

Output from redwing1.R

```
> # redwing1.R
>
> library(lsmmeans)
> library(car)
> 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)
>
> # fit the linear model
> m1<-lm(oil~treat+blockfac,data=redwing)
> summary(m1)
```

Call:

```
lm(formula = oil ~ treat + blockfac, data = redwing)
```

Residuals:

Min	1Q	Median	3Q	Max
-1.97083	-0.56458	0.07917	0.45000	2.57917

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	34.8375	0.7021	49.621	<2e-16 ***
treatb	-0.8000	0.8107	-0.987	0.3394
treatc	-1.1000	0.8107	-1.357	0.1949
treatd	1.6000	0.8107	1.974	0.0671 .
treate	0.9500	0.8107	1.172	0.2595
treatf	1.9250	0.8107	2.375	0.0313 *
blockfac2	-0.1667	0.6619	-0.252	0.8046
blockfac3	0.7333	0.6619	1.108	0.2854
blockfac4	0.4833	0.6619	0.730	0.4765

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 1.146 on 15 degrees of freedom

Multiple R-squared: 0.6383, Adjusted R-squared: 0.4454

F-statistic: 3.309 on 8 and 15 DF, p-value: 0.02193

>

```
> # get the lsmeans for treat
```

```

> lsmeans(m1, specs=~treat)
$`treat lsmeans`
  treat lsmean      SE df lower.CL upper.CL
    a 35.100 0.5732401 15 33.87817 36.32183
    b 34.300 0.5732401 15 33.07817 35.52183
    c 34.000 0.5732401 15 32.77817 35.22183
    d 36.700 0.5732401 15 35.47817 37.92183
    e 36.050 0.5732401 15 34.82817 37.27183
    f 37.025 0.5732401 15 35.80317 38.24683

>
> # 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)))
$`treat lsmeans`
  treat lsmean      SE df lower.CL upper.CL
    a 35.100 0.5732401 15 33.87817 36.32183
    b 34.300 0.5732401 15 33.07817 35.52183
    c 34.000 0.5732401 15 32.77817 35.22183
    d 36.700 0.5732401 15 35.47817 37.92183
    e 36.050 0.5732401 15 34.82817 37.27183
    f 37.025 0.5732401 15 35.80317 38.24683

$`treat lsm`
      estimate      SE df  t.ratio p.value
treat.v.control   -8.975 3.1397651 15  -2.85849 0.01196
seedling.v.other  -0.650 2.5636075 15  -0.25355 0.80329
bloom.v.ripening  -3.150 1.9857618 15  -1.58629 0.13353
within.bloom.i     0.300 0.8106839 15   0.37006 0.71651
within.bloom.ii   -5.100 1.4041456 15  -3.63210 0.00246
control.mean       37.025 0.5732401 15  64.58900 0.00000
  p values are not adjusted

>
>
> # Unfortunately, the lsmeans() function does not seem to be able to
> # test multiple degree of freedom hypotheses on contrasts, so the
> # Inoculation.timing line above is commented out (it won't work, although
> # one would hope that it would). Instead we'll have to use the
> # glht() function in the multcomp package. The documentation on glht

```

```

> # is hard to follow and the design of glht and related functions
> # is very complex, but I eventually figured out how to use it to do what
> # we need to do for this example.
>
> # Here is how to do the inoculation timing test with glht:
>
> 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:

	F	DF1	DF2	Pr(>F)
1	3.977	4	15	0.02146

```

> # And here are the Dunnett tests of each pairwise contrast with the best
> # treatment, which is treatment d.

```

```

> K2 <- rbind( "a - d" = c( 1, 0, 0, -1, 0, 0),
+             "b - d" = c( 0, 1, 0, -1, 0, 0),
+             "c - d" = c( 0, 0, 1, -1, 0, 0),
+             "e - d" = c( 0, 0, 0, -1, 1, 0),
+             "f - d" = c( 0, 0, 0, -1, 0, 1))
>
> summary(glht(m1, linfct = mcp(treat = K2 ),
+ alternative="less"))

```

Simultaneous Tests for General Linear Hypotheses

Multiple Comparisons of Means: User-defined Contrasts

```
Fit: lm(formula = oil ~ treat + blockfac, data = redwing)
```

Linear Hypotheses:

	Estimate	Std. Error	t value	Pr(<t)
a - d >= 0	-1.6000	0.8107	-1.974	0.11279
b - d >= 0	-2.4000	0.8107	-2.960	0.01904 *
c - d >= 0	-2.7000	0.8107	-3.331	0.00929 **
e - d >= 0	-0.6500	0.8107	-0.802	0.51239
f - d >= 0	0.3250	0.8107	0.401	0.92431

```
---
```

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
(Adjusted p values reported -- single-step method)

```
>
>
>
> # Alternatively, the linearHypothesis function in the car package
> # can be used to the multiple df test on inoculation timing.
> # To do this it is easier
> # to refit the model with the parameterization  $y_{ij} = \mu_i + \beta_j + e_{ij}$ 
>
> m1a <- lm(oil ~ treat + blockfac - 1, data = redwing)
> summary(m1a)
```

Call:
lm(formula = oil ~ treat + blockfac - 1, data = redwing)

Residuals:

	Min	1Q	Median	3Q	Max
	-1.97083	-0.56458	0.07917	0.45000	2.57917

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)	
treata	34.8375	0.7021	49.621	<2e-16	***
treatb	34.0375	0.7021	48.481	<2e-16	***
treatc	33.7375	0.7021	48.054	<2e-16	***
treatd	36.4375	0.7021	51.900	<2e-16	***
treate	35.7875	0.7021	50.974	<2e-16	***
treatf	36.7625	0.7021	52.363	<2e-16	***
blockfac2	-0.1667	0.6619	-0.252	0.805	
blockfac3	0.7333	0.6619	1.108	0.285	
blockfac4	0.4833	0.6619	0.730	0.477	

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 1.146 on 15 degrees of freedom
Multiple R-squared: 0.9994, Adjusted R-squared: 0.999
F-statistic: 2564 on 9 and 15 DF, p-value: < 2.2e-16

```
>
> # in the parameterization R uses, the estimated  $\mu_i$ 's are actually the
> # treatment means for block 1. This is because the constraint that R uses
> # on the  $\beta_j$ 's is that  $\beta_1 = 0$ , not that the sum of the  $\beta_j$ 's is 0.
> # However, in this additive model with no
> # treatment by block interactions, any contrasts among the  $\mu_i$ 's in any
> # given block will be the same as within any other block. Therefore, we
> # can go ahead and do our contrasts based on the previous model.
```

```
>
> c61a <- c(4, -1, -1, -1, -1, 0, 0, 0, 0)
> c62a <- c(0, 1, 1, 1, -3, 0, 0, 0, 0)
> c63a <- c(0, 1, -1, 0, 0, 0, 0, 0, 0)
> c64a <- c(0, 1, 1, -2, 0, 0, 0, 0, 0)
>
> linearHypothesis(m1a, rbind(c61a, c62a, c63a, c64a))
Linear hypothesis test
```

Hypothesis:

```

4 treata - treatb - treatc - treatd - treate = 0
treatb + treatc + treatd - 3 treate = 0
treatb - treatc = 0
treatb + treatc - 2 treatd = 0

```

Model 1: restricted model

Model 2: oil ~ treat + blockfac - 1

```

  Res.Df    RSS Df Sum of Sq      F Pr(>F)
1      19 40.628
2      15 19.716  4    20.912 3.9774 0.02146 *
---
```

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

>
> # Alternatively, if we reparameterize the model y_ij=mu_i +beta_j +e_ij
> # so that the sum of the beta_j's is zero, then the estimated mu_i's
> # will be the estimated treatment means averaged over the 4 blocks
> # That is, they will be the lsmeans of for each treatment (as given by
> # the LSMEANS statement in SAS or the lsmeans() function here in R)
>
> options()$contrasts # the default contrasts for unordered factors is
      unordered      ordered
"contr.treatment"    "contr.poly"
> # contr.treatment, so reset it to contr.sum
> op <- options(contrasts=c("contr.sum", "contr.poly"))
> options()$contrasts # now you can see that they've been changed
[1] "contr.sum" "contr.poly"
>
> mlb <-lm(oil~treat+blockfac-1,data=redwing)
> summary(mlb)

```

Call:

```
lm(formula = oil ~ treat + blockfac - 1, data = redwing)
```

Residuals:

```

      Min       1Q   Median       3Q      Max
-1.97083 -0.56458  0.07917  0.45000  2.57917

```

Coefficients:

```

      Estimate Std. Error t value Pr(>|t|)
treata    35.1000    0.5732   61.231 <2e-16 ***
treatb    34.3000    0.5732   59.835 <2e-16 ***
treatc    34.0000    0.5732   59.312 <2e-16 ***
treatd    36.7000    0.5732   64.022 <2e-16 ***
treate    36.0500    0.5732   62.888 <2e-16 ***
treatf    37.0250    0.5732   64.589 <2e-16 ***
blockfac1  -0.2625    0.4053  -0.648   0.527
blockfac2  -0.4292    0.4053  -1.059   0.306
blockfac3   0.4708    0.4053   1.162   0.264
---
```

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

Residual standard error: 1.146 on 15 degrees of freedom
Multiple R-squared:  0.9994,    Adjusted R-squared:  0.999
F-statistic: 2564 on 9 and 15 DF,  p-value: < 2.2e-16

```

>

```
> # now the following contrast will be in the lsmeans for trt. But as mentioned
> # previously, in this no interaction model, we'll get the same answer as
> # when we conducted the same contrast based on the trt means in block 1
> # that is, when we did this contrast based on model m1a
> linearHypothesis(m1b, rbind(c61a, c62a, c63a, c64a))
Linear hypothesis test
```

Hypothesis:

```
4 treata - treatb - treatc - treatd - treate = 0
treatb + treatc + treatd - 3 treate = 0
treatb - treatc = 0
treatb + treatc - 2 treatd = 0
```

Model 1: restricted model

Model 2: oil ~ treat + blockfac - 1

	Res.Df	RSS	Df	Sum of Sq	F	Pr(>F)
1	19	40.628				
2	15	19.716	4	20.912	3.9774	0.02146 *

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

>

```
> options(op) # reset contrasts to their original values
```

>

>