Mixed Effects Models
R lab:Preparing data

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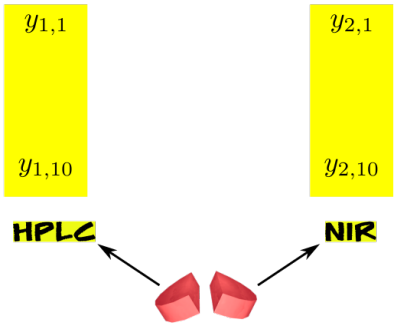
1 Introduction:

Now let us learn how to use **R** in order to fit a linear mixed effects model.In R there are two different functions in two different packages.Function lme is found in package nlme and the other function lmer which is the more recent one is found in package lme4.Both these packages are badly documented.

The reason we **prefer** lme over lmer is that it is more stable and more feature rich.Function lme is also backed by book **Mixed-Effects Models in S and S-PLUS** by Pinheiro and M.Bates who are also authors of package nlme.By default nlme package is installed in R.If not, We can install it by install.packages.

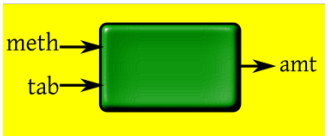
2 Data layout:

Consider our tablet study as example.We have 10 tablets and we break each one into two parts and measure the active content in two pieces using two different methods **HPLC** and **NIR**.



tab	HPLC	NIR
1	10.4	10.1
2	10.6	10.8
3	10.2	10.2
4	10.1	9.9
5	10.3	11.0
6	10.7	10.5
7	10.3	10.2
8	10.9	10.9
9	10.1	10.4
10	9.8	9.9

But it is not suitable to use this type of data in R.So consider it's black box diagram.



It has two inputs method used,tablet and one output amount of active content (random error is not shown in the figure).So the suitable data must also have 3 columns of which we have method in one column, tablets in one column, amount in one column.So we have a matrix of order 20x3.Now let us prepare our data file.

3 Preparing data file:

We have a file **tablet data.txt**.Let us read it using R.

```
    > data=read.table('tablet data.txt',head=T)
    > data
   tablet HPLC  NIR
1       1 10.4 10.1
2       2 10.6 10.8
3       3 10.2 10.2
4       4 10.1  9.9
5       5 10.3 11.0
6       6 10.7 10.5
7       7 10.3 10.2
8       8 10.9 10.9
9       9 10.1 10.4
10     10  9.8  9.9
>
```

In our suitable data, in one column we have 20 amounts measured by 2 methods of 10 each followed by method column which have 10 HPLC's and 10 NIR's followed by tab column which 1 to 10 replicated twice.
We create a new data frame with above properties and name it data1.

```
    > data1=with(data,data.frame(amt=c(HPLC,NIR),method=c(rep("HPLC",10),rep("NIR",10)),tab=
> data1
    amt method tab
1  10.4   HPLC   1
2  10.6   HPLC   2
3  10.2   HPLC   3
4  10.1   HPLC   4
5  10.3   HPLC   5
6  10.7   HPLC   6
7  10.3   HPLC   7
8  10.9   HPLC   8
```

```
9  10.1   HPLC   9
10  9.8   HPLC  10
11 10.1    NIR   1
12 10.8    NIR   2
13 10.2    NIR   3
14  9.9    NIR   4
15 11.0    NIR   5
16 10.5    NIR   6
17 10.2    NIR   7
18 10.9    NIR   8
19 10.4    NIR   9
20  9.9    NIR  10
```

This data can be used for fitting linear models.