

Output from mazemice.R

```
> # mazemice.R
>
> library(lsmmeans)
> library(lme4)
> library(pbkrtest)
> library(car)
>
> # get the data
> mazemice<-read.table(file="mazemice.dat",header=T,
+                       colClasses=c("factor","factor","factor","numeric"))
> head(mazemice)
  mouse day treat time
1     1   1     b    60
2     1   2     a    59
3     1   3     c    81
4     8   1     b    75
5     8   2     c    88
6     8   3     a    70
> is.factor(mazemice$mouse)
[1] TRUE
> is.factor(mazemice$time)
[1] FALSE
>
> # mixed effects model with random effects of mouse
> # using reml in the function lmer() from package lme4
> m1<-lmer(time~day+treat+(1|mouse),data=mazemice)
> summary(m1)
Linear mixed model fit by REML ['lmerMod']
Formula: time ~ day + treat + (1 | mouse)
Data: mazemice

REML criterion at convergence: 208.4711

Random effects:
Groups   Name              Variance Std.Dev.
mouse    (Intercept)  37.91   6.157
Residual                    16.15   4.019
Number of obs: 36, groups: mouse, 12

Fixed effects:
              Estimate Std. Error t value
(Intercept)  53.500     2.324   23.018
day2          6.833     1.641    4.165
day3          7.917     1.641    4.825
treatb       11.583     1.641    7.060
treatc       23.167     1.641   14.121

Correlation of Fixed Effects:
      (Intr) day2   day3   treatb
day2  -0.353
day3  -0.353  0.500
treatb -0.353  0.000  0.000
treatc -0.353  0.000  0.000  0.500
> anova(m1,type=3)
```

Analysis of Variance Table

```
      Df Sum Sq Mean Sq F value
day    2  442.2   221.08  13.689
treat  2 3220.2  1610.08  99.695
```

```
>
> # get the lsmeans for each level of treat and test the contrasts
> c1<-c(1,1,-2)
> c2<-c(1,-1,0)
>
> lsmeans(m1, specs=ls~treat, contr=list(lsm=list(control_vs_drugs=c1,
+                                           drugA_vs_drugB=c2)))
```

```
$`treat lsmeans`
  treat  lsmean      SE      df lower.CL upper.CL
  a 58.41667 2.122488 16.58737 53.93011 62.90323
  b 70.00000 2.122488 16.58737 65.51344 74.48656
  c 81.58333 2.122488 16.58737 77.09677 86.06989
```

```
$`treat lsm`
      estimate      SE df  t.ratio p.value
control_vs_drugs -34.75000 2.841657 20 -12.22878      0
drugA_vs_drugB   -11.58333 1.640632 20  -7.06029      0
p values are not adjusted
```

```
>
```