

Output from dishwash.R

```
> # dishwash.R
>
> library(lsmmeans)
> #library(phia)
> #library(doBy)
> library(car)
> library(effects)
> library(lme4)
> library(nlme)
>
> # get the data
> dishwash<-read.table(file="dishwash.dat",header=T,
+                       colClasses=c("factor","factor","numeric"))
> head(dishwash)
  block dishsoap dishes
1     1         a     19
2     1         b     17
3     1         c     11
4     2         d      6
5     2         e     26
6     2         f     23
> is.factor(dishwash$block)
[1] TRUE
> is.factor(dishwash$dishes)
[1] FALSE
> is.ordered(dishwash$block)
[1] FALSE
> is.ordered(dishwash$dishsoap)
[1] FALSE
>
> #### part 1
>
> # the intra-block analysis of a BIBD using ANOVA
> m1<-aov(dishes~dishsoap+block,data=dishwash)
> summary(m1)
          Df Sum Sq Mean Sq F value    Pr(>F)
dishsoap   8 1489.5   186.19   225.94 5.66e-15 ***
block      11   10.1    0.91     1.11   0.413
Residuals  16   13.2    0.82
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
> # note that the summary function gives F tests based on type I
> # or sequential sums of squares. To get F tests based on the type II and III
> # SS, we need the Anova() function from the car package.
>
> Anova(m1,type=2)
Anova Table (Type II tests)

Response: dishes
      Sum Sq Df  F value    Pr(>F)
dishsoap 1086.81  8 164.8539 6.809e-14 ***
block      10.06 11   1.1103   0.4127
Residuals  13.19 16
---
```

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

> Anova(m1,type=3)

Anova Table (Type III tests)

Response: dishes

	Sum Sq	Df	F value	Pr(>F)	
(Intercept)	629.69	1	764.1199	6.205e-15	***
dishsoap	1086.81	8	164.8539	6.809e-14	***
block	10.06	11	1.1103	0.4127	
Residuals	13.19	16			

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

>

> # get the contrasts of interest

> c1<-c(-1,-1,-1,-1,-1,-1,-1,-1,8)

> c2<-c(1,1,1,1,-1,-1,-1,-1,0)

> c3<-c(-3,-1,1,3,0,0,0,0,0)

> c41<-c(1,-1,-1,1,0,0,0,0,0)

> c42<-c(-1,3,-3,1,0,0,0,0,0)

> c5<-c(0,0,0,0,-3,-1,1,3,0)

> c61<-c(0,0,0,0,1,-1,-1,1,0)

> c62<-c(0,0,0,0,-1,3,-3,1,0)

>

> lsmeans(m1,specs=ls~dishsoap,contr=list(lsm=list(control_vs_others=c1,
+ detergentI_vs_detergentII=c2,

+ linear_in_additive_detergentI=c3,
+ #

+ nonlinear_in_additive_detergentI=list(c41,c42),
+ #

+ linear_in_additive_detergentII=c5
+ #

+ nonlinear_in_additive_detergentII=list(c61,c62)
+)))

\$`dishsoap lsmeans`

dishsoap	lsmean	SE	df	lower.CL	upper.CL
a	19.750000	0.5167795	16	18.654476	20.845524
b	17.194444	0.5167795	16	16.098921	18.289968
c	13.194444	0.5167795	16	12.098921	14.289968
d	6.527778	0.5167795	16	5.432254	7.623301
e	25.305556	0.5167795	16	24.210032	26.401079
f	22.972222	0.5167795	16	21.876699	24.067746
g	21.083333	0.5167795	16	19.987810	22.178857
h	19.194444	0.5167795	16	18.098921	20.289968
i	29.527778	0.5167795	16	28.432254	30.623301

\$`dishsoap lsm`

	estimate	SE	df	t.ratio	p.value
control_vs_others	91.00000	4.447221	16	20.46222	0
detergentI_vs_detergentII	-31.88889	1.482407	16	-21.51156	0
linear_in_additive_detergentI	-43.66667	2.343891	16	-18.62999	0
linear_in_additive_detergentII	-20.22222	2.343891	16	-8.62763	0

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

```

> # nonlinear_in_additive_detergentI and nonlinear_in_additive_detergentII lines
above
> # are 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 nonlinear_in_additive_detergentI and
> # nonlinear_in_additive_detergentII tests with glht:
>
> K1 <- rbind( "quadratic detergentI" = c41,
+             "cubic detergentI" = c42)
> K2 <- rbind( "quadratic detergentII" = c61,
+             "cubic detergentII" = c62)
>
>
> summary(glht(m1, linfct = mcp(dishsoap = K1 )),test=Ftest())

```

General Linear Hypotheses

Multiple Comparisons of Means: User-defined Contrasts

Linear Hypotheses:

	Estimate
quadratic detergentI == 0	-4.111
cubic detergentI == 0	-1.222

Global Test:

	F	DF1	DF2	Pr(>F)
1	7.827	2	16	0.004261

```

> summary(glht(m1, linfct = mcp(dishsoap = K2 )),test=Ftest())

```

General Linear Hypotheses

Multiple Comparisons of Means: User-defined Contrasts

Linear Hypotheses:

	Estimate
quadratic detergentII == 0	0.4444
cubic detergentII == 0	-0.4444

Global Test:

	F	DF1	DF2	Pr(>F)
1	0.1079	2	16	0.8984

```

>

```

```

> # use package effects to get means instead of lsmeans for each level of
> # dishsoap. These are inappropriate estimates of the treatment means in an
> # incomplete block design like this one; they are produced here only for
> # comparison with the ls means (or fitted means from the model), which are
> # appropriate here.
> effect("dishsoap",m1)

```

```

dishsoap effect

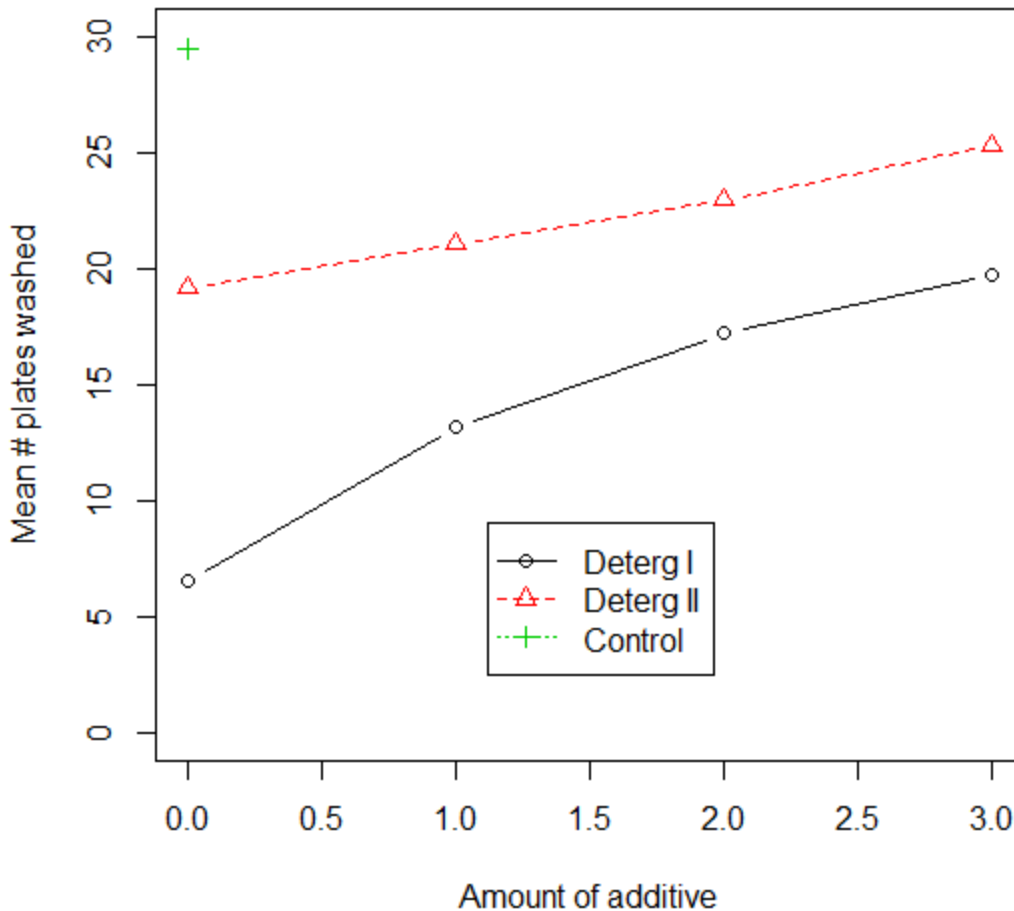
```

```

dishsoap
  a          b          c          d          e          f          g          h
19.750000 17.194444 13.194444  6.527778 25.305556 22.972222 21.083333 19.194444
  i
29.527778
>
> # get the profile plot
> # create variables "add" and "deterg"
>
>
> dsoapmeans <- lsmeans(m1, specs=~dishsoap)[[1]]
> dsoapmeans$add <- c(3,2,1,0,3,2,1,0,0)
> dsoapmeans$deterg <- c(1,1,1,1,2,2,2,2,3)
> head(dsoapmeans)
  dishsoap  lsmean      SE df  lower.CL  upper.CL  add deterg
    a 19.750000 0.5167795 16 18.654476 20.845524   3     1
    b 17.194444 0.5167795 16 16.098921 18.289968   2     1
    c 13.194444 0.5167795 16 12.098921 14.289968   1     1
    d  6.527778 0.5167795 16  5.432254  7.623301   0     1
    e 25.305556 0.5167795 16 24.210032 26.401079   3     2
    f 22.972222 0.5167795 16 21.876699 24.067746   2     2
>
> plot(dsoapmeans$add[1:4], dsoapmeans$lsmean[1:4], ylim=c(0,30), type="b",
+      lty=1, pch=1, col=1,
+      main="Mean # plates washed by amt of additive", ylab="Mean # plates washed",
+      xlab="Amount of additive")
> lines(dsoapmeans$add[5:8], dsoapmeans$lsmean[5:8], type="b", lty=2, pch=2, col=2)
> points(dsoapmeans$add[9], dsoapmeans$lsmean[9], type="b", pch=3, col=3)
> legend(locator(1), legend=c("Deterg I", "Deterg II", "Control"),
+       lty=c(1,2,3), pch=c(1,2,3), col=c(1,2,3))

```

Mean # plates washed by amt of additive



```
>
> #### part 2 mixed models (combined intra- and inter-block analysis)
> m2<-lmer(dishes~dishsoap+(1|block),data=dishwash)
> summary(m2)
Linear mixed model fit by REML ['lmerMod']
Formula: dishes ~ dishsoap + (1 | block)
Data: dishwash
```

REML criterion at convergence: 84.9649

Random effects:

Groups	Name	Variance	Std.Dev.
block	(Intercept)	0.05636	0.2374
	Residual	0.80437	0.8969

Number of obs: 36, groups: block, 12

Fixed effects:

	Estimate	Std. Error	t value
(Intercept)	19.7500	0.4625	42.70
dishsoapb	-2.9395	0.6484	-4.53
dishsoapc	-6.5076	0.6484	-10.04
dishsoapd	-13.2462	0.6484	-20.43
dishsoape	5.7235	0.6484	8.83
dishsoapf	3.4622	0.6484	5.34

```
dishsoapg    1.0454    0.6484    1.61
dishsoaph   -0.5076    0.6484   -0.78
dishsoapi    9.9697    0.6484   15.38
```

Correlation of Fixed Effects:

```
(Intr) dshspb dshspc dshspd dishsoape dshspf dshspg dshsph
dishsoapb -0.701
dishsoapc -0.701  0.500
dishsoapd -0.701  0.500  0.500
dishsoape -0.701  0.500  0.500  0.500
dishsoapf -0.701  0.500  0.500  0.500  0.500
dishsoapg -0.701  0.500  0.500  0.500  0.500    0.500
dishsoaph -0.701  0.500  0.500  0.500  0.500    0.500  0.500
dishsoapi -0.701  0.500  0.500  0.500  0.500    0.500  0.500  0.500
```

```
>
> # use the same contrasts
> lsmeans(m2, specs=ls~dishsoap, contr=list(lsm=list(control_vs_others=c1,
+                                             detergentI_vs_detergentII=c2,
+
+ linear_in_additive_detergentI=c3,
+                                             #
+ nonlinear_in_additive_detergentI=list(c41,c42),
+
+ linear_in_additive_detergentII=c5
+                                             #
+ nonlinear_in_additive_detergentII=list(c61,c62)
+                                             )))
```

```
$`dishsoap lsmeans`
  dishsoap    lsmean      SE      df  lower.CL  upper.CL
a  19.750000  0.4905492  20.96695  18.729749  20.770251
b  16.810523  0.4905492  20.96695  15.790273  17.830774
c  13.242435  0.4905492  20.96695  12.222184  14.262685
d   6.503783  0.4905492  20.96695   5.483532   7.524034
e  25.473521  0.4905492  20.96695  24.453270  26.493772
f  23.212173  0.4905492  20.96695  22.191922  24.232424
g  20.795393  0.4905492  20.96695  19.775142  21.815643
h  19.242435  0.4905492  20.96695  18.222184  20.262685
i  29.719738  0.4905492  20.96695  28.699487  30.739989
```

```
$`dishsoap lsm`
              estimate      SE      df  t.ratio p.value
control_vs_others      92.72764  4.159505  18.91116  22.29295     0
detergentI_vs_detergentII -32.41678  1.386502  18.91116 -23.38027     0
linear_in_additive_detergentI -43.30674  2.192252  18.91116 -19.75446     0
linear_in_additive_detergentII -21.11004  2.192252  18.91116  -9.62939     0
  p values are not adjusted
```

```
>
> # summary(glht(m2, linfct = mcp(dishsoap = K1)), test=Ftest())
> # summary(glht(m2, linfct = mcp(dishsoap = K2)), test=Ftest())
> # glht doesn't work for lmer, so refit the model using the lme function in
> # the nlme package
>
> # First create a groupedData data frame (same as the dishwash data frame
> # but adds a grouping structure to indicate that data are grouped by block)
> dish2 <- groupedData(dishes~dishsoap|block, data=dishwash)
>
```



```

+
nonlinear_in_additive_detergentI=list(c41,c42),
+
linear_in_additive_detergentII=c5
+
nonlinear_in_additive_detergentII=list(c61,c62)
+
))

```

```

$dishsoap lsmeans`
dishsoap    lsmean          SE df asymp.LCL asymp.UCL
a 19.750000 0.4624954 NA 18.843526 20.656474
b 16.810521 0.4624954 NA 15.904047 17.716996
c 13.242435 0.4624954 NA 12.335960 14.148909
d  6.503783 0.4624954 NA  5.597308  7.410257
e 25.473522 0.4624954 NA 24.567048 26.379996
f 23.212174 0.4624954 NA 22.305700 24.118649
g 20.795391 0.4624954 NA 19.888917 21.701865
h 19.242435 0.4624954 NA 18.335960 20.148909
i 29.719739 0.4624954 NA 28.813265 30.626214

```

```

$dishsoap lsm`
              estimate          SE df    z.ratio p.value
control_vs_others          92.72765 3.890480 NA  23.83450      0
detergentI_vs_detergentII    -32.41678 1.296827 NA -24.99700      0
linear_in_additive_detergentI -43.30674 2.050463 NA -21.12047      0
linear_in_additive_detergentII -21.11004 2.050463 NA -10.29526      0
p values are not adjusted

```

```

>
> # similarly, the tests for the 2 df contrasts given below are large sample
> # chisquare tests
> # not F tests. However the relationship between these chisq test statistics
> # and the F test statistics given by PROC MIXED is simple
> # (F test stat)*(num df) = chisq test stat.
>
> summary(glht(m2a, linfct = mcp(dishsoap = K1 )),test=Ftest())

```

General Linear Hypotheses

Multiple Comparisons of Means: User-defined Contrasts

Linear Hypotheses:

	Estimate
quadratic detergentI == 0	-3.799
cubic detergentI == 0	-2.542

Global Test:

```

Chisq DF Pr(>Chisq)
1 18.7 2 8.688e-05

```

Warning message:

```

In test(object) :

```

```

'df.residual' is not available for 'model' a Chisq test is performed instead of
the requested F test.

```

```

> summary(glht(m2a, linfct = mcp(dishsoap = K2 )),test=Ftest())

```

General Linear Hypotheses

Multiple Comparisons of Means: User-defined Contrasts

Linear Hypotheses:

	Estimate
quadratic detergentII == 0	0.7084
cubic detergentII == 0	1.0193

Global Test:

Chisq	DF	Pr(>Chisq)
1 0.8439	2	0.6558

Warning message:

In test(object) :

'df.residual' is not available for 'model' a Chisq test is performed instead of the requested F test.

>

>