Chapter25

```
calcium <- c( 3.28, 3.09, 3.03, 3.03, 3.52, 3.48, 3.38, 3.38, 2.88, 2.80, 2.81, 2.76, 3.34, 3.38, 3.23,
leaf <- rep(1:4, each=4)
leaf <- factor(leaf)
contrasts(leaf) <- contr.sum
result <- lm( calcium ~ leaf )
 anova(result)
```

```
## Analysis of Variance Table
##
## Response: calcium
##           Df  Sum Sq  Mean Sq F value   Pr(>F)
## leaf       3 0.88837 0.296123  44.853 8.52e-07 ***
## Residuals 12 0.07923 0.006602
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
 temp <- anova(result)
names(temp)
```

```
## [1] "Df"      "Sum Sq"  "Mean Sq" "F value" "Pr(>F)"
```

```
temp$"Mean Sq"
```

```
## [1] 0.296122917 0.006602083
```

```
MSTR <- temp$"Mean Sq"[1]
MSE <- temp$"Mean Sq"[2]

 # compute estimate and interval for Psi
 n <- 4
 a <- 4
 NT <- n*a
 sigma2 <- MSE
 sqrt(sigma2)
```

```
## [1] 0.08125321
```

```
 sigma2mu <- (MSTR-MSE)/n
 sqrt(sigma2mu)
```

```
## [1] 0.2690357
```

```
 Psi <- sigma2mu / sigma2
 LPsi <- (1/n) * ( (MSTR/MSE)/qf(.975,a-1,NT-a) - 1 )
 UPsi <- (1/n) * ( (MSTR/MSE)/qf(.025,a-1,NT-a) - 1 )
Psi
```

```
## [1] 10.96324
```

```
c(LPsi,UPsi)
```

```
## [1]   2.256208 160.509168
```

```
 # compute estimate and interval for rho
 rho <- sigma2mu / (sigma2mu + sigma2)
 Lrho <-LPsi / (LPsi + 1)
 Urho <-UPsi / (UPsi + 1)
rho
```

```
## [1] 0.9164106
```

```
c(Lrho,Urho)
```

```
## [1] 0.6928943 0.9938084
```

```
Ybari<- tapply( calcium, leaf, mean)
 Ybar=mean(Ybari)
 k<-4
 lower <- Ybar- qt(.975,k-1) * sqrt( var(Ybari) / k )
 upper <- Ybar+ qt(.975,k-1) * sqrt( var(Ybari) / k )
 Ybari
```

```
##      1      2      3      4
## 3.1075 3.4400 2.8125 3.3025
```

```
 Ybar
```

```
## [1] 3.165625
```

```
 c(lower, upper)
```

```
## [1] 2.732676 3.598574
```

```
#Using MLE

library(nlme)
result <- lme( calcium ~ 1, random = ~ 1 | leaf, method="ML" )
summary(result)
```

```
## Linear mixed-effects model fit by maximum likelihood
##  Data: NULL
##         AIC       BIC   logLik
##   -14.85706 -12.53929 10.42853
##
## Random effects:
##  Formula: ~1 | leaf
```

```
##         (Intercept)   Residual
## StdDev:   0.2321046 0.08125321
##
## Fixed effects: calcium ~ 1
##                Value Std.Error DF  t-value p-value
## (Intercept) 3.165625 0.1216805 12 26.01588       0
##
## Standardized Within-Group Residuals:
##        Min         Q1        Med         Q3        Max
## -0.9750738 -0.6723686 -0.2598367  0.6198881  2.1017279
##
## Number of Observations: 16
## Number of Groups: 4
```

```
library(lme4)
```

```
## Loading required package: Matrix
```

```
##
## Attaching package: 'lme4'
```

```
## The following object is masked from 'package:nlme':
##
##     lmList
```

```
lmer(calcium~(1|leaf),REML=F)
```

```
## Linear mixed model fit by maximum likelihood  ['lmerMod']
## Formula: calcium ~ (1 | leaf)
##      AIC      BIC   logLik deviance df.resid
## -14.8571 -12.5393  10.4285 -20.8571       13
## Random effects:
##  Groups   Name        Std.Dev.
##  leaf     (Intercept) 0.23210
##  Residual             0.08125
## Number of obs: 16, groups:  leaf, 4
## Fixed Effects:
## (Intercept)
##       3.166
```

```
setwd("/Users/qiongxiasong/Dropbox/myteaching/stat6338/Spring2017/data")
Mydata<-read.table("CH25PR17.txt")
names(Mydata)<-c("Y", "A","B")
 library(nlme)
 Y<-Mydata$Y
 A<-as.factor(Mydata$A)
 B<-as.factor(Mydata$B)
 library(nlme)
 result1<-lme(Y~A, random=~1|B)
 summary(result1)
```

```
## Linear mixed-effects model fit by REML
##  Data: NULL
##       AIC      BIC   logLik
##   217.868 226.9013 -103.934
##
## Random effects:
##  Formula: ~1 | B
##         (Intercept) Residual
## StdDev:    1.974262 2.044022
##
## Fixed effects: Y ~ A
##                Value Std.Error DF  t-value p-value
## (Intercept) 73.10625 1.1115549 42 65.76936       0
## A2           3.68750 0.7226709 42  5.10260       0
## A3           3.81875 0.7226709 42  5.28422       0
##  Correlation:
##    (Intr) A2
## A2 -0.325
## A3 -0.325  0.500
##
## Standardized Within-Group Residuals:
##        Min         Q1        Med         Q3        Max
## -2.1990458 -0.6281479  0.1033012  0.6554653  1.3637802
##
## Number of Observations: 48
## Number of Groups: 4
```

```
#result2<-lme(Y~A, random=~1|B, method="ML")
#summary(result2)

library(lme4)
result3<-lmer(Y~A+(1|B))
 summary(result3)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: Y ~ A + (1 | B)
##
## REML criterion at convergence: 207.9
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.1991 -0.6281  0.1033  0.6555  1.3638
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  B        (Intercept) 3.898    1.974
##  Residual             4.178    2.044
## Number of obs: 48, groups:  B, 4
##
## Fixed effects:
##             Estimate Std. Error t value
## (Intercept)  73.1062     1.1116   65.77
## A2            3.6875     0.7227    5.10
## A3            3.8188     0.7227    5.28
```

```
##
## Correlation of Fixed Effects:
##    (Intr) A2
## A2 -0.325
## A3 -0.325  0.500
```

```
 #result4<-lmer(Y~A+(1|B), REML=F)
#summary(result4)
```