Output from dioxin.R

```
> # dioxin.R
>
> library(lsmeans)
> library(lme4)
> library(pbkrtest)
> #library(car)
> #library(nlme)
>
> # get the data
> dioxin<-read.table(file="dioxin.dat",header=T,
+                    colClasses=c("factor","factor","factor","factor","numeric"))
> head(dioxin)
  site row column treat dioxin
1    1   1      1     b   92.7
2    1   1      2     a  299.1
3    1   1      3     c   63.7
4    1   2      1     a  287.5
5    1   2      2     c   86.8
6    1   2      3     b  102.7
> is.factor(dioxin$site)
[1] TRUE
> is.factor(dioxin$dioxin)
[1] FALSE
>
> # to fit this model with the lmer function in the lme4 package it is better
> # to avoid implicitly nested factors. Instead create a row factor (called
> # allrow below) that has 3*5=15 levels (a unique level for each row within
> # each site). Do the same for columns.
> dioxin <- within(dioxin , allrow <- factor(row:site))
> dioxin <- within(dioxin , allcol <- factor(column:site))
> head(dioxin)
  site row column treat dioxin allrow allcol
1    1   1      1     b   92.7    1:1    1:1
2    1   1      2     a  299.1    1:1    2:1
3    1   1      3     c   63.7    1:1    3:1
4    1   2      1     a  287.5    2:1    1:1
5    1   2      2     c   86.8    2:1    2:1
6    1   2      3     b  102.7    2:1    3:1
>
> # Replicated Latin square w/ rows & cols nested in squares
> # mixed effects model with random effects of row(site) column(site) site
> # using reml in the function lmer() from package lme4
> m1<-lmer(dioxin~treat+(1|site)+(1|allrow)+(1|allcol),data=dioxin)
> summary(m1)
Linear mixed model fit by REML ['lmerMod']
Formula: dioxin ~ treat + (1 | site) + (1 | allrow) + (1 | allcol)
   Data: dioxin

REML criterion at convergence: 398.0167

Random effects:
 Groups   Name        Variance Std.Dev.
 allcol   (Intercept)  52.71    7.261
 allrow   (Intercept)  82.43    9.079
```

```
 site     (Intercept) 548.30   23.416
 Residual             403.30   20.082
Number of obs: 45, groups: allcol, 15; allrow, 15; site, 5

Fixed effects:
            Estimate Std. Error t value
(Intercept)  254.793     12.065   21.12
treatb      -191.620      7.333  -26.13
treatc      -195.500      7.333  -26.66

Correlation of Fixed Effects:
       (Intr) treatb
treatb -0.304
treatc -0.304  0.500
> anova(m1,type=3)
Analysis of Variance Table
      Df Sum Sq Mean Sq F value
treat  2 374768  187384  464.62
>
> # get the lsmeans for each level of treat
> lsmeans(m1,specs=~treat)
$`treat lsmeans`
 treat    lsmean       SE       df  lower.CL  upper.CL
     a 254.79333 12.06471 5.179696 224.10085 285.48582
     b  63.17333 12.06471 5.179696  32.48085  93.86582
     c  59.29333 12.06471 5.179696  28.60085  89.98582

>
> # test the contrasts of interest
> c1<-c(2,-1,-1)
> c2<-c(0,1,-1)
>
> lsmeans(m1,specs=lsm~treat,contr=list(lsm=list(control_vs_remed=c1,
+                                                remed1_vs_remed2=c2)))
$`treat lsmeans`
 treat    lsmean       SE       df  lower.CL  upper.CL
     a 254.79333 12.06471 5.179696 224.10085 285.48582
     b  63.17333 12.06471 5.179696  32.48085  93.86582
     c  59.29333 12.06471 5.179696  28.60085  89.98582

$`treat lsm`
                 estimate        SE df  t.ratio p.value
control_vs_remed   387.12 12.701204 18 30.47900 0.00000
remed1_vs_remed2     3.88  7.333043 18  0.52911 0.60319
    p values are not adjusted
```