

MANOVA. PLS206 Fall 2013

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Concept and elements

```
> ddig <- read.csv("../Examples/digMANOVA.dat", header=TRUE)
> str(ddig)

'data.frame':      24 obs. of  6 variables:
 $ animal: int   578 583 589 594 599 577 580 585 591 576 ...
 $ diet  : Factor w/ 5 levels "AA","A0","MM",...: 1 1 1 1 1 2 2 2 2 3 ...
 $ dmd   : num   64.8 62.5 62.1 64.9 68.8 57.9 63.3 60 59.3 61.4 ...
 $ ndfd  : num   49.2 46.7 44 49.2 54.5 43.8 51.3 48.9 45.5 33.5 ...
 $ adfd  : num   47.8 43.6 42.2 46.7 52.1 43.6 50.1 45.5 43.8 44 ...
 $ cellud: num   37.8 41.8 44.2 38.9 35.5 46.5 39.1 43.8 45.2 39.9 ...

> ddig$animal <- factor(ddig$animal)
> # options(contrasts =c("contr.treatment", "contr.poly"))
> man1 <- manova(cbind(dmd,ndfd,adfd,cellud) ~ diet, ddig)
> str(man1)

List of 13
 $ coefficients : num [1:5, 1:4] 64.62 -4.5 -3.34 -2.6 -4.2 ...
 ..- attr(*, "dimnames")=List of 2
 .. ..$ : chr [1:5] "(Intercept)" "dietA0" "dietMM" "dietM0" ...
 .. ..$ : chr [1:4] "dmd" "ndfd" "adfd" "cellud"
 $ residuals    : num [1:24, 1:4] 0.18 -2.12 -2.52 0.28 4.18 ...
 ..- attr(*, "dimnames")=List of 2
 .. ..$ : chr [1:24] "1" "2" "3" "4" ...
 .. ..$ : chr [1:4] "dmd" "ndfd" "adfd" "cellud"
 $ effects      : num [1:24, 1:4] -302.553 -3.578 -2.079 -0.913 -6.641 ...
 ..- attr(*, "dimnames")=List of 2
 .. ..$ : chr [1:24] "(Intercept)" "dietA0" "dietMM" "dietM0" ...
 .. ..$ : chr [1:4] "dmd" "ndfd" "adfd" "cellud"
 $ rank         : int 5
 $ fitted.values: num [1:24, 1:4] 64.6 64.6 64.6 64.6 64.6 ...
 ..- attr(*, "dimnames")=List of 2
 .. ..$ : chr [1:24] "1" "2" "3" "4" ...
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.. ..$ : chr [1:4] "dmd" "ndfd" "adfd" "cellud"
$ assign      : int [1:5] 0 1 1 1 1
$ qr          :List of 5
..$ qr       : num [1:24, 1:5] -4.899 0.204 0.204 0.204 0.204 ...
.. ..- attr(*, "dimnames")=List of 2
.. .. ..$ : chr [1:24] "1" "2" "3" "4" ...
.. .. ..$ : chr [1:5] "(Intercept)" "dietAO" "dietMM" "dietMO" ...
.. ..- attr(*, "assign")= int [1:5] 0 1 1 1 1
.. ..- attr(*, "contrasts")=List of 1
.. .. ..$ diet: chr "contr.treatment"
..$ qraux: num [1:5] 1.2 1.08 1.1 1.13 1.2
..$ pivot: int [1:5] 1 2 3 4 5
..$ tol   : num 1e-07
..$ rank  : int 5
..- attr(*, "class")= chr "qr"
$ df.residual : int 19
$ contrasts    :List of 1
..$ diet: chr "contr.treatment"
$ xlevels      :List of 1
..$ diet: chr [1:5] "AA" "AO" "MM" "MO" ...
$ call         : language manova(cbind(dmd, ndfd, adfd, cellud) ~ diet, ddig)
$ terms        :Classes 'terms', 'formula' length 3 cbind(dmd, ndfd, adfd, cellud) ~ diet
.. ..- attr(*, "variables")= language list(cbind(dmd, ndfd, adfd, cellud), diet)
.. ..- attr(*, "factors")= int [1:2, 1] 0 1
.. .. ..- attr(*, "dimnames")=List of 2
.. .. ..$ : chr [1:2] "cbind(dmd, ndfd, adfd, cellud)" "diet"
.. .. ..$ : chr "diet"
.. ..- attr(*, "term.labels")= chr "diet"
.. ..- attr(*, "order")= int 1
.. ..- attr(*, "intercept")= int 1
.. ..- attr(*, "response")= int 1
.. ..- attr(*, ".Environment")=<environment: R_GlobalEnv>
.. ..- attr(*, "predvars")= language list(cbind(dmd, ndfd, adfd, cellud), diet)
.. ..- attr(*, "dataClasses")= Named chr [1:2] "nmatrix.4" "factor"
.. .. ..- attr(*, "names")= chr [1:2] "cbind(dmd, ndfd, adfd, cellud)" "diet"
$ model        :'data.frame':      24 obs. of  2 variables:
..$ cbind(dmd, ndfd, adfd, cellud): num [1:24, 1:4] 64.8 62.5 62.1 64.9 68.8 57.9 63.3 60
.. ..- attr(*, "dimnames")=List of 2
.. .. ..$ : NULL
.. .. ..$ : chr [1:4] "dmd" "ndfd" "adfd" "cellud"
..$ diet       : Factor w/ 5 levels "AA","AO","MM",...: 1 1 1 1 1 2 2 2
..- attr(*, "terms")=Classes 'terms', 'formula' length 3 cbind(dmd, ndfd, adfd, cellud) ~
.. ..- attr(*, "variables")= language list(cbind(dmd, ndfd, adfd, cellud), diet)
.. .. ..- attr(*, "factors")= int [1:2, 1] 0 1
.. .. ..- attr(*, "dimnames")=List of 2
.. .. ..$ : chr [1:2] "cbind(dmd, ndfd, adfd, cellud)" "diet"

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.. .. ..$ : chr "diet"
.. .. ..- attr(*, "term.labels")= chr "diet"
.. .. ..- attr(*, "order")= int 1
.. .. ..- attr(*, "intercept")= int 1
.. .. ..- attr(*, "response")= int 1
.. .. ..- attr(*, ".Environment")=<environment: R_GlobalEnv>
.. .. ..- attr(*, "predvars")= language list(cbind(dmd, ndfd, adfd, cellud), diet)
.. .. ..- attr(*, "dataClasses")= Named chr [1:2] "nmatrix.4" "factor"
.. .. ..- attr(*, "names")= chr [1:2] "cbind(dmd, ndfd, adfd, cellud)" "diet"
- attr(*, "class")= chr [1:5] "manova" "maov" "aov" "mlm" ...

> (sum.man1 <- summary(man1, test="Wilks"))

           Df      Wilks approx F num Df den Df      Pr(>F)
diet           4 0.0018831    21.04      16 49.518 < 2.2e-16 ***
Residuals 19
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> str(sum.man1)

List of 4
 $ row.names : chr [1:2] "diet" "Residuals"
 $ SS        :List of 2
  ..$ diet    : num [1:4, 1:4] 62.06 3.63 -12.95 -37.01 3.63 ...
  .. ..- attr(*, "dimnames")=List of 2
  .. .. ..$ : chr [1:4] "dmd" "ndfd" "adfd" "cellud"
  .. .. ..$ : chr [1:4] "dmd" "ndfd" "adfd" "cellud"
  ..$ Residuals: num [1:4, 1:4] 157 216 212 -167 216 ...
  .. ..- attr(*, "dimnames")=List of 2
  .. .. ..$ : chr [1:4] "dmd" "ndfd" "adfd" "cellud"
  .. .. ..$ : chr [1:4] "dmd" "ndfd" "adfd" "cellud"
 $ Eigenvalues: num [1, 1:4] 62.11196 5.88714 0.219 0.00224
  ..- attr(*, "dimnames")=List of 2
  .. ..$ : chr "diet"
  .. ..$ : NULL
 $ stats      : num [1:2, 1:6] 4 19 0.00188 NA 21.04044 ...
  ..- attr(*, "dimnames")=List of 2
  .. ..$ : chr [1:2] "diet" "Residuals"
  .. ..$ : chr [1:6] "Df" "Wilks" "approx F" "num Df" ...
  - attr(*, "class")= chr "summary.manova"

> library(car)
> Anova(man1, test="Wilks")

Type II MANOVA Tests: Wilks test statistic
           Df test stat approx F num Df den Df      Pr(>F)

```

```

diet  4 0.0018831    21.04    16 49.518 < 2.2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> library(candisc)
> man1.can1 <-candisc(man1, term="diet")
> plot(man1.can1)

Vector scale factor set to 14

> library(heplots)
> heplot3d(man1.can1, scale=6, fill=TRUE)
>

```