DNA Example: Random Effects Two-Way

An analysis of a 3x3 factorial design using data from Ott & Longnecerk. Three randomly selected subjects analyzed by three randomly selected analysts. Two replicates for each subject by analyst combination.

```
library(lme4)
library(pbkrtest)
library(lmerTest)
DNA <- read.csv("C:/hess/STAT512/RNotes/Random1/R1_DNA_2way.csv")
str(DNA)
```

```
## 'data.frame':    18 obs. of  3 variables:
##  $ subject: int  1 1 1 1 1 1 2 2 2 2 ...
##  $ analyst: int  1 1 2 2 3 3 1 1 2 2 ...
##  $ DNAcont: num  13.2 12.3 12.5 12.9 13 12.4 10.6 9.8 9.6 10.7 ...
```

```
#Important: Need to define subject and analyst as.factor!!!!
DNA$subject <- as.factor(DNA$subject)
DNA$analyst <- as.factor(DNA$analyst)
```

Full Model

```
Model1 <- lmer(DNAcont ~ (1|subject) + (1|analyst) + (1|subject:analyst), data = DNA)
```

```
## singular fit
```

```
summary(Model1)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: DNAcont ~ (1 | subject) + (1 | analyst) + (1 | subject:analyst)
##    Data: DNA
##
## REML criterion at convergence: 29.2
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.42824 -0.75416  0.01546  0.70062  1.42039
##
## Random effects:
##  Groups          Name        Variance Std.Dev.
##  subject:analyst (Intercept) 0.0000   0.0000
##  analyst         (Intercept) 0.0000   0.0000
##  subject         (Intercept) 4.6217   2.1498
##  Residual                    0.1491   0.3862
## Number of obs: 18, groups:  subject:analyst, 9; analyst, 3; subject, 3
##
## Fixed effects:
##             Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)   10.433      1.245   2.000   8.383   0.0139 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
## convergence code: 0
## singular fit
```

```
rand(Model1)
```

```
## singular fit
```

```
## ANOVA-like table for random-effects: Single term deletions
##
## Model:
## DNAcont ~ (1 | subject) + (1 | analyst) + (1 | subject:analyst)
##                       npar  logLik    AIC    LRT Df Pr(>Chisq)
## <none>                   5 -14.622 39.244
## (1 | subject)           4 -26.404 60.809 23.565  1  1.208e-06 ***
## (1 | analyst)           4 -14.622 37.244  0.000  1     1.0000
## (1 | subject:analyst)   4 -14.622 37.244  0.000  1     0.9983
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Reduced Model

In the "full" model above two of the variance components (subject:analyst and analyst) were estimated to be zero. Dropping those terms from the model does not change the reuslts.

```
Model2 <- lmer(DNAcont ~ (1|subject), data = DNA)
summary(Model2)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: DNAcont ~ (1 | subject)
##    Data: DNA
##
## REML criterion at convergence: 29.2
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.42824 -0.75417  0.01546  0.70062  1.42040
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  subject  (Intercept) 4.6221   2.1499
##  Residual             0.1491   0.3861
## Number of obs: 18, groups:  subject, 3
##
## Fixed effects:
##             Estimate Std. Error     df t value Pr(>|t|)
## (Intercept)   10.433      1.245  2.000   8.383   0.0139 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```