Pharmaceutical Example: Nested Design (Sites as Random)

Example 17.11 from Ott and Longnecker. This is a two-stage nested design with batch nested within site (and tablet nested with batch). Batch should clearly be considered a random factor, but site could be considered random or fixed depending on the emphasis of the experimenter.

Notes:

1. The model notation A/B is equivalent to A + A:B!

2. When there is nesting, I prefer to work with unique names to prevent confusion/mistakes!

```
library(lme4)
Tablet <- read.csv("C:/hess/STAT512/RNotes/Random1/R1_Pharm_Nested.csv")
str(Tablet)
```

```
## 'data.frame':    30 obs. of  3 variables:
##  $ site   : int  1 1 1 1 1 1 1 1 1 1 ...
##  $ batch  : int  1 1 1 1 1 2 2 2 2 2 ...
##  $ content: num  5.03 5.1 5.25 4.98 5.05 4.64 4.73 4.82 4.95 5.06 ...
```

```
#Important: Need to define site and batch as.factors!!!!
Tablet$site <- as.factor(Tablet$site)
Tablet$batch <- as.factor(Tablet$batch)
with( table(batch, site), data = Tablet)
```

```
##      site
## batch 1 2
##     1 5 5
##     2 5 5
##     3 5 5
```

```
Tablet$BatchUnique <- paste("S", Tablet$site, "B", Tablet$batch, sep = "")
with( table(BatchUnique, site), data = Tablet)
```

```
##            site
## BatchUnique 1 2
##        S1B1 5 0
##        S1B2 5 0
##        S1B3 5 0
##        S2B1 0 5
##        S2B2 0 5
##        S2B3 0 5
```

Three Model Statements with Identical Results

```
Model1 <- lmer( content ~ (1|site/batch), data = Tablet)
summary(Model1)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: content ~ (1 | site/batch)
##    Data: Tablet
```

```
## 
## REML criterion at convergence: -32.1
## 
## Scaled residuals:
##     Min      1Q  Median      3Q     Max 
## -2.0555 -0.4256 -0.1264  0.4865  2.4200 
## 
## Random effects:
##  Groups      Name        Variance Std.Dev.
##  batch:site (Intercept) 0.01647  0.1283  
##  site       (Intercept) 0.00000  0.0000  
##  Residual               0.01209  0.1100  
## Number of obs: 30, groups:  batch:site, 6; site, 2
## 
## Fixed effects:
##             Estimate Std. Error t value
## (Intercept)  5.04333    0.05611   89.88
```

```r
Model2 <- lmer( content ~ (1|site) + (1|site:batch), data = Tablet)
summary(Model2)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: content ~ (1 | site) + (1 | site:batch)
##    Data: Tablet
## 
## REML criterion at convergence: -32.1
## 
## Scaled residuals:
##     Min      1Q  Median      3Q     Max 
## -2.0555 -0.4256 -0.1264  0.4865  2.4200 
## 
## Random effects:
##  Groups      Name        Variance Std.Dev.
##  site:batch (Intercept) 0.01647  0.1283  
##  site       (Intercept) 0.00000  0.0000  
##  Residual               0.01209  0.1100  
## Number of obs: 30, groups:  site:batch, 6; site, 2
## 
## Fixed effects:
##             Estimate Std. Error t value
## (Intercept)  5.04333    0.05611   89.88
```

```r
Model3 <- lmer( content ~ (1|site) + (1|BatchUnique), data = Tablet)
summary(Model3)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: content ~ (1 | site) + (1 | BatchUnique)
##    Data: Tablet
## 
## REML criterion at convergence: -32.1
## 
## Scaled residuals:
##     Min      1Q  Median      3Q     Max 
## -2.0555 -0.4256 -0.1264  0.4865  2.4200 
## 
```

```
## Random effects:
##  Groups       Name        Variance Std.Dev.
##  BatchUnique (Intercept) 0.01647  0.1283
##  site        (Intercept) 0.00000  0.0000
##  Residual                0.01209  0.1100
## Number of obs: 30, groups:  BatchUnique, 6; site, 2
##
## Fixed effects:
##             Estimate Std. Error t value
## (Intercept)  5.04333    0.05611   89.88
```