

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

```
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

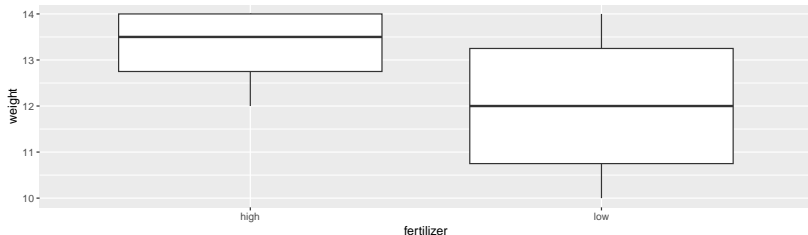
```
ggplot(hilo, aes(x = fertilizer, y = yield)) + geom_boxplot
```



Yields overlap for fertilizer groups.

Boxplot for weight for each fertilizer group

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



Weights overlap for fertilizer groups.

ANOVAs for yield and weight

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

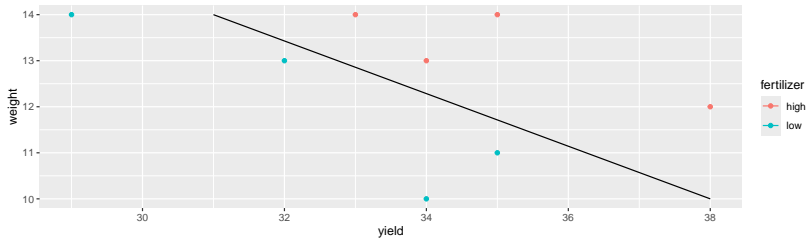
| | Df | Sum Sq | Mean Sq | F value | Pr(>F) |
|------------|----|--------|---------|---------|--------|
| fertilizer | 1 | 12.5 | 12.500 | 2.143 | 0.194 |
| Residuals | 6 | 35.0 | 5.833 | | |

```
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...

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))  
response
```

| | yield | weight |
|------|-------|--------|
| [1,] | 34 | 10 |
| [2,] | 29 | 14 |
| [3,] | 35 | 11 |
| [4,] | 32 | 13 |
| [5,] | 33 | 14 |
| [6,] | 38 | 12 |
| [7,] | 34 | 13 |
| [8,] | 35 | 14 |

```
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 | | | | | |

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

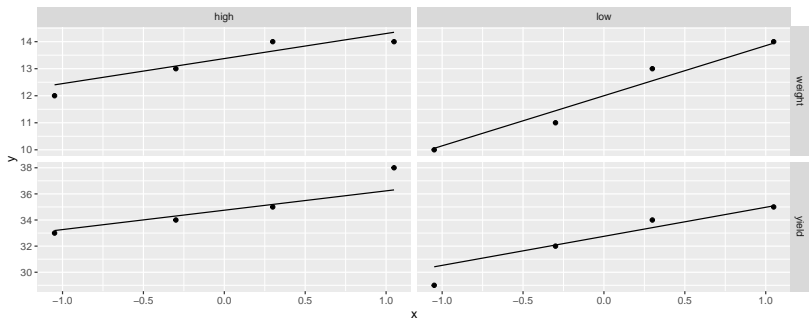
For normal quantile plots, need “extra-long” with all the data values in one column:

```
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

gg



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 `$`).

```
library(MVTests)
# hilo %>% select(yield, weight) -> numeric_values
summary(BoxM(response, 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)

```
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

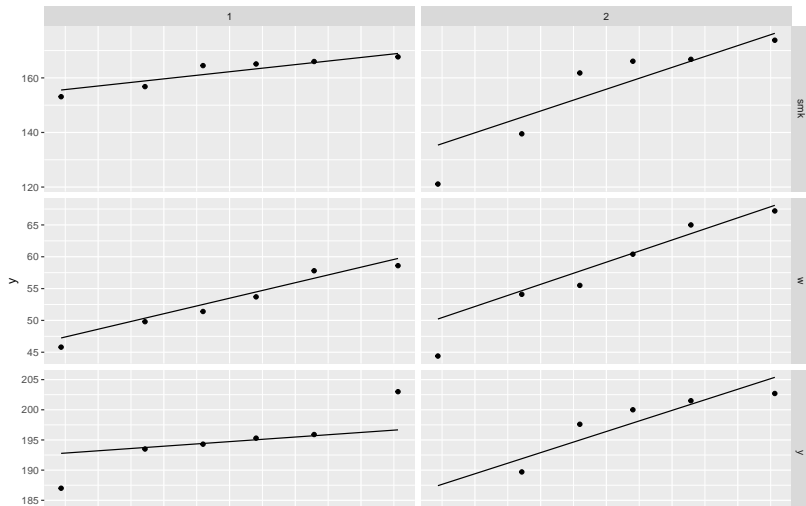
- ▶ Interaction not quite significant, but main effects are.
- ▶ Combined response variable (y, smk, w) definitely depends on location and on variety
- ▶ Weak dependence of (y, smk, w) on the location-variety *combination*.
- ▶ Understanding that dependence beyond our scope right now.

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).

Assessing normality

```
peanuts %>% pivot_longer(y:w, names_to = "yname", values_to = "y") %>%  
  ggplot(aes(sample = y)) + stat_qq() + stat_qq_line() +  
  facet_grid(yname ~ location, scales = "free_y")
```



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.)