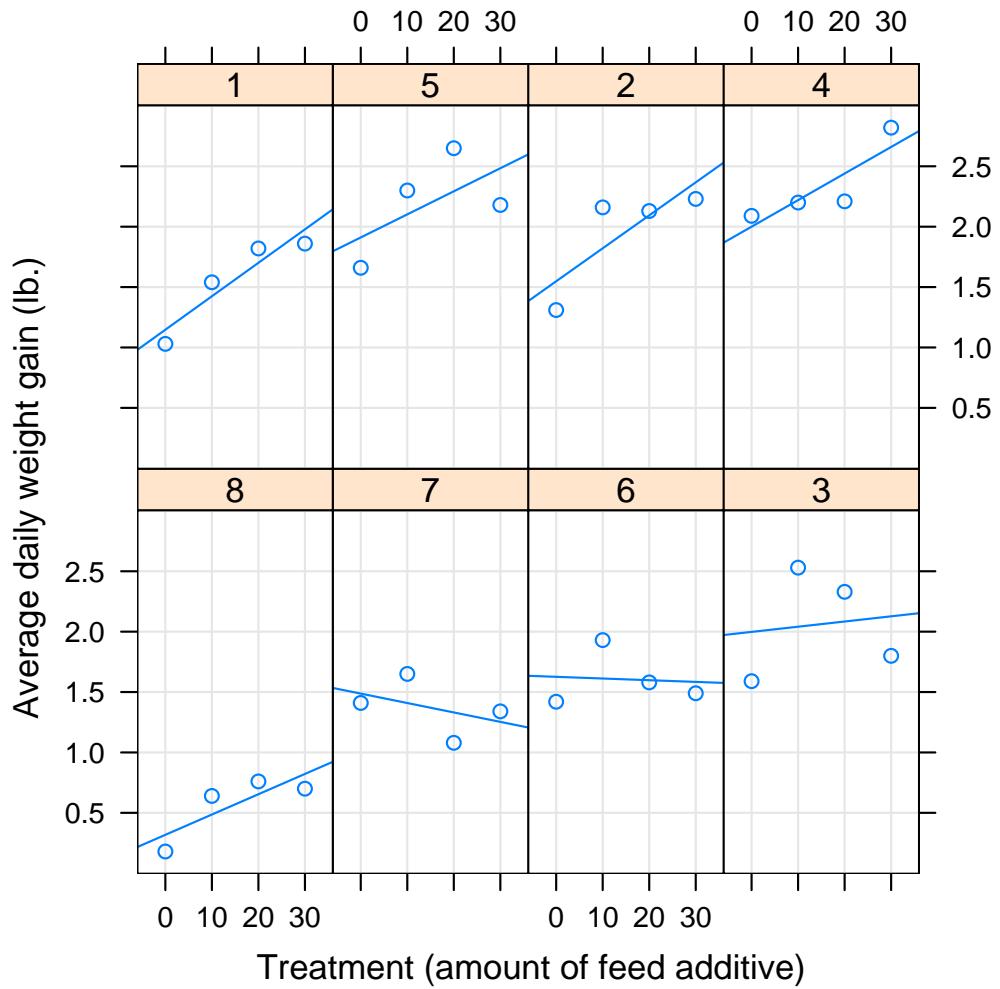


Figure 1: Average daily weight gain

```

> (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
83.33 96.52 -32.66      10.10      65.33
Random effects:
Groups   Name        Variance Std.Dev.
Block    (Intercept) 0.25930  0.50922
Residual           0.04943  0.22233
number of obs: 32, groups: Block, 8

Fixed effects:
            Estimate Std. Error t value
Treatment0     0.439128  0.711092  0.6175
Treatment10    1.426113  0.637549  2.2369
Treatment20    0.479621  0.548889  0.8738
Treatment30    0.200115  0.775204  0.2581
InitWt         0.004448  0.002082  2.1368
Treatment0:InitWt -0.002154  0.002786 -0.7732
Treatment10:InitWt -0.003365  0.002515 -1.3381
Treatment20:InitWt -0.001082  0.002488 -0.4351

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
48.34 57.13 -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) 0.8011075 0.3556610 2.252
InitWt       0.0027797 0.0008334 3.336
Treatment0  -0.5520737 0.1148132 -4.808
Treatment10 -0.0685662 0.1189691 -0.576
Treatment20 -0.0881292 0.1162879 -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
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
48.34 57.13 -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	0.2490338	0.3776318	0.659
Treatment10	0.7325413	0.3903798	1.876
Treatment20	0.7129784	0.3827685	1.863
Treatment30	0.8011075	0.3556610	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)))

> (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
122.9 133.5 -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) 22.36784   3.10182  7.211
Treatment1   4.42949   3.36504  1.316
```

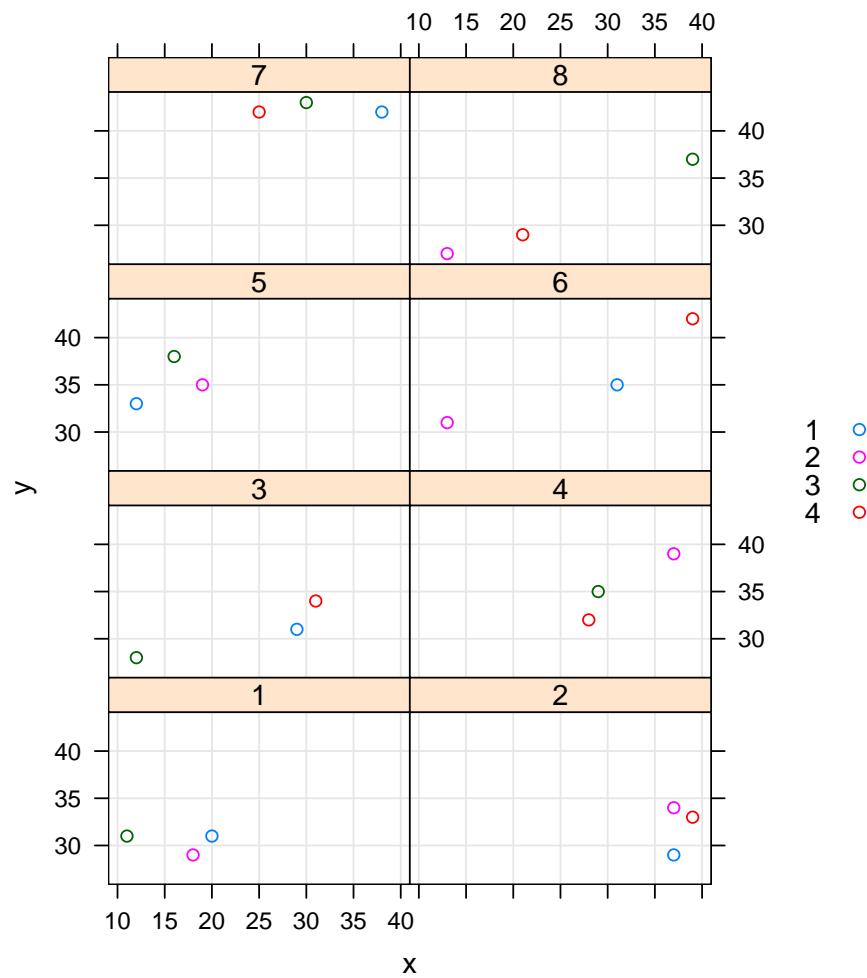


Figure 2: Balanced incomplete block design

```

Treatment2    -0.43737    2.93320   -0.149
Treatment3     6.27864    3.28203    1.913
x             0.44255    0.08706    5.083
Treatment1:x -0.22377    0.10608   -2.109
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)
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
113.2 121.4 -49.59      94.09      99.18
Random effects:
Groups   Name        Variance Std.Dev.
Block    (Intercept) 18.5214  4.3036
Residual           1.0380  1.0188
number of obs: 24, groups: Block, 8

Fixed effects:
  Estimate Std. Error t value
(Intercept) 20.94523   2.06223 10.157
Treatment1   5.34139   1.97584  2.703
Treatment2   1.13555   0.71404  1.590
Treatment3   8.18098   1.77022  4.621

```

```

x:Grp13      0.23952    0.04297   5.575
x:Grp24      0.48923    0.04412  11.087

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
115.8 120.0 -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
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

```

```

84.49 93.91 -34.24      76.7      68.49
Random effects:
Groups   Name        Variance Std.Dev.
Block    (Intercept) 1.2073   1.0988
Cult     (Intercept) 1.0634   1.0312
Residual           1.1963   1.0938
number of obs: 24, groups: Block, 4; Cult, 2

Fixed effects:
            Estimate Std. Error t value
(Intercept) 33.5250   1.2901 25.987
Inoccon     -5.5000   0.7734 -7.111
Inocdea     -2.8750   0.7734 -3.717
Culta       -0.3750   1.6508 -0.227
Inoccon:Culta 0.2500   1.0938  0.229
Inocdea:Culta -1.0250   1.0938 -0.937

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
85.75 92.82 -36.88      78.65      73.75
Random effects:
Groups   Name        Variance Std.Dev.
Block    (Intercept) 1.2128   1.1013

```

```

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

```

**Fixed effects:**

	Estimate	Std. Error	t value
(Intercept)	33.6542	1.2373	27.201
Inoccon	-5.3750	0.5392	-9.968
Inocdea	-3.3875	0.5392	-6.282
Culta	-0.6333	1.5038	-0.421

**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
85.68	91.57	-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
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
-226.2 -209.8 120.1     -260.5       -240.2
Random effects:
Groups   Name        Variance Std.Dev.
Year     (Intercept) 0.00026466 0.016268
State    (Intercept) 0.02950854 0.171781
Residual           0.00111697 0.033421
number of obs: 77, groups: Year, 11; State, 7

Fixed effects:
            Estimate Std. Error t value
(Intercept) -1.28377  0.72344 -1.775
log(y)       1.06977  0.10393 10.294
log(rd)      -0.29532  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

```
> (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
787.6 815.5 -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) 33.9776   10.2830   3.304
Time        -3.1970    3.0849  -1.036
Druga        3.5992    4.2314   0.851
Drugb        7.0912    4.2094   1.685
baseHR       0.5434    0.1161   4.679
Time:Druga   -7.5013    4.3627  -1.719
Time:Drugb   -3.9894    4.3627  -0.914

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        1 379.23 379.23
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
795.8  818.1 -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  -0.570
Residual            24.361   4.9357
number of obs: 120, groups: Patient, 24

Fixed effects:
              Estimate Std. Error t value
(Intercept)  36.0464   10.1945   3.536
Time         -7.0273    1.8179  -3.866
Druga        -0.4524    3.5146  -0.129
Drugb         4.9365    3.4881   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  0.050
> anova(fm3HR)

Analysis of Variance Table
  Df Sum Sq Mean Sq
Time   1 364.03 364.03
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
803.1  819.9 -395.6      794.3        791.1

```

```

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

```

```

Fixed effects:
          Estimate Std. Error t value
(Intercept) 36.9314    9.9014   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
Time      1 364.03 364.03
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
256.4 259.6 -126.2      256.6      252.4
Random effects:
Groups   Name      Variance Std.Dev.
influent (Intercept) 63.324   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   6.189

```

```

> (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
 260.6 263.8 -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(fm1MLMiss)
An object of class "ranef.lmer"
[[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 "ranef.lmer"
[[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
242.5 249.0 -117.3      247.5      234.5
Random effects:
Groups   Name        Variance Std.Dev.
influent (Intercept) 14.970   3.8691
Residual            42.514   6.5202
number of obs: 37, groups: influent, 6

Fixed effects:
            Estimate Std. Error t value
(Intercept) 36.400     4.845    7.513
Type1       -20.800    5.934   -3.505
Type2       -16.462    5.517   -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
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
84.65 183.9 -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	-0.328
LoctnE:Trt1	0.464	-0.328	-0.328	-0.328	-0.328	-0.656	-0.328	-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	-0.328
LoctnG:Trt1	0.464	-0.328	-0.328	-0.328	-0.328	-0.328	-0.328	-0.656	-0.328	-0.328
LoctnH:Trt1	0.464	-0.328	-0.328	-0.328	-0.328	-0.328	-0.328	-0.328	-0.656	-0.328
LoctnA:Trt2	0.464	-0.656	-0.328	-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	-0.328
LoctnC:Trt2	0.464	-0.328	-0.328	-0.656	-0.328	-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	-0.328
LoctnE:Trt2	0.464	-0.328	-0.328	-0.328	-0.328	-0.656	-0.328	-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	-0.328
LoctnG:Trt2	0.464	-0.328	-0.328	-0.328	-0.328	-0.328	-0.328	-0.656	-0.328	-0.328
LoctnH:Trt2	0.464	-0.328	-0.328	-0.328	-0.328	-0.328	-0.328	-0.328	-0.656	-0.328
LoctnA:Trt3	0.464	-0.656	-0.328	-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	-0.328
LoctnC:Trt3	0.464	-0.328	-0.328	-0.656	-0.328	-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	-0.328
LoctnE:Trt3	0.464	-0.328	-0.328	-0.328	-0.328	-0.656	-0.328	-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	-0.328
LoctnG:Trt3	0.464	-0.328	-0.328	-0.328	-0.328	-0.328	-0.328	-0.656	-0.328	-0.328
LoctnH:Trt3	0.464	-0.328	-0.328	-0.328	-0.328	-0.328	-0.328	-0.328	-0.656	-0.328
	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	0.500	0.500
LoctnA:Trt2	-0.354	-0.707	-0.354	0.500	0.250	0.250	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	0.250	0.250
LoctnC:Trt2	-0.354	-0.707	-0.354	0.250	0.250	0.500	0.250	0.250	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	0.250	0.250
LoctnE:Trt2	-0.354	-0.707	-0.354	0.250	0.250	0.250	0.250	0.500	0.250	0.250	0.250
LoctnF:Trt2	-0.354	-0.707	-0.354	0.250	0.250	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	0.250	0.250
LoctnH:Trt2	-0.354	-0.707	-0.354	0.250	0.250	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	0.250	0.250
LoctnB:Trt3	-0.354	-0.354	-0.707	0.250	0.500	0.250	0.250	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	0.250	0.250
LoctnD:Trt3	-0.354	-0.354	-0.707	0.250	0.250	0.250	0.500	0.250	0.250	0.250	0.250
LoctnE:Trt3	-0.354	-0.354	-0.707	0.250	0.250	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	0.250	0.250	0.500
LoctnG:Trt3	-0.354	-0.354	-0.707	0.250	0.250	0.250	0.250	0.250	0.250	0.250	0.250
LoctnH:Trt3	-0.354	-0.354	-0.707	0.250	0.250	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
 20 54.87 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        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
 29.82 56.64 -4.91     -22.17       9.82
Random effects:
Groups   Name        Variance Std.Dev.
Grp     (Intercept) 0.0016543 0.040673
Residual           0.0504389 0.224586
number of obs: 108, groups: Grp, 27

Fixed effects:
```

	Estimate	Std. Error	t value
(Intercept)	2.52149	0.06895	36.57
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

#### 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
41.51	54.92	-15.75	14.95	31.51

#### Random effects:

Groups	Name	Variance	Std.Dev.
Grp	(Intercept)	0.110923	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-effects model fit by REML
Formula: Adj ~ 1 + (1 | Grp)
Data: Multilocation
      AIC    BIC logLik MLdeviance REMLdeviance
 51.33 56.69 -23.66       43.75       47.33

Random effects:
 Groups   Name        Variance Std.Dev.
 Grp     (Intercept) 0.107491  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   42.79

> 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      58.1951: 0.888889 0.888889 0.888889 0.888889  0.00000  0.00000  0.00
  1      24.0707: 1.03246 0.969626 0.994050 0.990267 -0.406756 -0.437447 -0.
  2      15.9680: 0.884835 0.815370 1.10073 1.41171 -0.341165 -0.401696 -0.
  3      15.4463: 0.977776 0.604681 0.969811 1.58336 0.0457936 -0.0495801 -1.
  4      15.4463: 0.977776 0.604681 0.969811 1.58336 0.0457936 -0.0495801 -1.
  5      15.4463: 0.977776 0.604681 0.969811 1.58336 0.0457936 -0.0495801 -1.

Linear mixed-effects model fit by REML
Formula: Adj ~ Trt + (Trt - 1 | Location) + (1 | Block)
Data: Multilocation
      AIC    BIC logLik MLdeviance REMLdeviance
 45.45 85.68 -7.723       2.553       15.45

Random effects:
 Groups   Name        Variance Std.Dev. Corr

```

```

Location Trt1      1.4556e-01 3.8152e-01
          Trt2      7.6956e-02 2.7741e-01 0.716
          Trt3      1.0610e-01 3.2574e-01 0.719 0.653
          Trt4      5.8897e-02 2.4269e-01 0.866 0.840 0.812
Block     (Intercept) 1.8599e-11 4.3126e-06
Residual            3.7197e-02 1.9287e-01
number of obs: 108, groups: Location, 9; Block, 3

```

**Fixed effects:**

	Estimate	Std. Error	t value
(Intercept)	2.86567	0.08900	32.20
Trt1	0.05834	0.08755	0.67
Trt2	-0.18802	0.07271	-2.59
Trt3	0.08379	0.08257	1.01

**Correlation of Fixed Effects:**

	(Intr)	Trt1	Trt2
Trt1	0.126		
Trt2	-0.253	0.181	
Trt3	-0.107	0.249	0.177

## 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()
> (fmlPBIB <- 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
 83.98  117.5 -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) 2.891311  0.166413 17.374
Treatment1  -0.073789  0.222061 -0.332
Treatment10 -0.400249  0.222061 -1.802
Treatment11  0.007388  0.222061  0.033
Treatment12  0.161510  0.222061  0.727
Treatment13 -0.273542  0.222061 -1.232
Treatment14 -0.400000  0.227200 -1.761
Treatment15 -0.032078  0.222061 -0.144
Treatment2  -0.485996  0.222061 -2.189
Treatment3  -0.436368  0.222061 -1.965
Treatment4  -0.107481  0.227200 -0.473
Treatment5  -0.086413  0.222061 -0.389
Treatment6   0.019383  0.222061  0.087
Treatment7  -0.102326  0.222061 -0.461
Treatment8  -0.109706  0.222061 -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 0.500 0.512 0.500 0.500
Treatment7 -0.667 0.500 0.500 0.500 0.477 0.500 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 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
22391 22422 -11190      22373      22381
Random effects:
Groups   Name        Variance Std.Dev. Corr
Class    (Intercept) 14.4894933 3.806507
          Pretot       0.0092028 0.095931 -0.641
Residual           22.2357557 4.715480
number of obs: 3691, groups: Class, 190

Fixed effects:
            Estimate Std. Error t value
(Intercept)  7.0596    0.3659   19.29
Pretot       -0.1860   0.0161  -11.56

Correlation of Fixed Effects:
  (Intr)
Pretot -0.760

```