Multivariate Analysis of Variance

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STAT 4690-Applied Multivariate Analysis

Quick Overview

What do we mean by Analysis of Variance?

- ANOVA is a collection of statistical models that aim to analyze and understand the differences in means between different subgroups of the data.
 - As such, it can be seen as a generalisation of the t-test (or of Hotelling's T^2).
 - Note that there could be multiple, overlapping ways of defining the subgroups (e.g multiway ANOVA)
- It also provides a framework for hypothesis testing.
 - Which can be recovered from a suitable regression model.
- Most importantly, ANOVA provides a framework for understanding and comparing the various sources of variation in the data.

Review of univariate ANOVA i

Assume the data comes from g populations:

$$X_{11}, \ldots, X_{1n_1}$$
 $\vdots \quad \ddots \quad \vdots$
 X_{g1}, \ldots, X_{gn_g}

- Assume that $X_{\ell 1}, \ldots, X_{\ell n_{\ell}}$ is a random sample from $N(\mu_{\ell}, \sigma^2)$, for $\ell = 1, \ldots, g$.
 - Homoscedasticity
- We are interested in testing the hypothesis that $\mu_1 = \ldots = \mu_g$.

Review of univariate ANOVA ii

- Reparametrisation: We will write the mean $\mu_{\ell} = \mu + \tau_{\ell}$ as a sum of an overall component μ (i.e. shared by all populations) and a population-specific component τ_{ℓ} .
 - Our hypothesis can now be rewritten as $\tau_\ell=0$, for all ℓ .
 - We can write our observations as

$$X_{\ell i} = \mu + \tau_{\ell} + \varepsilon_{\ell i},$$

where $\varepsilon_{\ell i} \sim N(0, \sigma^2)$.

• Identifiability: We need to assume $\sum_{\ell=1}^g \tau_\ell = 0$, otherwise there are infinitely many models that lead to the same data-generating mechanism.

Review of univariate ANOVA ii

- Sample statistics: Set $n = \sum_{\ell=1}^g n_\ell$.
 - Overall sample mean: $\bar{X} = \frac{1}{n} \sum_{\ell=1}^g \sum_{i=1}^{n_\ell} X_{\ell i}$.
 - Population-specific sample mean: $\bar{X}_{\ell} = \frac{1}{n_{\ell}} \sum_{i=1}^{n_{\ell}} X_{\ell i}$.
- We get the following decomposition:

$$(X_{\ell i} - \bar{X}) = (\bar{X}_{\ell} - \bar{X}) + (X_{\ell i} - \bar{X}_{\ell}).$$

- Squaring the left-hand side and summing over both ℓ and i, we get

$$\sum_{\ell=1}^{g} \sum_{i=1}^{n_{\ell}} \left(X_{\ell i} - \bar{X} \right)^2 = \sum_{\ell=1}^{g} n_{\ell} \left(\bar{X}_{\ell} - \bar{X} \right)^2 + \sum_{\ell=1}^{g} \sum_{i=1}^{n_{\ell}} \left(X_{\ell i} - \bar{X}_{\ell} \right)^2.$$

Review of univariate ANOVA iv

- This is typically summarised as $SS_T = SS_M + SS_R$:
 - The total sum of squares:

$$SS_T = \sum_{\ell=1}^g \sum_{i=1}^{n_\ell} \left(X_{\ell i} - \bar{X} \right)^2$$

The model (or treatment) sum of squares:

$$SS_M = \sum_{\ell=1}^g n_\ell \left(\bar{X}_\ell - \bar{X} \right)^2$$

• The residual sum of squares:

$$SS_R = \sum_{\ell=1}^g \sum_{i=1}^{n_\ell} \left(X_{\ell i} - \bar{X}_\ell \right)^2$$

Review of univariate ANOVA v

• Yet another representation is the ANOVA table:

Source of Variation	Sum of Squares	Degrees of freedom
Model	SS_M	g-1
Residual	SS_R	n-g
Total	SS_T	n-1

- The usual test statistic used for testing $\tau_\ell=0$ for all ℓ is

$$F = \frac{SS_M/(g-1)}{SS_R/(n-g)} \sim F(g-1, n-g).$$

Review of univariate ANOVA vi

 We could also instead reject the null hypothesis for small values of

$$\frac{SS_R}{SS_R + SS_M} = \frac{SS_R}{SS_T}.$$

This is the test statistic that we will generalize to the multivariate setting.

Multivariate ANOVA i

The setting is similar: Assume the data comes from g populations:

$$egin{array}{ccccc} \mathbf{Y}_{11}, & \ldots, & \mathbf{Y}_{1n_1} \\ drain & \ddots & drain \\ \mathbf{Y}_{g1}, & \ldots, & \mathbf{Y}_{gn_g} \end{array}$$

- Assume that $\mathbf{Y}_{\ell 1}, \dots, \mathbf{Y}_{\ell n_{\ell}}$ is a random sample from $N_p(\mu_{\ell}, \Sigma)$, for $\ell = 1, \dots, g$.
 - Homoscedasticity is key here again.
- We are again interested in testing the hypothesis that $\mu_1=\ldots=\mu_g.$

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Multivariate ANOVA i

- Reparametrisation: We will write the mean as $\mu_\ell = \mu + au_\ell$
 - $\mathbf{Y}_{\ell i} = \mu + \tau_{\ell} + \mathbf{E}_{\ell i}$, where $\mathbf{E}_{\ell i} \sim N_p(0, \Sigma)$.
- **Identifiability**: We need to assume $\sum_{\ell=1}^g \tau_\ell = 0$.
- Instead of a decomposition of the sum of squares, we get a decomposition of the outer product:

$$(\mathbf{Y}_{\ell i} - \bar{\mathbf{Y}})(\mathbf{Y}_{\ell i} - \bar{\mathbf{Y}})^T.$$

Multivariate ANOVA iii

The decomposition is given as

$$\sum_{\ell=1}^{g} \sum_{i=1}^{n_{\ell}} (\mathbf{Y}_{\ell i} - \bar{\mathbf{Y}}) (\mathbf{Y}_{\ell i} - \bar{\mathbf{Y}})^{T} = \sum_{\ell=1}^{g} n_{\ell} (\bar{\mathbf{Y}}_{\ell} - \bar{\mathbf{Y}}) (\bar{\mathbf{Y}}_{\ell} - \bar{\mathbf{Y}})^{T} + \sum_{\ell=1}^{g} \sum_{i=1}^{n_{\ell}} (\mathbf{Y}_{\ell i} - \bar{\mathbf{Y}}_{\ell}) (\mathbf{Y}_{\ell i} - \bar{\mathbf{Y}}_{\ell})^{T}.$$

Between sum of squares and cross products matrix:

$$B = \sum_{\ell=1}^{g} n_{\ell} (\bar{\mathbf{Y}}_{\ell} - \bar{\mathbf{Y}}) (\bar{\mathbf{Y}}_{\ell} - \bar{\mathbf{Y}})^{T}.$$

Within sum of squares and cross products matrix:

$$\mathbf{W} = \sum_{\ell=1}^{g} \sum_{i=1}^{n_{\ell}} (\mathbf{Y}_{\ell i} - \bar{\mathbf{Y}}_{\ell}) (\mathbf{Y}_{\ell i} - \bar{\mathbf{Y}}_{\ell})^{T}.$$

Multivariate ANOVA iv

- Note that $W = \sum_{\ell=1}^g (n_\ell 1) S_\ell$.
- Similarly as above, we have a MANOVA table:

Source of Variation	Sum of Squares	Degrees of freedom
Model	В	g-1
Residual	W	n-g
Total	B+W	n-1

■ To test the null hypothesis $H_0: \tau_\ell = 0$ for all $\ell = 1, \ldots, g$, we will use Wilk's lambda as our test statistic:

$$\Lambda = \frac{|W|}{|B+W|}.$$

Multivariate ANOVA v

• There is actually no closed-form for the null distribution of Λ , so we will use Bartlett's approximation:

$$-\left(n-1-\frac{1}{2}(p+g)\right)\log\Lambda\approx\chi^2((g-1)p).$$

In particular, if we let $c=\chi^2_{\alpha}((n-1)p)$ be the critical value, we reject the null hypothesis if

$$\Lambda \le \exp\left(\frac{-c}{n - 1 - 0.5(p + g)}\right).$$

Example i

```
## Example on producing plastic film
## from Krzanowski (1998, p. 381)
tear \leftarrow c(6.5, 6.2, 5.8, 6.5, 6.5, 6.9, 7.2,
          6.9, 6.1, 6.3, 6.7, 6.6, 7.2, 7.1,
          6.8.\ 7.1.\ 7.0.\ 7.2.\ 7.5.\ 7.6
gloss \leftarrow c(9.5, 9.9, 9.6, 9.6, 9.2, 9.1, 10.0,
           9.9. 9.5. 9.4. 9.1. 9.3. 8.3. 8.4.
           8.5, 9.2, 8.8, 9.7, 10.1, 9.2)
opacity \leftarrow c(4.4, 6.4, 3.0, 4.1, 0.8, 5.7, 2.0,
              3.9, 1.9, 5.7, 2.8, 4.1, 3.8, 1.6,
              3.4, 8.4, 5.2, 6.9, 2.7, 1.9
```

Example ii

```
Y <- cbind(tear, gloss, opacity)
Y low <- Y[1:10,]
Y high <- Y[11:20,]
n <- nrow(Y); p <- ncol(Y); g <- 2
W \leftarrow (nrow(Y low) - 1)*cov(Y low) +
  (nrow(Y high) - 1)*cov(Y high)
B < -(n-1)*cov(Y) - W
(Lambda <- det(W)/det(W+B))
```

[1] 0.4136192

Example iii

```
transf_lambda \leftarrow -(n - 1 - 0.5*(p + g))*log(Lambda)
transf lambda > qchisq(0.95, p*(g-1))
## [1] TRUE
# Or if you want a p-value
pchisq(transf lambda, p*(g-1), lower.tail = FALSE)
## [1] 0.002227356
```

Example iv

```
# R has a function for MANOVA
# But first, create factor variable
rate <- gl(g, 10, labels = c("Low", "High"))

fit <- manova(Y ~ rate)
summary_tbl <- broom::tidy(fit, test = "Wilks")
# Or you can use the summary function</pre>
```

```
knitr::kable(summary_tbl, digits = 3)
```

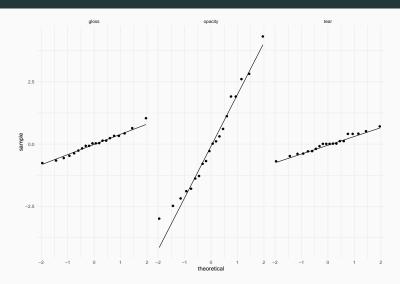
Example v

term	df	wilks	statistic	num.df	den.df	p.value
rate	1	0.414	7.561	3	16	0.002
Residuals	18	-	-	-	-	-

Example vi

```
# Check residuals for evidence of normality
library(tidyverse)
fit %>%
  residuals %>%
  as.data.frame() %>%
  gather(variable, residual) %>%
  ggplot(aes(sample = residual)) +
  stat qq() + stat qq line() +
  facet grid(. ~ variable) +
  theme minimal()
```

Example vii



Comments i

- The output from R shows a different approximation to the Wilk's lambda distribution, due to Rao.
- There are actually 4 tests available in R (we will discuss them in the next lecture):
 - Wilk's lambda;
 - Pillai-Bartlett;
 - Hotelling-Lawley;
 - Roy's Largest Root.

Comments ii

- Since we only had two groups in the above example, we were only comparing two means.
 - Wilk's lambda was therefore equivalent to Hotelling's T^2 .
 - But of course MANOVA is much more general.
- We can assess the normality assumption by looking at the residuals $\mathbf{E}_{\ell i} = \mathbf{Y}_{\ell i} \bar{\mathbf{Y}}_{\ell}.$

Testing for Equality of Covariance Matrices i

- Last lecture, when comparing two multivariate means, and again today, we talked about homoscedasticity as an important assumption.
- This is a testable assumption, i.e. we can devise a corresponding hypothesis test.
- Our null hypothesis: $H_0: \Sigma_1 = \cdots = \Sigma_g$, where Σ_ℓ is the covariance matrix for population ℓ .
- In this course, we will discuss Box' M-test
 - This test is based on a comparison of generalized variances.

Testing for Equality of Covariance Matrices ii

 Under the normality assumption, the likelihood ratio statistic for the null hypothesis above is

$$\Lambda = \prod_{\ell=1}^{g} \left(\frac{|S_{\ell}|}{|S_{pool}|} \right)^{(n_{\ell}-1)/2}.$$

■ Here, S_{ℓ} is the sample covariance for population ℓ , and S_{pool} is the pooled estimator:

$$S_{pool} = \frac{1}{n-1} \left(\sum_{\ell=1}^{g} (n_{\ell} - 1) S_{\ell} \right) = \frac{1}{n-1} W.$$

Testing for Equality of Covariance Matrices iii

Box's M-statistic is defined as

$$M = -2 \log \Lambda$$
.

■ The general theory of Likelihood Ratio Tests tells us that $M \approx \chi^2(\nu)$ for an appropriate value $\nu>0$.

Testing for Equality of Covariance Matrices iv

Box's Test for Equality of Covariance Matrices Set

$$u = \left(\sum_{\ell=1}^{g} \frac{1}{n_{\ell} - 1} - \frac{1}{n - g}\right) \left(\frac{2p^2 + 3p - 1}{6(p + 1)(g - 1)}\right).$$

Then C=(1-u)M has approximate $\chi^2(\nu)$ distribution, where

$$\nu = \frac{1}{2}p(p+1)(g-1).$$

Comments about Box's M-test

- Good approximation if $n_{\ell} > 20$ for all ℓ and both $g, p \leq 5$.
 - Not very realistic for modern datasets...
- There is another approximation using the F distribution when the conditions above are not met.
 - See Rencher (1998), Section 4.3.
- However, Box's M-test is especially sensitive to departures from normality.
- In general, one can also use graphical tests.
- Key result: With large and approximately equal sample sizes, MANOVA is relatively robust to heteroscedasticity.

Example (cont'd) i

```
S_low <- cov(Y_low)
S_high <- cov(Y_high)
S_pool <- W/(n - 1)

c("pool" = log(det(S_pool)),
    "low" = log(det(S_low)),
    "high" = log(det(S_high)))</pre>
```

```
## pool low high
## -2.370911 -2.949096 -2.013061
```

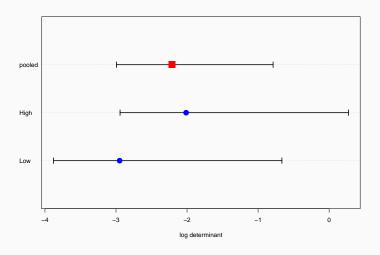
Example (cont'd) ii

```
library(heplots)
(boxm res <- boxM(Y, rate))
##
   Box's M-test for Homogeneity of Covariance Matrices
##
##
## data: Y
## Chi-Sq (approx.) = 4.0175, df = 6, p-value = 0.6743
```

Example (cont'd) iii

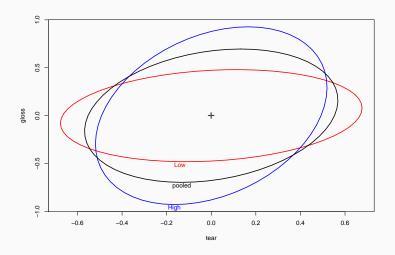
```
# You can plot the log generalized variances
# The plot function adds 95% CI
plot(boxm_res)
```

Example (cont'd) iv



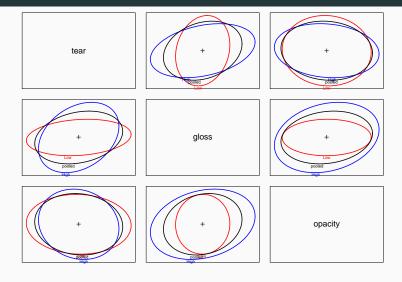
Example (cont'd) v

Example (cont'd) vi



Example (cont'd) vii

Example (cont'd) viii



Strategy for Multivariate Comparison of Treatments

- 1. Try to identify outliers.
 - This should be done graphically at first.
 - Once the model is fitted, you can also look at influence measures.
- 2. Perform a multivariate test of hypothesis.
- 3. If there is evidence of a multivariate difference, calculate Bonferroni confidence intervals and investigate component-wise differences.
 - The projection of the confidence region onto each variable generally leads to confidence intervals that are too large.