

# **lmer for SAS PROC MIXED Users**

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## **1 Introduction**

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

A file on the SAS Institute web site (<http://www.sas.com>) contains all the data sets in the book and all the SAS programs used in Littell et al. (1996). We have converted the data sets from the tabular representation used for SAS PROC MIXED to the `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")=<R_GlobalEnv>
 ..$ order.groups:List of 2
 .. ..$ Sire: logi TRUE
 .. ..$ Dam : logi TRUE
 ..$ FUN          :function (x)
 ..$ outer        : NULL
 ..$ inner        : NULL
 ..$ labels       :List of 1
 .. ..$ AvgDailyGain: chr "Average Daily Weight Gain"
 ..$ units        : list()
```

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]))
```

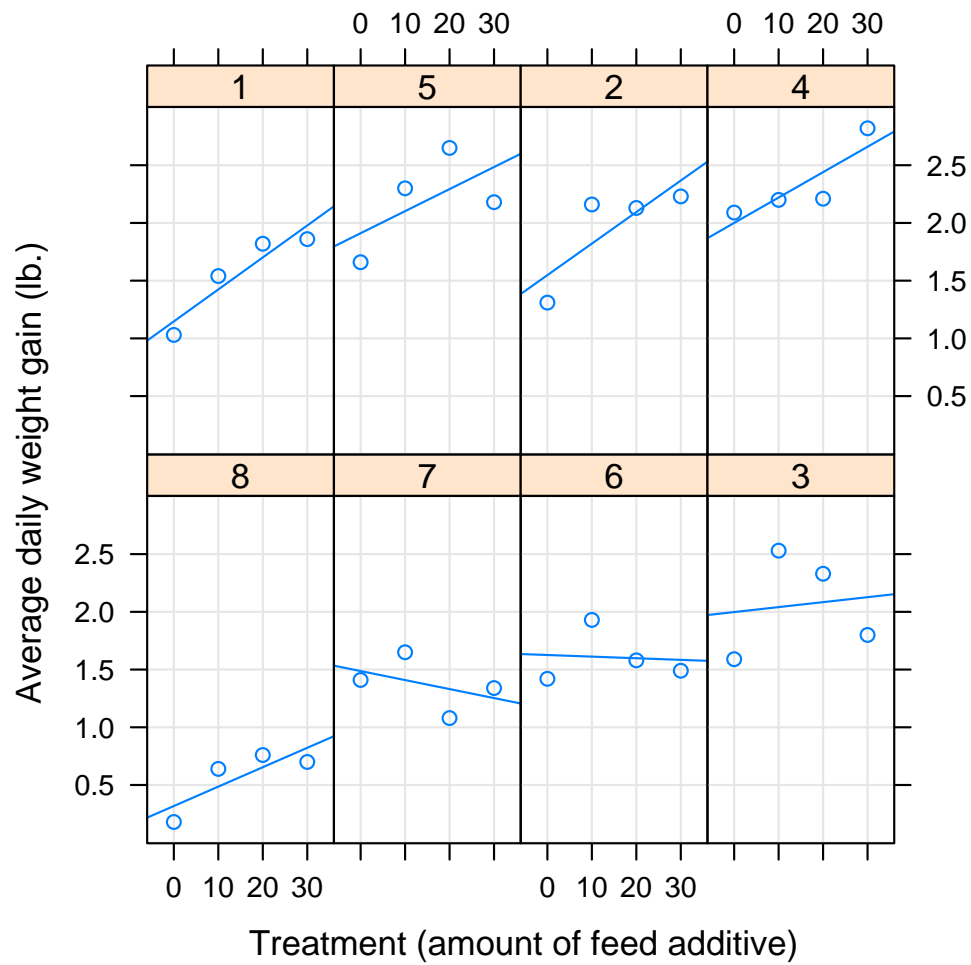


Figure 1: Average daily weight gain

```

> (fmlAdg <- lmer(adg ~ (Treatment - 1) * InitWt + (1 | Block),
+   AvgDailyGain))
Linear mixed model fit by REML
Formula: adg ~ (Treatment - 1) * InitWt + (1 | Block)
Data: AvgDailyGain
   AIC   BIC logLik deviance REMLdev
85.33 99.98 -32.66   10.10   65.33
Random effects:
Groups   Name             Variance Std.Dev.
Block    (Intercept) 0.25930   0.50921
Residual                    0.04943   0.22233
Number of obs: 32, groups: Block, 8

Fixed effects:
              Estimate Std. Error t value
Treatment0      0.439126   0.711093   0.6175
Treatment10     1.426112   0.637550   2.2369
Treatment20     0.479620   0.548890   0.8738
Treatment30     0.200117   0.775205   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(fmlAdg)
Analysis of Variance Table
              Df Sum Sq Mean Sq F value
Treatment      4  5.7251   1.4313  28.9552
InitWt         1  0.5495   0.5495  11.1174
Treatment:InitWt 3  0.1381   0.0460   0.9312
> (fm2Adg <- lmer(adg ~ InitWt + Treatment + (1 | Block), AvgDailyGain))

```

```

Linear mixed model fit by REML
Formula: adg ~ InitWt + Treatment + (1 | Block)
Data: AvgDailyGain
AIC BIC logLik deviance REMLdev
50.34 60.6 -18.17 13.62 36.34
Random effects:
Groups Name Variance Std.Dev.
Block (Intercept) 0.240833 0.49075
Residual 0.050081 0.22379
Number of obs: 32, groups: Block, 8

Fixed effects:
Estimate Std. Error t value
(Intercept) 0.8011046 0.3556609 2.252
InitWt 0.0027797 0.0008334 3.336
Treatment0 -0.5520740 0.1148138 -4.808
Treatment10 -0.0685666 0.1189697 -0.576
Treatment20 -0.0881295 0.1162885 -0.758

Correlation of Fixed Effects:
(Intr) InitWt Trtmn0 Trtm10
InitWt -0.844
Treatment0 0.036 -0.224
Treatment10 0.139 -0.340 0.534
Treatment20 0.079 -0.272 0.530 0.545
> anova(fm2Adg)
Analysis of Variance Table
Df Sum Sq Mean Sq F value
InitWt 1 0.51456 0.51456 10.275
Treatment 3 1.52670 0.50890 10.162
> (fm3Adg <- lmer(adg ~ InitWt + Treatment - 1 + (1 | Block),
+ AvgDailyGain))
Linear mixed model fit by REML
Formula: adg ~ InitWt + Treatment - 1 + (1 | Block)
Data: AvgDailyGain
AIC BIC logLik deviance REMLdev
50.34 60.6 -18.17 13.62 36.34
Random effects:
Groups Name Variance Std.Dev.
Block (Intercept) 0.240833 0.49075

```

```

Residual                0.050081 0.22379
Number of obs: 32, groups: Block, 8

```

Fixed effects:

	Estimate	Std. Error	t value
InitWt	0.0027797	0.0008334	3.336
Treatment0	0.2490307	0.3776319	0.659
Treatment10	0.7325380	0.3903800	1.876
Treatment20	0.7129751	0.3827687	1.863
Treatment30	0.8011046	0.3556609	2.252

Correlation of Fixed Effects:

	InitWt	Trtmn0	Trtml0	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)))

```

```

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

```

Linear mixed model fit by REML

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

Data: BIB

	AIC	BIC	logLik	deviance	REMLdev
	124.9	136.7	-52.45	93.5	104.9

Random effects:

Groups	Name	Variance	Std.Dev.
Block	(Intercept)	18.2488	4.2719
Residual		1.2005	1.0957

Number of obs: 24, groups: Block, 8

Fixed effects:

	Estimate	Std. Error	t value
(Intercept)	22.36787	3.10185	7.211
Treatment1	4.42948	3.36511	1.316

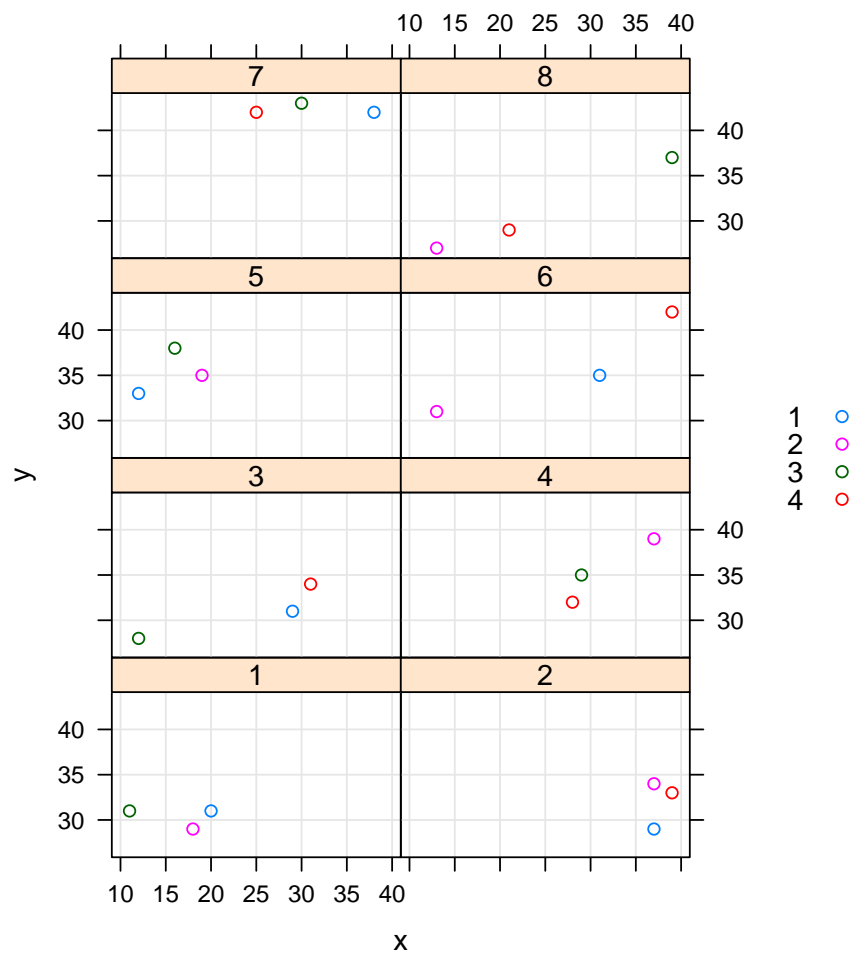


Figure 2: Balanced incomplete block design

Treatment2	-0.43738	2.93326	-0.149
Treatment3	6.27861	3.28210	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	-1.548

#### Correlation of Fixed Effects:

	(Intr)	Trtmn1	Trtmn2	Trtmn3	x	Trtml:	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(fmlBIB)

#### Analysis of Variance Table

	Df	Sum Sq	Mean Sq	F value
Treatment	3	23.447	7.816	6.5107
x	1	136.809	136.809	113.9640
Treatment:x	3	18.427	6.142	5.1166

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

Linear mixed model fit by REML

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

Data: BIB

AIC	BIC	logLik	deviance	REMLdev
115.2	124.6	-49.59	94.09	99.18

#### Random effects:

Groups	Name	Variance	Std.Dev.
Block	(Intercept)	18.5245	4.3040
Residual		1.0379	1.0188

Number of obs: 24, groups: Block, 8

#### Fixed effects:

	Estimate	Std. Error	t value
(Intercept)	20.94518	2.06228	10.156
Treatment1	5.34143	1.97574	2.704
Treatment2	1.13556	0.71400	1.590
Treatment3	8.18102	1.77013	4.622

```

x:Grp13      0.23952      0.04296      5.575
x:Grp24      0.48923      0.04412     11.088

Correlation of Fixed Effects:
      (Intr) Trtmn1 Trtmn2 Trtmn3 x:Gr13
Treatment1 -0.501
Treatment2 -0.431  0.559
Treatment3 -0.527  0.942  0.581
x:Grp13     0.027 -0.663 -0.165 -0.605
x:Grp24    -0.639  0.651  0.452  0.688  0.042
> anova(fm2BIB)
Analysis of Variance Table
      Df  Sum Sq Mean Sq F value
Treatment  3   23.424    7.808   7.5233
x:Grp      2  154.733   77.366  74.5441

```

## C Bond

```

> (fm1Bond <- lmer(pressure ~ Metal + (1 | Ingot), Bond))
Linear mixed model fit by REML
Formula: pressure ~ Metal + (1 | Ingot)
Data: Bond
      AIC      BIC logLik deviance REMLdev
117.8 123.0  -53.9   115.7   107.8
Random effects:
Groups   Name             Variance Std.Dev.
Ingot    (Intercept)  11.447     3.3833
Residual                  10.372     3.2206
Number of obs: 21, groups: Ingot, 7

Fixed effects:
              Estimate Std. Error t value
(Intercept)  71.1000     1.7655   40.27
Metalc       -0.9143     1.7215   -0.53
Metali        4.8000     1.7215    2.79

```

```

Correlation of Fixed Effects:
      (Intr) Metalc
Metalc -0.488
Metali -0.488  0.500

```

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

    Df Sum Sq Mean Sq F value
Metal  2 131.90   65.95   6.3585
```

## 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")=<R_GlobalEnv>
 ..$ order.groups:List of 2
 .. ..$ Block: logi TRUE
 .. ..$ Cult : logi TRUE
 ..$ FUN          :function (x)
 ..$ outer        : NULL
 ..$ inner        :List of 1
 .. ..$ Cult:Class 'formula' length 2 ~Inoc
 .. .. - attr(*, ".Environment")=<R_GlobalEnv>
 ..$ labels       :List of 1
 .. ..$ drywt: chr "Yield"
 ..$ units        : list()
> xtabs(~Block + Cult, Cultivation)
      Cult
Block a b
  1 3 3
  2 3 3
  3 3 3
  4 3 3
> (fmlCult <- lmer(drywt ~ Inoc * Cult + (1 | Block) + (1 |
+      Cult), Cultivation))
Linear mixed model fit by REML
Formula: drywt ~ Inoc * Cult + (1 | Block) + (1 | Cult)
Data: Cultivation
AIC    BIC logLik deviance REMLdev
```

```

86.49 97.09 -34.24    74.94    68.49
Random effects:
Groups   Name             Variance Std.Dev.
Block    (Intercept) 1.20728  1.09876
Cult     (Intercept) 0.26565  0.51541
Residual                   1.19633  1.09377
Number of obs: 24, groups: Block, 4; Cult, 2

```

```

Fixed effects:
              Estimate Std. Error t value
(Intercept)   33.5250    0.9309   36.01
Inoccon       -5.5000    0.7734   -7.11
Inocdea       -2.8750    0.7734   -3.72
Culta         -0.3750    1.0628   -0.35
Inoccon:Culta  0.2500    1.0938    0.23
Inocdea:Culta -1.0250    1.0938   -0.94

```

```

Correlation of Fixed Effects:
              (Intr) Inoccn Inocde Culta  Incc:C
Inoccon      -0.415
Inocdea      -0.415  0.500
Culta        -0.571  0.364  0.364
Inoccon:Clt  0.294 -0.707 -0.354 -0.515
Inocdea:Clt  0.294 -0.354 -0.707 -0.515  0.500
> anova(fm1Cult)

```

Analysis of Variance Table

```

              Df  Sum Sq Mean Sq F value
Inoc          2 118.176   59.088 49.3908
Cult          1   0.657    0.657  0.5489
Inoc:Cult     2   1.826    0.913  0.7631

```

```

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

```

Linear mixed model fit by REML

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

Data: Cultivation

AIC BIC logLik deviance REMLdev

```

87.75 96 -36.88    76.9   73.75

```

Random effects:

```

Groups   Name             Variance Std.Dev.
Block    (Intercept) 1.21283  1.10129

```

```

Cult      (Intercept) 0.25824  0.50817
Residual                1.16299  1.07842
Number of obs: 24, groups: Block, 4; Cult, 2

```

Fixed effects:

	Estimate	Std. Error	t value
(Intercept)	33.6542	0.8691	38.72
Inoccon	-5.3750	0.5392	-9.97
Inocdea	-3.3875	0.5392	-6.28
Culta	-0.6333	0.8428	-0.75

Correlation of Fixed Effects:

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

```
> anova(fm2Cult)
```

Analysis of Variance Table

	Df	Sum Sq	Mean Sq	F value
Inoc	2	118.176	59.088	50.8069
Cult	1	0.657	0.657	0.5647

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

Linear mixed model fit by REML

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

Data: Cultivation

	AIC	BIC	logLik	deviance	REMLdev
	87.68	94.75	-37.84	77.32	75.68

Random effects:

Groups	Name	Variance	Std.Dev.
Block	(Intercept)	1.21285	1.10129
Cult	(Intercept)	0.10360	0.32188
Residual		1.16300	1.07842

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

Fixed effects:

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

```

Correlation of Fixed Effects:
      (Intr) Inoccn
Inoccon -0.381
Inocdea -0.381  0.500
> anova(fm3Cult)
Analysis of Variance Table
      Df  Sum Sq Mean Sq F value
Inoc   2 118.176  59.088  50.806

```

## E Demand

```

> (fmlDemand <- lmer(log(d) ~ log(y) + log(rd) + log(rt) +
+   log(rs) + (1 | State) + (1 | Year), Demand))
Linear mixed model fit by REML
Formula: log(d) ~ log(y) + log(rd) + log(rt) + log(rs) + (1 | State) +
Data: Demand
      AIC      BIC logLik deviance REMLdev
-224.2 -205.4  120.1   -260.5   -240.2
Random effects:
Groups   Name             Variance Std.Dev.
Year     (Intercept) 0.00026466 0.016268
State    (Intercept) 0.02950232 0.171762
Residual                    0.00111699 0.033421
Number of obs: 77, groups: Year, 11; State, 7

```

```

Fixed effects:
              Estimate Std. Error t value
(Intercept) -1.28386    0.72343  -1.775
log(y)       1.06978    0.10393  10.294
log(rd)      -0.29533    0.05246  -5.629
log(rt)       0.03988    0.02789   1.430
log(rs)      -0.32673    0.11438  -2.856

```

```

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

```

## F HR

```
> (fm1HR <- lmer(HR ~ Time * Drug + baseHR + (Time | Patient),
+               HR))
```

Linear mixed model fit by REML

Formula: HR ~ Time \* Drug + baseHR + (Time | Patient)

Data: HR

AIC	BIC	logLik	deviance	REMLdev
789.6	820.3	-383.8	788.1	767.6

Random effects:

Groups	Name	Variance	Std.Dev.	Corr
Patient	(Intercept)	60.633	7.7867	
	Time	37.789	6.1473	-0.563
Residual		24.361	4.9357	

Number of obs: 120, groups: Patient, 24

Fixed effects:

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

Correlation of Fixed Effects:

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

```
> anova(fm1HR)
```

Analysis of Variance Table

	Df	Sum Sq	Mean Sq	F value
Time	1	379.20	379.20	15.5661
Drug	2	92.89	46.45	1.9066
baseHR	1	533.30	533.30	21.8915
Time:Drug	2	72.11	36.06	1.4801

```
> (fm3HR <- lmer(HR ~ Time + Drug + baseHR + (Time | Patient),
+ HR))
```

Linear mixed model fit by REML

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

Data: HR

AIC	BIC	logLik	deviance	REMLdev
797.8	822.9	-389.9	791.2	779.8

Random effects:

Groups	Name	Variance	Std.Dev.	Corr
Patient	(Intercept)	61.560	7.8460	
	Time	40.968	6.4006	-0.571
Residual		24.361	4.9357	

Number of obs: 120, groups: Patient, 24

Fixed effects:

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

Correlation of Fixed Effects:

	(Intr)	Time	Druga	Drugb
Time	-0.096			
Druga	-0.297	0.000		
Drugb	-0.219	0.000	0.502	
baseHR	-0.966	0.000	0.132	0.050

```
> anova(fm3HR)
```

Analysis of Variance Table

	Df	Sum Sq	Mean Sq	F value
Time	1	364.01	364.01	14.9423
Drug	2	92.89	46.45	1.9066
baseHR	1	533.29	533.29	21.8915

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

Linear mixed model fit by REML

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

Data: HR

AIC	BIC	logLik	deviance	REMLdev
805.1	824.7	-395.6	794.3	791.1

Random effects:

Groups	Name	Variance	Std.Dev.	Corr
Patient	(Intercept)	63.026	7.9389	
	Time	40.968	6.4006	-0.553
Residual		24.361	4.9357	

Number of obs: 120, groups: Patient, 24

Fixed effects:

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

Correlation of Fixed Effects:

	(Intr)	Time
Time	-0.098	
baseHR	-0.984	0.000

> anova(fm4HR)

Analysis of Variance Table

	Df	Sum Sq	Mean Sq	F value
Time	1	364.0	364.0	14.942
baseHR	1	534.9	534.9	21.957

## G Mississippi

```
> (fm1Miss <- lmer(y ~ 1 + (1 | influent), Mississippi))
```

Linear mixed model fit by REML

Formula: y ~ 1 + (1 | influent)

Data: Mississippi

AIC	BIC	logLik	deviance	REMLdev
258.4	263.2	-126.2	256.6	252.4

Random effects:

Groups	Name	Variance	Std.Dev.
influent	(Intercept)	63.313	7.9570
Residual		42.659	6.5314

Number of obs: 37, groups: influent, 6

Fixed effects:

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

```

> (fmlMLMiss <- lmer(y ~ 1 + (1 | influent), Mississippi, method = "ML"))
Linear mixed model fit by maximum likelihood
Formula: y ~ 1 + (1 | influent)
Data: Mississippi
      AIC      BIC logLik deviance REMLdev
262.6 267.4 -128.3   256.6   252.4
Random effects:
Groups      Name      Variance Std.Dev.
influente (Intercept) 51.250    7.1589
Residual              42.698    6.5344
Number of obs: 37, groups: influente, 6

Fixed effects:
              Estimate Std. Error t value
(Intercept)   21.217      3.122    6.796
> ranef(fmlMLMiss)
$influente
  (Intercept)
1    0.3097835
2   -6.5771551
3   -3.7862180
4    2.8826386
5   -5.8434348
6   13.0143857
> ranef(fmlMiss)
$influente
  (Intercept)
1    0.3092865
2   -6.7192205
3   -3.8978570
4    2.9460546
5   -6.0128502
6   13.3745867
> VarCorr(fmlMiss)
$influente
              (Intercept)
(Intercept)   63.31329
attr(,"stddev")
(Intercept)
  7.956965

```

```

attr(,"correlation")
      (Intercept)
(Intercept)      1

attr(,"sc")
sigmaREML
  6.53139
> (fm2Miss <- lmer(y ~ Type + (1 | influent), Mississippi))
Linear mixed model fit by REML
Formula: y ~ Type + (1 | influent)
Data: Mississippi
      AIC      BIC logLik deviance REMLdev
244.5 252.6 -117.3   247.5   234.5
Random effects:
Groups      Name      Variance Std.Dev.
influent (Intercept) 14.966    3.8686
Residual              42.514    6.5203
Number of obs: 37, groups: influent, 6

Fixed effects:
              Estimate Std. Error t value
(Intercept)   36.400      4.845    7.514
Type1        -20.800      5.933   -3.506
Type2        -16.462      5.516   -2.984

Correlation of Fixed Effects:
      (Intr) Type1
Type1 -0.816
Type2 -0.878  0.717
> anova(fm2Miss)
Analysis of Variance Table
      Df Sum Sq Mean Sq F value
Type   2 541.85  270.93  6.3726

```

## 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")=<R_GlobalEnv>
..$ order.groups:List of 2
.. ..$ Location: logi TRUE
.. ..$ Block    : logi TRUE
..$ FUN          :function (x)
..$ outer        : NULL
..$ inner        :List of 1
.. ..$ Block:Class 'formula' length 2 ~Trt
.. .. ..- attr(*, ".Environment")=<R_GlobalEnv>
..$ labels       :List of 1
.. ..$ Adj: chr "Adjusted yield"
..$ units        : list()
> Multilocation$Grp <- with(Multilocation, Block:Location)
> (fmlMult <- lmer(Adj ~ Location * Trt + (1 | Grp), Multilocation))
Linear mixed model fit by REML
Formula: Adj ~ Location * Trt + (1 | Grp)
Data: Multilocation
AIC      BIC logLik deviance REMLdev
86.65 188.6 -5.323  -87.15  10.65
Random effects:
Groups   Name             Variance Std.Dev.
Grp      (Intercept)  0.0056191 0.074961
Residual                    0.0345788 0.185954
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	0.946
LocationH:Trt1	-0.14953	0.21472	-0.696
LocationA:Trt2	-0.09347	0.21472	-0.435
LocationB:Trt2	-0.32273	0.21472	-1.503
LocationC:Trt2	0.08960	0.21472	0.417
LocationD:Trt2	-0.29693	0.21472	-1.383
LocationE:Trt2	-0.30693	0.21472	-1.429
LocationF:Trt2	-0.30993	0.21472	-1.443
LocationG:Trt2	-0.10860	0.21472	-0.506
LocationH:Trt2	-0.33060	0.21472	-1.540
LocationA:Trt3	-0.40247	0.21472	-1.874
LocationB:Trt3	-0.56550	0.21472	-2.634
LocationC:Trt3	-0.12247	0.21472	-0.570
LocationD:Trt3	-0.54840	0.21472	-2.554
LocationE:Trt3	-0.32863	0.21472	-1.531
LocationF:Trt3	-0.46257	0.21472	-2.154
LocationG:Trt3	-0.25297	0.21472	-1.178
LocationH:Trt3	-0.37203	0.21472	-1.733

Correlation of Fixed Effects:

	(Intr)	LoctnA	LoctnB	LoctnC	LoctnD	LoctnE	LoctnF	LoctnG	LoctnH
LocationA	-0.707								
LocationB	-0.707	0.500							
LocationC	-0.707	0.500	0.500						
LocationD	-0.707	0.500	0.500	0.500					
LocationE	-0.707	0.500	0.500	0.500	0.500				
LocationF	-0.707	0.500	0.500	0.500	0.500	0.500			
LocationG	-0.707	0.500	0.500	0.500	0.500	0.500	0.500		

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

LoctnA:Trt1	-0.707	-0.354	-0.354							
LoctnB:Trt1	-0.707	-0.354	-0.354	0.500						
LoctnC:Trt1	-0.707	-0.354	-0.354	0.500	0.500					
LoctnD:Trt1	-0.707	-0.354	-0.354	0.500	0.500	0.500				
LoctnE:Trt1	-0.707	-0.354	-0.354	0.500	0.500	0.500	0.500			
LoctnF:Trt1	-0.707	-0.354	-0.354	0.500	0.500	0.500	0.500	0.500		
LoctnG:Trt1	-0.707	-0.354	-0.354	0.500	0.500	0.500	0.500	0.500	0.500	
LoctnH:Trt1	-0.707	-0.354	-0.354	0.500	0.500	0.500	0.500	0.500	0.500	0.500
LoctnA:Trt2	-0.354	-0.707	-0.354	0.500	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
LoctnC:Trt2	-0.354	-0.707	-0.354	0.250	0.250	0.500	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
LoctnE:Trt2	-0.354	-0.707	-0.354	0.250	0.250	0.250	0.250	0.500	0.250	0.250
LoctnF:Trt2	-0.354	-0.707	-0.354	0.250	0.250	0.250	0.250	0.250	0.250	0.500
LoctnG:Trt2	-0.354	-0.707	-0.354	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
LoctnA:Trt3	-0.354	-0.354	-0.707	0.500	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
LoctnC:Trt3	-0.354	-0.354	-0.707	0.250	0.250	0.500	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
LoctnE:Trt3	-0.354	-0.354	-0.707	0.250	0.250	0.250	0.250	0.500	0.250	0.250
LoctnF:Trt3	-0.354	-0.354	-0.707	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
LoctnH:Trt3	-0.354	-0.354	-0.707	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(fmlMult)
Analysis of Variance Table

            Df Sum Sq Mean Sq F value
Location      8 6.9476  0.8684 25.1149
Trt           3 1.2217  0.4072 11.7774
Location:Trt 24 0.9966  0.0415  1.2008
> (fm2Mult <- lmer(Adj ~ Location + Trt + (1 | Grp), Multilocation))
Linear mixed model fit by REML
Formula: Adj ~ Location + Trt + (1 | Grp)
Data: Multilocation
AIC   BIC logLik deviance REMLdev
22 59.55 3.001 -51.22 -6.001
Random effects:
Groups   Name             Variance Std.Dev.
Grp      (Intercept) 0.0050851 0.07131
Residual                    0.0367154 0.19161
Number of obs: 108, groups: Grp, 27

Fixed effects:
            Estimate Std. Error t value
(Intercept) 2.53296    0.07599 33.33
LocationA    0.47818    0.09752 4.90
LocationB   -0.22443    0.09752 -2.30
LocationC    0.52712    0.09752 5.41

```

LocationD	0.02902	0.09752	0.30
LocationE	0.32537	0.09752	3.34
LocationF	0.73709	0.09752	7.56
LocationG	0.32098	0.09752	3.29
LocationH	0.80099	0.09752	8.21
Trt1	0.05834	0.05215	1.12
Trt2	-0.18802	0.05215	-3.61
Trt3	0.08379	0.05215	1.61

#### Correlation of Fixed Effects:

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

LocationA  
LocationB  
LocationC  
LocationD  
LocationE  
LocationF  
LocationG  
LocationH  
Trt1

Trt2 0.500  
Trt3 0.500 0.500

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

Linear mixed model fit by REML

Formula: Adj ~ Location + (1 | Grp)

Data: Multilocation

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

Random effects:

Groups	Name	Variance	Std.Dev.
Grp	(Intercept)	3.3652e-11	5.8011e-06
Residual		5.1642e-02	2.2725e-01

Number of obs: 108, groups: Grp, 27

Fixed effects:

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

Correlation of Fixed Effects:

	(Intr)	LoctnA	LoctnB	LoctnC	LoctnD	LoctnE	LoctnF	LoctnG
LocationA	-0.707							
LocationB	-0.707	0.500						
LocationC	-0.707	0.500	0.500					
LocationD	-0.707	0.500	0.500	0.500				
LocationE	-0.707	0.500	0.500	0.500	0.500			
LocationF	-0.707	0.500	0.500	0.500	0.500	0.500		
LocationG	-0.707	0.500	0.500	0.500	0.500	0.500	0.500	
LocationH	-0.707	0.500	0.500	0.500	0.500	0.500	0.500	0.500

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

Linear mixed model fit by REML

Formula: Adj ~ Trt + (1 | Grp)

Data: Multilocation

AIC	BIC	logLik	deviance	REMLdev
43.51	59.6	-15.75	14.95	31.51

Random effects:

Groups	Name	Variance	Std.Dev.
Grp	(Intercept)	0.110920	0.33305
Residual		0.036716	0.19161

Number of obs: 108, groups: Grp, 27

Fixed effects:

	Estimate	Std. Error	t value
(Intercept)	2.86567	0.07395	38.75
Trt1	0.05834	0.05215	1.12
Trt2	-0.18802	0.05215	-3.61
Trt3	0.08379	0.05215	1.61

Correlation of Fixed Effects:

	(Intr)	Trt1	Trt2
Trt1	-0.353		
Trt2	-0.353	0.500	
Trt3	-0.353	0.500	0.500

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

Linear mixed model fit by REML

Formula: Adj ~ 1 + (1 | Grp)

Data: Multilocation

AIC	BIC	logLik	deviance	REMLdev
53.33	61.37	-23.66	43.75	47.33

Random effects:

Groups	Name	Variance	Std.Dev.
Grp	(Intercept)	0.107489	0.32785
Residual		0.050439	0.22459

Number of obs: 108, groups: Grp, 27

Fixed effects:

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

```
> anova(fm2Mult)
```

Analysis of Variance Table

	Df	Sum Sq	Mean Sq	F value
Location	8	7.3768	0.9221	25.115
Trt	3	1.2217	0.4072	11.092

```
> (fm2MultR <- lmer(Adj ~ Trt + (Trt - 1 | Location) + (1 |
+ Block), Multilocation, control = list(msV = 1, niterEM = 200)))
```

Linear mixed model fit by REML

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

Data: Multilocation

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

Random effects:

Groups	Name	Variance	Std.Dev.	Corr
Location	Trt1	1.3589e-01	3.6863e-01	
	Trt2	1.0700e-01	3.2710e-01	0.989
	Trt3	1.1909e-01	3.4509e-01	0.998 0.996
	Trt4	1.1411e-01	3.3780e-01	0.927 0.972 0.948
Block	(Intercept)	2.3486e-14	1.5325e-07	
Residual		3.7773e-02	1.9435e-01	

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

Fixed effects:

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

Correlation of Fixed Effects:

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

## I PBIB

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

Linear mixed model fit by REML

Formula: response ~ Treatment + (1 | Block)

Data: PBIB

AIC BIC logLik deviance REMLdev

85.98 121.6 -25.99 22.83 51.98

Random effects:

Groups	Name	Variance	Std.Dev.
--------	------	----------	----------

Block	(Intercept)	0.046519	0.21568
-------	-------------	----------	---------

Residual		0.085560	0.29251
----------	--	----------	---------

Number of obs: 60, groups: Block, 15

Fixed effects:

	Estimate	Std. Error	t value
(Intercept)	2.891309	0.166413	17.374
Treatment1	-0.073788	0.222062	-0.332
Treatment10	-0.400249	0.222062	-1.802
Treatment11	0.007392	0.222062	0.033
Treatment12	0.161514	0.222062	0.727
Treatment13	-0.273542	0.222062	-1.232
Treatment14	-0.400000	0.227201	-1.761
Treatment15	-0.032076	0.222062	-0.144
Treatment2	-0.485995	0.222062	-2.189
Treatment3	-0.436366	0.222062	-1.965
Treatment4	-0.107474	0.227201	-0.473
Treatment5	-0.086411	0.222062	-0.389
Treatment6	0.019385	0.222062	0.087
Treatment7	-0.102323	0.222062	-0.461
Treatment8	-0.109705	0.222062	-0.494

Correlation of Fixed Effects:

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

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

## J SIMS

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

```

Linear mixed model fit by REML
Formula: Gain ~ Pretot + (Pretot | Class)
Data: SIMS
AIC    BIC logLik deviance REMLdev
22393 22430 -11190    22373    22381
Random effects:
Groups   Name             Variance Std.Dev. Corr
Class    (Intercept) 14.489586 3.806519
          Pretot      0.009206 0.095947 -0.641
Residual                22.235943 4.715500
Number of obs: 3691, groups: Class, 190

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

Correlation of Fixed Effects:
      (Intr)
Pretot -0.760

```