Multivariate Analysis of Variance

Multivariate analysis of variance

- Standard ANOVA has just one response variable.
- What if you have more than one response?
- Try an ANOVA on each response separately.
- But might miss some kinds of interesting dependence between the responses that distinguish the groups.

Packages

```r
library(car) # may need to install first
library(tidyverse)
library(MVTests) # also may need to install
```

Small example

- Measure yield and seed weight of plants grown under 2 conditions: low and high amounts of fertilizer.
- Data (fertilizer, yield, seed weight):

```
url <- "http://ritsokiguess.site/datafiles/manova1.txt"
hilo <- read_delim(url, " ")
```

- 2 responses, yield and seed weight.

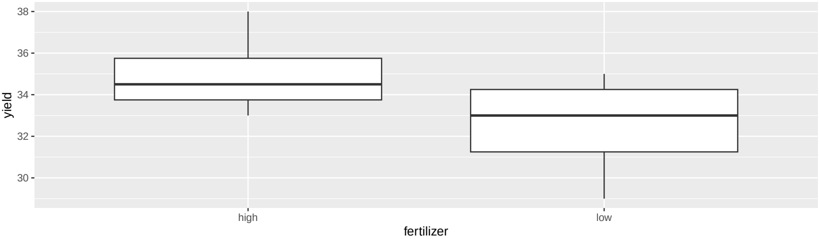
The data

```
hilo
```

```
# A tibble: 8 x 3
  fertilizer yield weight
  <chr>      <dbl>  <dbl>
1 low           34     10
2 low           29     14
3 low           35     11
4 low           32     13
5 high          33     14
6 high          38     12
7 high          34     13
8 high          35     14
```

Boxplot for yield for each fertilizer group

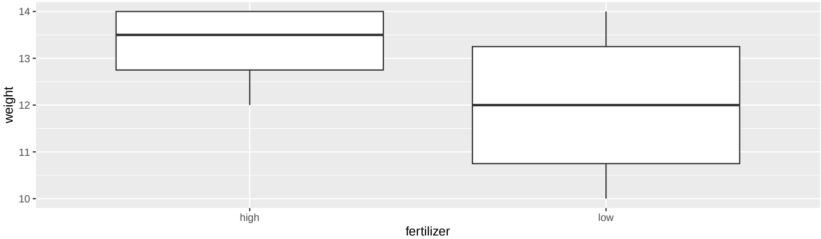
```
ggplot(hilo, aes(x = fertilizer, y = yield)) + geom_boxplot
```



Yields overlap for fertilizer groups.

Boxplot for weight for each fertilizer group

```
ggplot(hilo, aes(x = fertilizer, y = weight)) + geom_boxplo
```



Weights overlap for fertilizer groups.

ANOVAs for yield and weight

```
hilo.y <- aov(yield ~ fertilizer, data = hilo)
summary(hilo.y)
```

```
            Df Sum Sq Mean Sq F value Pr(>F)
fertilizer   1   12.5  12.500   2.143  0.194
Residuals    6   35.0   5.833
```

```
hilo.w <- aov(weight ~ fertilizer, data = hilo)
summary(hilo.w)
```

```
            Df Sum Sq Mean Sq F value Pr(>F)
fertilizer   1  3.125   3.125   1.471  0.271
Residuals    6 12.750   2.125
```

Neither response depends significantly on fertilizer. But…

Plotting both responses at once

- Have two response variables (not more), so can plot the response variables against *each other*, labelling points by which fertilizer group they're from.

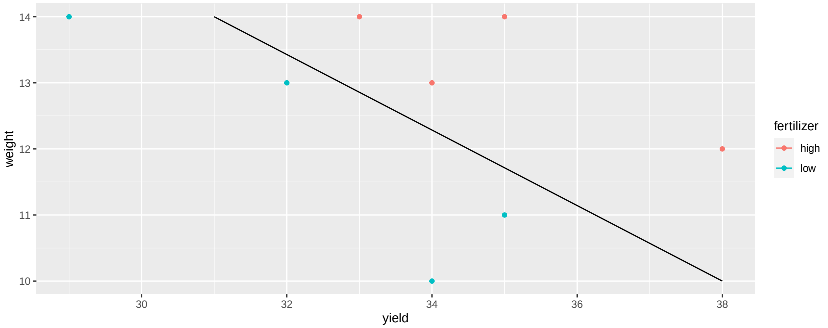
- First, create data frame with points $(31, 14)$ and $(38, 10)$ (why? Later):

```
d <- tribble(
  ~line_x, ~line_y,
  31, 14,
  38, 10
)
```

- Then plot data as points, and add line through points in `d`:

```
ggplot(hilo, aes(x = yield, y = weight,
                     colour = fertilizer)) + geom_point() +
  geom_line(data = d,
            aes(x = line_x, y = line_y, colour = NULL)) -> g
```

The plot



Comments

- Graph construction:
  - Joining points in `d` by line.
  - `geom_line` inherits `colour` from `aes` in `ggplot`.
  - Data frame `d` has no `fertilizer` (previous `colour`), so have to unset.
- Results:
  - High-fertilizer plants have both yield and weight high.
  - True even though no sig difference in yield or weight individually.
  - Drew line separating highs from lows on plot.

MANOVA finds multivariate differences

- Is difference found by diagonal line significant? MANOVA finds out.

```
response <- with(hilo, cbind(yield, weight))
hilo.1 <- manova(response ~ fertilizer, data = hilo)
summary(hilo.1)
```

```
           Df  Pillai approx F num Df den Df  Pr(>F)  
fertilizer  1 0.80154   10.097      2      5 0.01755 *
Residuals   6                                         
---
Signif. codes:  
0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

- Yes! Difference between groups is *diagonally*, not just up/down (weight) or left-right (yield). The *yield-weight combination* matters.

Strategy

- Create new response variable by gluing together columns of responses, using `cbind`.
- Use `manova` with new response, looks like `lm` otherwise.
- With more than 2 responses, cannot draw graph. What then?
- If MANOVA test significant, cannot use Tukey. What then?
- Use *discriminant analysis* (of which more later).

Another way to do MANOVA

using Manova from package car:

```
hilo.2.lm <- lm(response ~ fertilizer, data = hilo)
hilo.2 <- Manova(hilo.2.lm)
summary(hilo.2)
```

```
Type II MANOVA Tests:

Sum of squares and products for error:
       yield weight
yield     35 -18.00
weight   -18  12.75

------------------------------------------

Term: fertilizer

Sum of squares and products for the hypothesis:
       yield weight
yield  12.50  6.250
weight  6.25  3.125

Multivariate Tests: fertilizer
                 Df test stat approx F num Df den Df   Pr(>F)
Pillai            1  0.801542 10.09714      2      5 0.017546 *
Wilks             1  0.198458 10.09714      2      5 0.017546 *
Hotelling-Lawley  1  4.038855 10.09714      2      5 0.017546 *
Roy               1  4.038855 10.09714      2      5 0.017546 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Comments

- Same result as small-m `manova`.
- `Manova` will also do *repeated measures*, coming up later.

Assumptions

- normality of each response variable within each treatment group
    - this is actually *multivariate* normality, with correlations
- equal spreads: each response variable has same variances and correlations (with other response variables) within each treatment group. Here:
    - yield has same spread for low and high fertilizer
    - weight has same spread for low and high fertilizer
    - correlation between yield and weight is same for low and high fertilizer
- test equal spread using Box's M test
    - a certain amount of unequalness is OK, so only a concern if P-value from M-test is very small (eg. less than 0.001).

Assumptions for yield-weight data

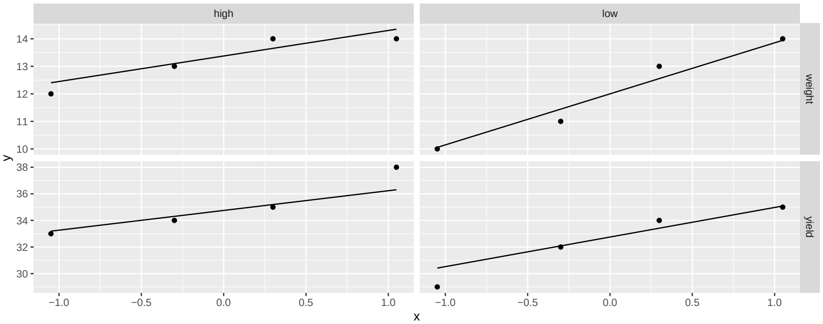
For normal quantile plots, need “extra-long” with all the data values in one column:

```
hilo %>%
  pivot_longer(-fertilizer, names_to = "xname",
                 values_to = "xvalue") %>%
  ggplot(aes(sample = xvalue)) + stat_qq() +
    stat_qq_line() +
    facet_grid(xname ~ fertilizer, scales = "free") -> g
```

There are only four observations per response variable - treatment group combination, so graphs are not very informative (over):

The plots

```
g
```


high
low
weight
yield
y
x
14
13
12
11
10
38
36
34
32
30
−1.0
−0.5
0.0
0.5
1.0

Box M test

- Make sure package `MVTests` loaded first.
- inputs:
  - the response matrix (or, equivalently, the response-variable columns from your dataframe)
  - the column with the grouping variable in it (most easily gotten with $).

```r
hilo %>% select(yield, weight) -> numeric_values
summary(BoxM(numeric_values, hilo$fertilizer))
```

```
        Box's M Test 

Chi-Squared Value = 1.002964 , df = 3  and p-value: 0.801 
```

- No problem at all with unequal spreads.

Another example: peanuts

- Three different varieties of peanuts (mysteriously, 5, 6 and 8) planted in two different locations.
- Three response variables: `y`, `smk` and `w`.

```
u <- "http://ritsokiguess.site/datafiles/peanuts.txt"
peanuts.orig <- read_delim(u, " ")
```

The data

```
peanuts.orig
```

```
# A tibble: 12 x 6
     obs location variety     y   smk     w
   <dbl>    <dbl>   <dbl> <dbl> <dbl> <dbl>
 1     1        1       5  195.  153.  51.4
 2     2        1       5  194.  168.  53.7
 3     3        2       5  190.  140.  55.5
 4     4        2       5  180.  121.  44.4
 5     5        1       6  203   157.  49.8
 6     6        1       6  196.  166   45.8
 7     7        2       6  203.  166.  60.4
 8     8        2       6  198.  162.  54.1
 9     9        1       8  194.  164.  57.8
10    10        1       8  187   165.  58.6
11    11        2       8  202.  167.  65  
12    12        2       8  200   174.  67.2
```

Setup for analysis

```
peanuts.orig %>%
  mutate(
    location = factor(location),
    variety = factor(variety)
  ) -> peanuts
response <- with(peanuts, cbind(y, smk, w))
head(response)
```

```
         y   smk    w
[1,] 195.3 153.1 51.4
[2,] 194.3 167.7 53.7
[3,] 189.7 139.5 55.5
[4,] 180.4 121.1 44.4
[5,] 203.0 156.8 49.8
[6,] 195.9 166.0 45.8
```

Analysis (using Manova)

```r
peanuts.1 <- lm(response ~ location * variety, data = peanuts)
peanuts.2 <- Manova(peanuts.1)
summary(peanuts.2)
```

```
Type II MANOVA Tests:

Sum of squares and products for error:
          y     smk       w
y   104.205  49.365  76.480
smk  49.365 352.105 121.995
w    76.480 121.995  94.835

------------------------------------------

Term: location

Sum of squares and products for the hypothesis:
              y       smk           w
y     0.7008333  -10.6575    7.129167
smk -10.6575000  162.0675 -108.412500
w     7.1291667 -108.4125   72.520833

Multivariate Tests: location
                 Df test stat approx F num Df den Df   Pr(>F)
Pillai            1  0.893484 11.18432      3      4 0.020502 *
Wilks             1  0.106516 11.18432      3      4 0.020502 *
Hotelling-Lawley  1  8.388243 11.18432      3      4 0.020502 *
Roy               1  8.388243 11.18432      3      4 0.020502 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

------------------------------------------

Term: variety
```

Comments

- Interaction not quite significant, but main effects are.
- Combined response variable `(y,smk,w)` definitely depends on location and on variety
- Weak dependence of `(y,smk,w)` on the location-variety *combination.*
- Understanding that dependence beyond our scope right now.

Comments

- this time there are only six observations per location and four per variety, so normality is still difficult to be confident about
- `y` at location 1 seems to be the worst for normality (long tails / outliers), and maybe `y` at location 2 is skewed left, but the others are not bad
- there is some evidence of unequal spread (slopes of lines), but is it bad enough to worry about? (Box M-test, over).

Box's M tests

- One for location, one for variety:

```r
summary(BoxM(response, peanuts$location))
```

```
       Box's M Test

Chi-Squared Value = 12.47797 , df = 6  and p-value: 0.0521
```

```r
summary(BoxM(response, peanuts$variety))
```

```
       Box's M Test

Chi-Squared Value = 10.56304 , df = 12  and p-value: 0.567
```

- Neither of these P-values is low enough to worry about. (Remember, the P-value here has to be *really* small to indicate a problem.)