Output from redwing2.R

```
> # redwing2.R
>
> library(lsmeans)
> library(nlme)
> #library(lme4) # not used
> #library(lmerTest) # not used
> library(multcomp)
>
> # get the data
> # you may want to change the path to where you put the data set
> redwing<-read.table(file="redwing1.dat",header=T)
> head(redwing)
  treat block  oil
1     a     1 34.4
2     a     2 35.9
3     a     3 36.0
4     a     4 34.1
5     b     1 33.3
6     b     2 31.9
>
>
> is.factor(redwing$block)
[1] FALSE
> redwing$blockfac <- factor(redwing$block)
>
> redwing2 <- groupedData(oil~treat|blockfac, data=redwing)
>
> # fit the linear model
> m1<-lme(oil~treat,data=redwing2, random= ~1|blockfac)
> summary(m1)
Linear mixed-effects model fit by REML
 Data: redwing2
       AIC      BIC    logLik
  79.69989 86.82286 -31.84994

Random effects:
 Formula: ~1 | blockfac
         (Intercept) Residual
StdDev: 4.870195e-05 1.126881

Fixed effects: oil ~ treat
             Value Std.Error DF  t-value p-value
(Intercept) 35.100 0.5634406 15 62.29583  0.0000
treatb      -0.800 0.7968253 15 -1.00398  0.3313
treatc      -1.100 0.7968253 15 -1.38048  0.1877
treatd       1.600 0.7968253 15  2.00797  0.0630
treate       0.950 0.7968253 15  1.19223  0.2517
treatf       1.925 0.7968253 15  2.41584  0.0289
 Correlation:
       (Intr) treatb treatc treatd treate
treatb -0.707
treatc -0.707  0.500
treatd -0.707  0.500  0.500
treate -0.707  0.500  0.500  0.500
```

```
treatf -0.707  0.500  0.500  0.500  0.500

Standardized Within-Group Residuals:
        Min          Q1         Med          Q3         Max
-2.12977208 -0.57126699  0.04437026  0.46588764  2.48473410

Number of Observations: 24
Number of Groups: 4
>
> anova(m1,Terms="treat",type="marginal")
F-test for: treat
  numDF denDF  F-value p-value
1     5    15 4.985125  0.0069
>
> # Notice that the F test for treatments given above is different
> # from the one given in redwing1.R when block effects are fixed.
> # This contradicts what I said in class that the F test for treatments
> # is unaffected by whether block effects are fixed or random. Actually,
> # when Type 3 estimation of the mixed effect model is used, by statement
> # is correct. For Type 3 estimation, the F test for treatments is the same
> # regardless of whether block effects are fixed or random. However, the lme()
> # function does not use Type 3 estimation. It uses REML estimation. REML
> # and Type 3 estiamtion give the same results in the RCB model unless
> # the Type 3 estimate of the block-to-block variance component is <0.
> # If it is >=0, then reml and type 3 coincide and it remains true that
> # treating block effects as fixed or random does not alter the F test on
> # the treatments. However, in the unusual case that there is no
> # evidence of block to block variability, then the type 3 estimate of the
> # block variance component can be negative, whereas the REML estimator
> # corrects this estimate and makes it 0. In that case (only) the F test for
> # treatments given by REML estimation of the mixed effect model
> # (block effects random) differs from that of the fixed effect model (block
> # effects fixed). The truth is that this example (the redwing flaxseed
> # example) is anomolous, it is unusual for there to be no block to block
> # variance. In such a situation (and in general), you are really better off
> # using REML estimation.
> # Note that if you change the method of estimation used in PROC MIXED in
> # redwing2.sas, you will see that it gives the same results as provided
> # here in this program where we use lme to fit our model.
>
> # Now get the lsmeans for treat. Note the SEs are different than when
> # block effects are fixed (see redwing1.R).
> lsmeans(m1,specs=~treat)
Error in eval(expr, envir, enclos) : object 'oil' not found
>
> # test the contrasts of interest
> # Here we use the lsmeans() function in package lsmeans
> c1<-c(1,1,1,1,1,-5)
> c2<-c(4,-1,-1,-1,-1,0)
> c3<-c(0,1,1,1,-3,0)
> c4<-c(0,1,-1,0,0,0)
> c5<-c(0,1,1,-2,0,0)
> c61<-c(4,-1,-1,-1,-1,0)
> c62<-c(0,1,1,1,-3,0)
> c63<-c(0,1,-1,0,0,0)
> c64<-c(0,1,1,-2,0,0)
> c7<-c(0,0,0,0,0,1)
```

```
>
> lsmeans(m1,specs=lsm~factor(treat),contr=list(lsm=list(treat.v.control=c1,
+                                                        seedling.v.other=c2,
+                                                        bloom.v.ripening=c3,
+                                                        within.bloom.i=c4,
+                                                        within.bloom.ii=c5,
+                                       #Inoculation.timing=list(c61,c62,c63,c64)
+                                                        control.mean=c7)))
Error in eval(expr, envir, enclos) : object 'oil' not found
>
> # The lsmeans function call above gives test statistics that agree with those
> # from SAS's PROC MIXED, but it treats these test statistics as Z tests, not
> # t-tests. They are contrasts tests of the form C/s.e.(C) where C is the
> # estimated contrast, but the lsmeans function does not implement these as
> # t tests. Their squares are still the F statistics produced by the CONTRAST
> # statement in SAS, but lsmeans in R treats these as Z tests and uses their
> # large sample distribution, which is standard normal under the null
> # hypothesis, rather than t (or F if squared). This is emphasized by the
> # fact that the denominator DF given by lsmeans is listed as NA.
> # Because the lsmeans function refers the statistics to their large sample
> # std normal distribution rather than to a t distribution, it gives
> # different p-values than does PROC MIXED.
>
> # Similarly, if we use glht to do the 4 df test on the inoculation timing
> # contrasts, it uses a large sample chisquare test rather than an F test.
> # The chisq test statistic it uses is numDF*F where numDF=4 for this
> # hypothesis (there are four contrasts being tested simultaneously) and
> # F is the usual F statistic for the contrast (e.g., the F statistic produced
> # by SAS' PROC MIXED.
>
> K1 <- rbind(  "seed.v.other" = c61,
+              "blm.v.rip" = c62,
+              "w/in blm (i)" = c63,
+              "w/in blm (ii)" = c64)
>
> summary(glht(m1, linfct = mcp(treat = K1 )),test=Ftest())

         General Linear Hypotheses

Multiple Comparisons of Means: User-defined Contrasts


Linear Hypotheses:
                     Estimate
seed.v.other == 0     -0.65
blm.v.rip == 0        -3.15
w/in blm (i) == 0      0.30
w/in blm (ii) == 0    -5.10

Global Test:
  Chisq DF Pr(>Chisq)
1 16.47  4   0.002451
Warning message:
In test(object) :
  'df.residual' is not available for 'model' a Chisq test is performed instead of
the requested F test.
>
```

```
> # The anova function can be used to test hypotheses on the treatment means
> # with F tests. It is easier, though, if we first refit the model without
> # an intercept (that is, in the parameterization y_ij=mu_i+b_j+e_ij)
> # Then the fitted mu_i's are the estimated treatment means and specifying
> # the contrasts become a but easier:
>
> # refit with alternate parameterization:
> m1a <-lme(oil~treat-1,data=redwing2, random= ~1|blockfac)
> summary(m1a)
Linear mixed-effects model fit by REML
 Data: redwing2
       AIC      BIC    logLik
  79.69989 86.82286 -31.84994

Random effects:
 Formula: ~1 | blockfac
         (Intercept) Residual
StdDev: 4.870178e-05 1.126881

Fixed effects: oil ~ treat - 1
        Value Std.Error DF  t-value p-value
treata 35.100 0.5634406 15 62.29583       0
treatb 34.300 0.5634406 15 60.87599       0
treatc 34.000 0.5634406 15 60.34354       0
treatd 36.700 0.5634406 15 65.13553       0
treate 36.050 0.5634406 15 63.98190       0
treatf 37.025 0.5634406 15 65.71234       0
 Correlation:
       treata treatb treatc treatd treate
treatb 0
treatc 0      0
treatd 0      0      0
treate 0      0      0      0
treatf 0      0      0      0      0

Standardized Within-Group Residuals:
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-2.12977208 -0.57126699  0.04437026  0.46588764  2.48473410

Number of Observations: 24
Number of Groups: 4
>
> # Test inoculation timing:
> anova(m1a,type="marginal", L=K1)
F-test for linear combination(s)
             treata treatb treatc treatd treate
seed.v.other       4     -1     -1     -1     -1
blm.v.rip          0      1      1      1     -3
w/in blm (i)       0      1     -1      0      0
w/in blm (ii)      0      1      1     -2      0
  numDF denDF  F-value p-value
1     4    15 4.116986   0.019
>
> # Test average of inoculation treatment means vs control mean:
> anova(m1a,type="marginal", L=c1)
F-test for linear combination(s)
treata treatb treatc treatd treate treatf
```

```
     1      1      1      1      1     -5
  numDF denDF  F-value p-value
1     1    15 8.457683  0.0108
>
>
> # Again, note that the tests given above agree with PROC MIXED when
> # method = REML is used. Given the negative variance component for blocks
> # here, REML is the better metod. If blocks had not had a negative variance
> # component, the REML and TYPE 3 results (including the above F tests)
> # would have agreed.
>
```