Multivariate analysis of variance (MANOVA)

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, " ")
```

```
## Rows: 8 Columns: 3
## -- Column specification ----------------------------
## Delimiter: " "
## chr (1): fertilizer
## dbl (2): yield, weight
##
## i Use `spec()` to retrieve the full column specification fo
## i Specify the column types or set `show_col_types = FALSE`
```

- 2 responses, yield and seed weight.

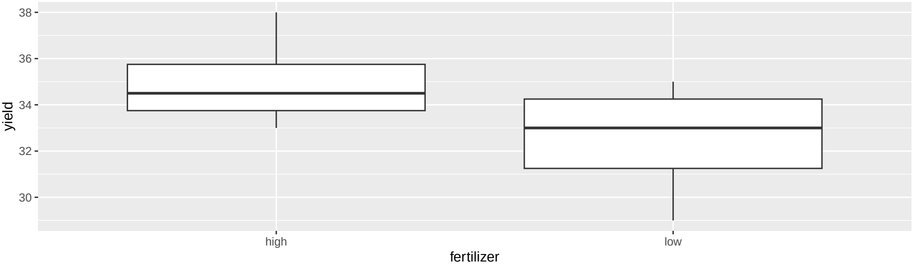
The data

```
hilo
```

fertilizer	yield	weight
low	34	10
low	29	14
low	35	11
low	32	13
high	33	14
high	38	12
high	34	13
high	35	14

Boxplot for yield for each fertilizer group

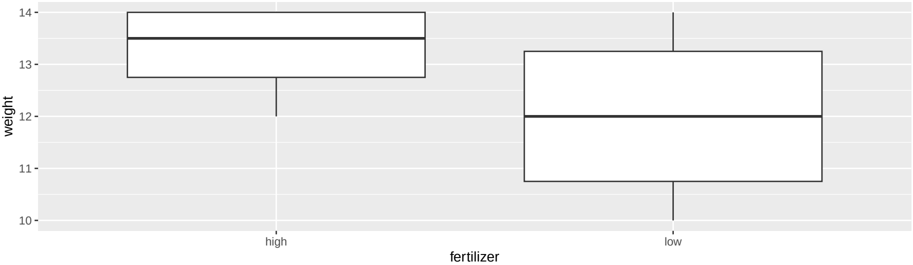
```
ggplot(hilo, aes(x = fertilizer, y = yield)) + geom_boxplot()
```



Yields overlap for fertilizer groups.

Boxplot for weight for each fertilizer group

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



Weights overlap for fertilizer groups.

ANOVAs for yield and weight

```r
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
```

```r
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.

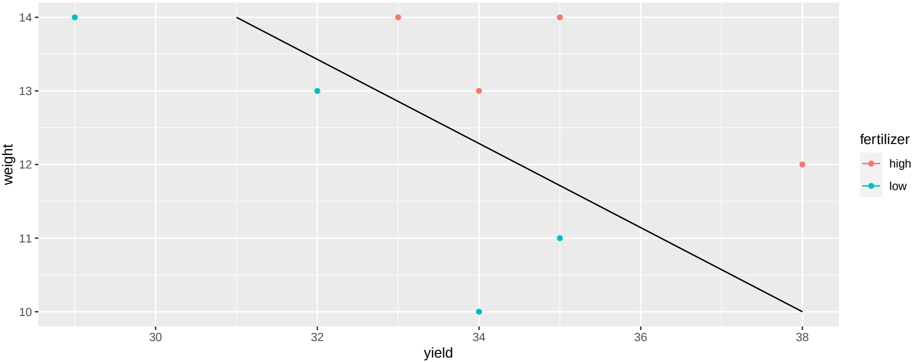
- First, create data frame with points $(31, 14)$ and $(38, 10)$ (why? Later):

```
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

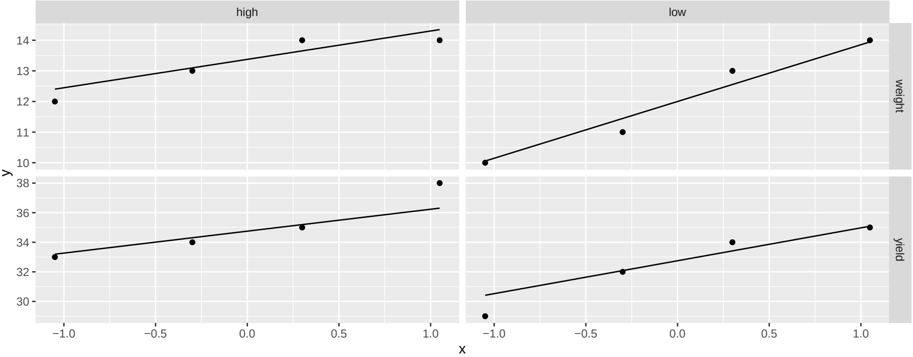
For normal quantile plots, need “extra-long” with all the data values in one column:

```r
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 $).

```
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, " ")
```

```
## Rows: 12 Columns: 6
## -- Column specification -------------------------------
## Delimiter: " "
## dbl (6): obs, location, variety, y, smk, w
##
## i Use `spec()` to retrieve the full column specification fo
## i Specify the column types or set `show_col_types = FALSE`
```

The data

```
peanuts.orig
```

obs	location	variety	y	smk	w
1	1	5	195.3	153.1	51.4
2	1	5	194.3	167.7	53.7
3	2	5	189.7	139.5	55.5
4	2	5	180.4	121.1	44.4
5	1	6	203.0	156.8	49.8
6	1	6	195.9	166.0	45.8
7	2	6	202.7	166.1	60.4
8	2	6	197.6	161.8	54.1
9	1	8	193.5	164.5	57.8
10	1	8	187.0	165.1	58.6
11	2	8	201.5	166.8	65.0
12	2	8	200.0	173.8	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)

```
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
##
```

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.

Normal quantile plots

Setup for normal quantile plots

```
peanuts %>%
  pivot_longer(y:w, names_to = "xname",
               values_to = "xvals") -> d
```

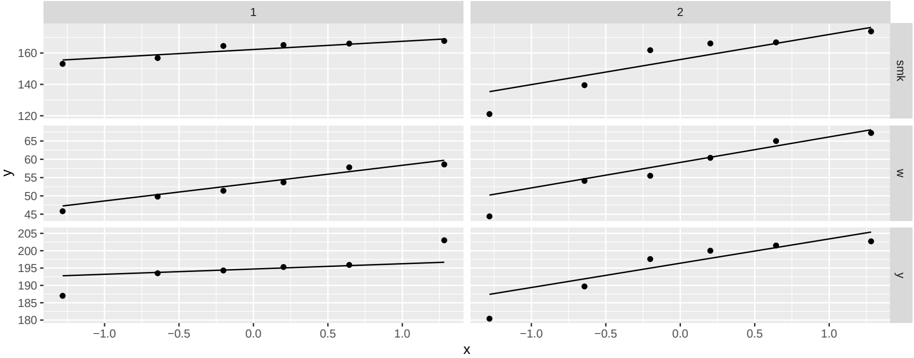
Make the plots (save to show on next pages)

```
ggplot(d, aes(sample = xvals)) + stat_qq() +
  stat_qq_line() +
  facet_grid(xname ~ location, scales = "free") -> g1

ggplot(d, aes(sample = xvals)) + stat_qq() +
  stat_qq_line() +
  facet_grid(xname ~ variety, scales = "free") -> g2
```

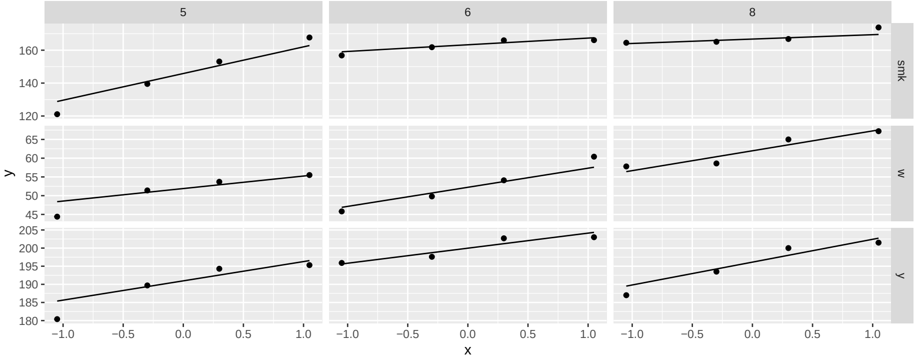
The plot for location

```
g1
```



The plot for variety

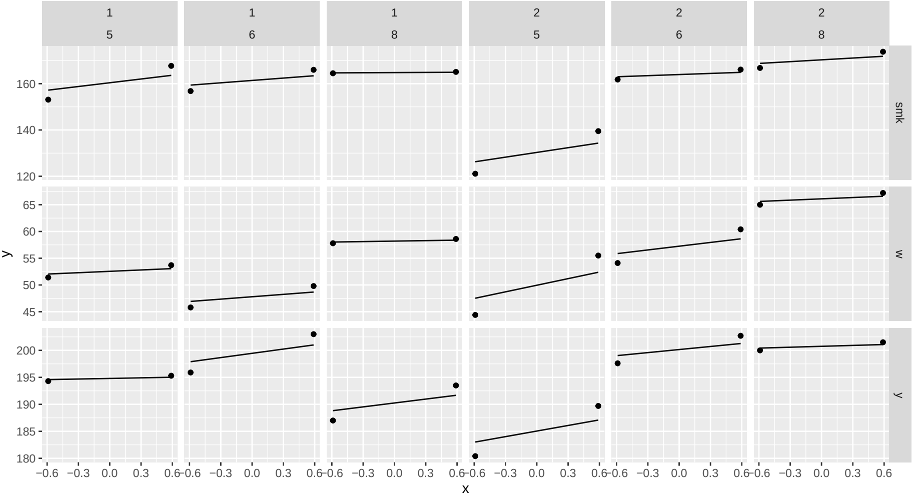
```
g2
```



Alternative: show both these plots at once:

```
ggplot(d, aes(sample = xvals)) + stat_qq() +
  stat_qq_line() +
  facet_grid(xname ~ location + variety,
             scales = "free") -> g3
```

The combined plot



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:

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

```
##         Box's M Test
##
## Chi-Squared Value = 12.47797 , df = 6  and p-value: 0.0521
```

```
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.)