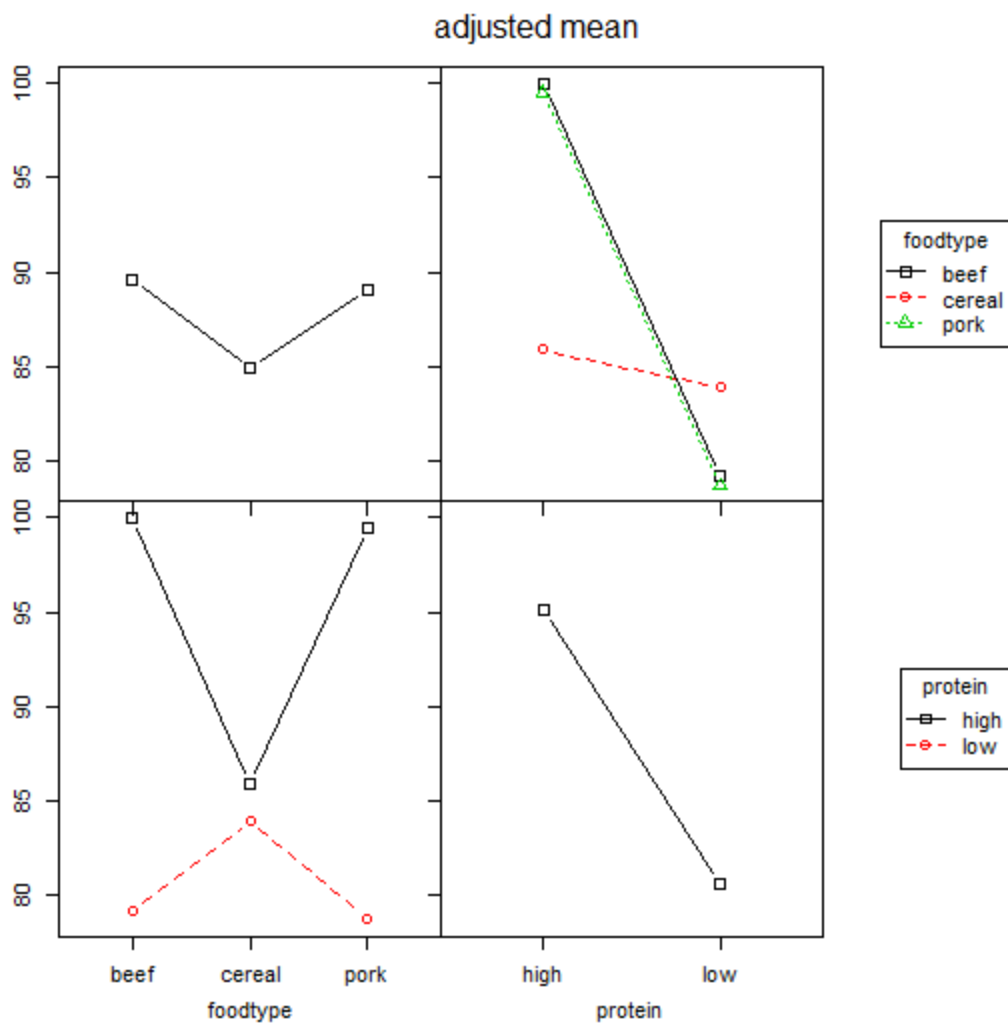


Output from rats.R

```
> #rats.R
>
> library(lsmmeans)
Loading required package: plyr
Loading required package: multcomp
Loading required package: mvtnorm
Loading required package: survival
Loading required package: splines
Warning messages:
1: package 'lsmmeans' was built under R version 3.0.2
2: package 'plyr' was built under R version 3.0.2
3: package 'multcomp' was built under R version 3.0.2
> library(phia)
Loading required package: car
Warning messages:
1: package 'phia' was built under R version 3.0.2
2: package 'car' was built under R version 3.0.2
>
> # get the data
> ratdata <- read.table(file="ratdata.dat",header=T)
> head(ratdata)
  wgtgain foodtype protein
1      73    beef    high
2      98  cereal    high
3      94    pork    high
4      90    beef    low
5     107  cereal    low
6      49    pork    low
> levels(ratdata$foodtype)
[1] "beef" "cereal" "pork"
> levels(ratdata$protein)
[1] "high" "low"
>
> # fit the two-way anova model
> m1 <- aov(wgtgain~foodtype*protein,data=ratdata)
> summary(m1)

              Df Sum Sq Mean Sq F value    Pr(>F)
foodtype      2    267    133  0.621 0.541132
protein       1   3168   3168 14.767 0.000322 ***
foodtype:protein 2   1178    589  2.746 0.073188 .
Residuals    54  11586    215

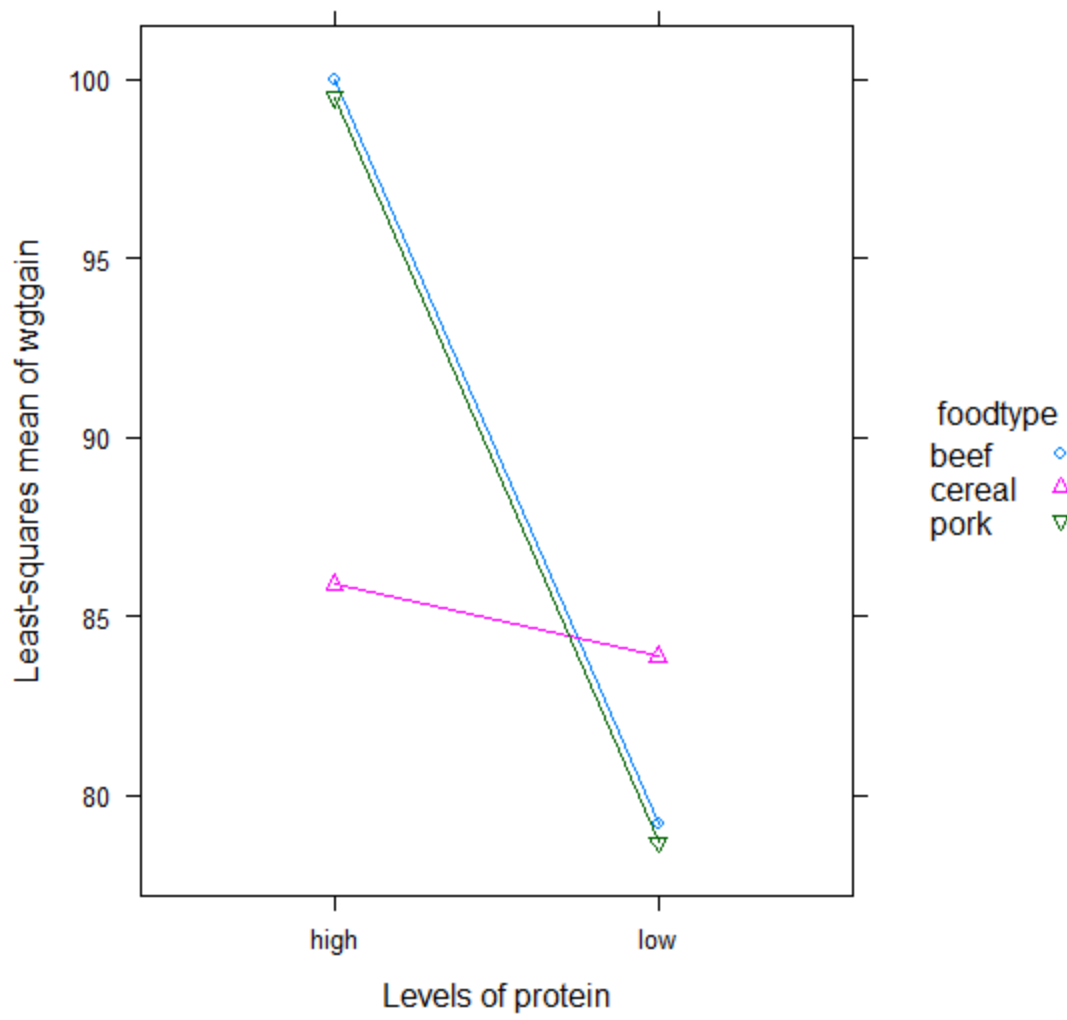
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
>
> # get profile plots (uses package phia)
> ( trtmns <- interactionMeans(m1) )
  foodtype protein adjusted mean
1    beef    high    100.0
2  cereal    high    85.9
3   pork    high    99.5
4    beef    low    79.2
5  cereal    low    83.9
6   pork    low    78.7
> plot(trtmns)
```



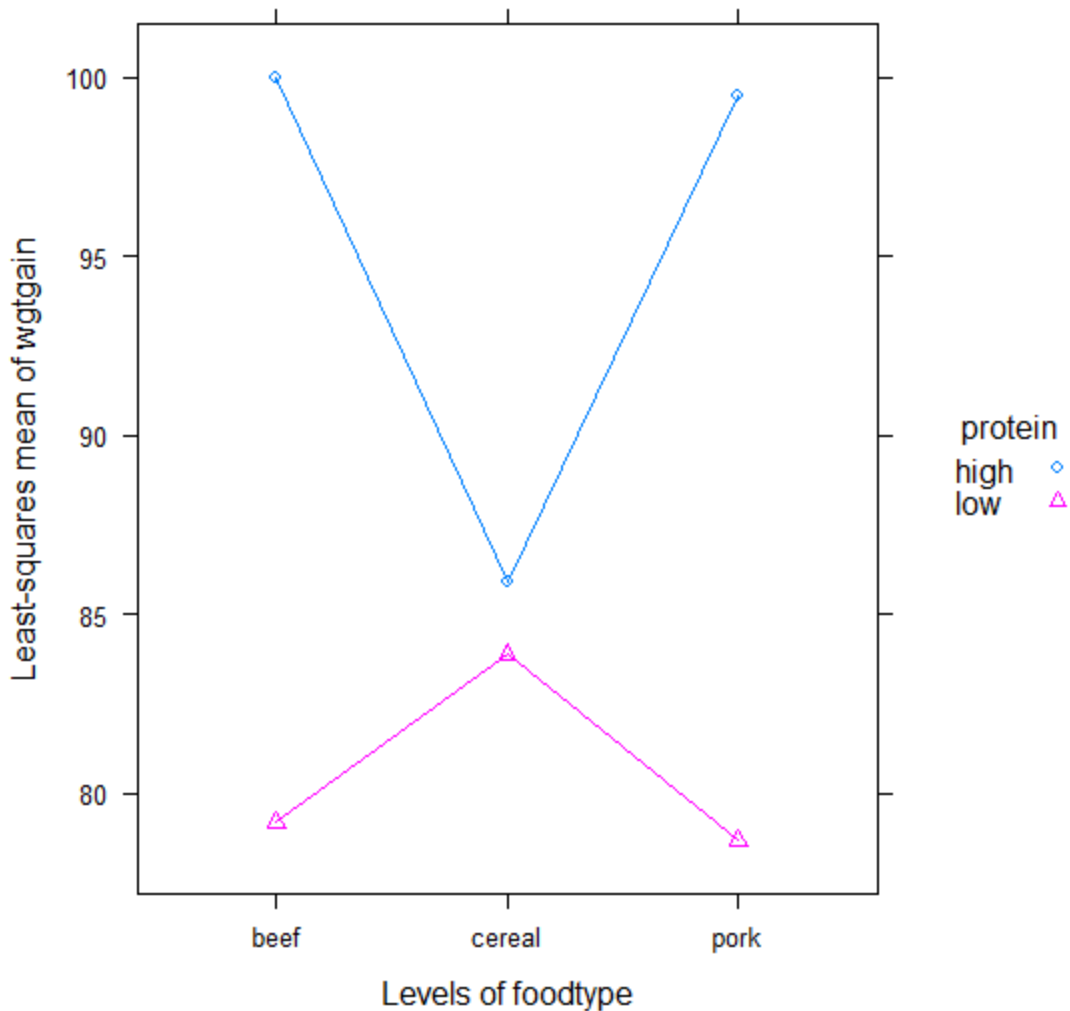
```

>
> # alternatively can use function lsmip from lsmeans package
> # for profile plots:
> lsmip(m1, foodtype~protein)
Loading required package: lattice

```



```
> lsmip(m1,protein~foodtype)
```



```

>
> # test effects slices (aka simple effects) (uses package phia)
> testInteractions(m1, fixed="foodtype", across="protein", adjustment="none")
F Test:
P-value adjustment method: none
      Value Df Sum of Sq      F    Pr(>F)
beef    20.8  1    2163.2 10.0822 0.002474 **
cereal   2.0  1     20.0  0.0932 0.761302
pork    20.8  1    2163.2 10.0822 0.002474 **
Residuals      54    11586.0
---
Signif. codes:  0 '****' 0.001 '***' 0.01 '**' 0.05 '.' 0.1 ' ' 1
> testInteractions(m1, fixed="protein", across="foodtype", adjustment="none")
F Test:
P-value adjustment method: none
      foodtype1 foodtype2 Df Sum of Sq      F    Pr(>F)
high          0.5     -13.6  2    1280.1 2.9831 0.05904 .
low           0.5       5.2  2     164.6 0.3836 0.68326
Residuals                54    11586.0
---
Signif. codes:  0 '****' 0.001 '***' 0.01 '**' 0.05 '.' 0.1 ' ' 1
>
> # set up and test interaction contrasts (uses package phia)
> (custom.contr <- contrastCoefficients(

```

```

+ foodtype ~ cereal - (beef + pork)/2,
+ foodtype ~ beef - pork,
+ protein ~ high - low,
+ data=ratdata, normalize=FALSE))
$foodtype
      foodtype foodtype.1
beef      -0.5           1
cereal     1.0           0
pork      -0.5          -1

$protein
      protein
high     1
low     -1

>
> names(custom.contr$foodtype) <- c("cereal.vs.meat", "beef.vs.pork")
> names(custom.contr$protein) <- c("high.vs.low")
>
> testInteractions(m1, custom=custom.contr, adjust="none")
F Test:
P-value adjustment method: none

              Value Df Sum of Sq      F Pr(>F)
cereal.vs.meat : high.vs.low -18.8  1    1178.1 5.491 0.02283 *
  beef.vs.pork : high.vs.low   0.0  1         0.0 0.000 1.00000
Residuals                54    11586.0
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

>
>
> # main effect contrasts (uses package lsmeans)
> # These are not advisable in this example
> lsmeans(m1, specs = lsm ~ foodtype,
+   contr=list(lsm=custom.contr$foodtype ) )
$`foodtype lsmeans`
  foodtype lsmean      SE df lower.CL upper.CL
    beef     89.6 3.275329 54 83.03336 96.16664
   cereal     84.9 3.275329 54 78.33336 91.46664
    pork     89.1 3.275329 54 82.53336 95.66664

$`foodtype lsm`
              estimate      SE df  t.ratio p.value
cereal.vs.meat    -4.45 4.011442 54 -1.10933 0.27220
beef.vs.pork       0.50 4.632014 54  0.10794 0.91444
  p values are not adjusted

Warning message:
In lsmeans(m1, specs = lsm ~ foodtype, contr = list(lsm = custom.contr$foodtype))
:
  lsmeans of foodtype may be misleading due to interaction with other
predictor(s)
> lsmeans(m1, specs = lsm ~ protein,
+   contr=list(lsm=custom.contr$protein ) )
$`protein lsmeans`
  protein  lsmean      SE df lower.CL  upper.CL
    high 95.13333 2.674295 54 89.77170 100.49497
    low  80.60000 2.674295 54 75.23836  85.96164

```

```

$`protein lsm`
      estimate      SE df t.ratio p.value
high.vs.low 14.53333 3.782024 54 3.84274 0.00032
p values are not adjusted

```

Warning message:

```

In lsmeans(m1, specs = lsm ~ protein, contr = list(lsm = custom.contr$protein)) :
  lsmeans of protein may be misleading due to interaction with other predictor(s)

```

```

>
> # now test the contrasts of interest among foodtypes separately for
> # each protein level
>
> c1 <- c(1,-2,1,0,0,0)/2
> c2 <- c(1,0,-1,0,0,0)
> c3 <- c(0,0,0,1,-2,1)/2
> c4 <- c(0,0,0,1,0,-1)
>

```

```

> lsmeans(m1, specs = lsm ~ foodtype:protein,
+   contr=list(lsm=list(meat.v.cer.high=c1,b.v.p.high=c2,
+   meat.v.cer.low=c3,b.v.p.low=c4  ) ) )

```

```

$`foodtype:protein lsmeans`
  foodtype protein lsmean      SE df lower.CL upper.CL
  beef      high   100.0 4.632014 54 90.71337 109.28663
  cereal    high    85.9 4.632014 54 76.61337  95.18663
  pork      high    99.5 4.632014 54 90.21337 108.78663
  beef      low     79.2 4.632014 54 69.91337  88.48663
  cereal    low     83.9 4.632014 54 74.61337  93.18663
  pork      low     78.7 4.632014 54 69.41337  87.98663

```

```

$`foodtype:protein lsm`
      estimate      SE df  t.ratio p.value
meat.v.cer.high   13.85 5.673036 54  2.44137 0.01794
b.v.p.high         0.50 6.550657 54  0.07633 0.93944
meat.v.cer.low    -4.95 5.673036 54 -0.87255 0.38677
b.v.p.low         0.50 6.550657 54  0.07633 0.93944
p values are not adjusted

```

```

>
>

```