G E P BOX'S M-TEST FOR EQUALITY OF POPULATION COVARIANCE MATRICES
FINAL PROJECT : UIC STAT522 (SPRING 2023)

QAYUM KHAN

1. EXECUTIVE SUMMARY

When each of independent observations has several components, we are in the situation of multivariate statistics. When those responses are organized into finitely many known groups and we would like to test for similarity of the subpopulations (typically, of their intragroup mean vectors and intragroup covariance matrices), we would then like to apply multivariate analysis of variance (MANOVA). Typically the model is set up with a grand mean, then a fixed treatment-effect offset to each group's mean, possibly more offsets if studying multiway (multifactor) effects, and idiosyncratic errors. However, the mechanism of MANOVA has three assumptions (see textbook's two models [JW07, 6-38, 6-59]):

(1) the errors have intergroup independence (the subpopulations don't influence each other) as well as intragroup independence,
(2) per group the errors are identically multinormally distributed with population mean zero, and
(3) population covariance matrices between groups are identical.

The purpose of G E P Box's M-test is to check whether the latter condition (3) is satisfied, given that the former two conditions are satisfied. Thus, it is a critical tool for the correct setup of any MANOVA model.

Box's M-test works well when both the dimension of observations and the number of groups are each less than five, and the number of observations per group is more than twenty. Besides limited ranges, it is known to be sensitive to the normality assumption (2), whereas Wilks' Λ^* for testing equality of means is more robust to nonnormality.

In Sections 2–3, we consider the rigorous mathematics behind the statistical test, especially its weighting coefficient. In subsequent sections, we discuss the appendices in which R programs are run on various multivariate datasets. There is a prebuilt function `boxM()` in the CRAN library `heplots`. This library of Michael Friendly handles sum-of-squares-and-cross-products (SSP) matrices for linear hypotheses (H) and errors (E) using intervals/ellipses; graphics are drawn via `plot()`.

2. Historical Context and Scientific Statement

The main source of this exposition is Box's original paper [Box49]. We use the same notation, except we write g for the number of population groups rather than k, which we reserve for a summation index.

Consider g mutually independent groups (1) of random multivariate samples $x_{lj} \in \mathbb{R}^p$. Suppose that they are multinormally (2) distributed:

$$X_{l1}, \ldots, X_{ln_l} \overset{\text{iid}}{\sim} \mathcal{N}_p(\mu_l, A_l) \quad \text{for all } 1 \leqslant l \leqslant g.$$

Here, the l-th group nonuniformly has n_l samples, $\mu_l \in \mathbb{R}^p$ is unknown population mean, and $A_l \in \mathbb{R}^{p \times p}$ is the unknown population covariance.

Write $\nu_l := n_l - 1$ for the l-th degree of freedom, $N := \nu_1 + \cdots + \nu_g$ for total number of degrees of freedom, and $\nu := N/g$ for average number of degrees of freedom. The (unbiased) **sample covariance matrix** is

$$S_l := \nu_l^{-1} \sum_{j=1}^{n_l} (x_{lj} - \overline{x}_l)(x_{lj} - \overline{x}_l)' \in \mathbb{R}^{p \times p}$$

where $\overline{x}_l := n_l^{-1} \sum_{j=1}^{n_l} x_{lj} \in \mathbb{R}^p$ is the l-th sample mean. Abbreviate $n := N + g = \sum_{l=1}^{g} n_l$. The **pooled sample covariance matrix** is

$$S_0 := N^{-1} \sum_{l=1}^{g} \nu_l S_l \in \mathbb{R}^{p \times p}.$$

Consider the null hypothesis that population covariances are equal

$$H_0 : A_1 = \ldots = A_g =: A.$$

The likelihood ratio (LR) statistic is introduced in [NP28, xix]. Our 3rd textbook [And03, 10.2:8] and Homework5#3 ($g = 2$) both calculate the maximum likelihood estimate (MLE) and LR in general and under H_0.

Result 2.1. *The likelihood ratio test (LRT) statistic of H_0 is*

$$\Lambda_0 = \prod_{l=1}^{g} \left(\frac{|\widehat{A}_l|}{|\widehat{A}_0|} \right)^{n_l/2} \in [0, 1]$$

where $\widehat{A}_l = \frac{\nu_l}{n_l} S_l$ is MLE of A_l and $\widehat{A}_0 = \frac{N}{n} S_0$ is MLE of A under H_0.

The ratio of likelihoods of null hypothesis over none is in [NP33, 12].

Theorem 2.2 (Neyman–Pearson 1933)**.** *For any significance level $0 < \alpha < 1$, most powerful (MP) is the hypothesis test that is defined by rejection of H_0 if LRT statistic $\Lambda_0 < \lambda_\alpha$, for appropriate constant λ_α.*

In the univariate case ($p = 1$), the above Λ_0 reduces to the so-called L_1-statistic of Neyman–Pearson (1931), which was proven an unbiased test by Brown [Bro39]. Here, a hypothesis test at level α with binary loss is **unbiased** if the **power function** $\beta(\theta) := \mathbb{P}[\text{reject } H_0|\theta]$ satisfies $\beta \leqslant \alpha$ under assumption H_0 is true and $\beta > \alpha$ assuming H_0 is false.

The constant λ_α can be determined asymptotically also, as follows. The following statement and a sketch is in [Wil38]; with appropriate hypotheses, a simple rigorous proof is provided by R M Dudley [Dud03].

Theorem 2.3 (Wilks 1938). *Under suitable regularity hypotheses (such as for existence and uniqueness of an interior-point MLE), the statistic $M_0 := -2 \log \Lambda_0$ is asymptotically distributed as $\chi^2((p+1)(g-1)p/2)$.*

A correction to the univariate case ($p = 1$) of Result 2.1 was offered in [Bar37, 15]. We state it for multivariate observations via determinants.

Definition 2.4 (Bartlett 1937). Consider the non-MLE based statistic

$$\Lambda = \prod_{l=1}^{g} \left(\frac{|S_l|}{|S_0|}\right)^{\nu_l/2} \in [0,1].$$

Write $M := -2 \log \Lambda$. The univariate M was used and studied by H O Hartley [Har40]. The unbiasedness of the multivariate Bartlett's Λ-test was eventually proven rigorously by M D Perlman [Per80, 2.1].

G E P Box is responsible for the development of multivariate M, so the test is named after him, and proposed a further correction [Box49].

Definition 2.5 (Box 1949, "Box's M-test"). Consider the constant

$$1 - \rho := \frac{2p^2 + 3p - 1}{6(p+1)(g-1)} \left(\sum_{l=1}^{g} \nu_l^{-1} - N^{-1}\right).$$

Reject the above H_0 if $\rho M > \chi_\alpha^2((p+1)(g-1)p/2)$, for a given level α.

Remark 2.6. In practice it seems to work well if $p, g < 5$ and all $n_l > 20$.

3. PARTLY DERIVING THE ρ-FACTOR

The purpose of this section is to begin to reveal some of the mystery of the formula for ρ in Definition 2.5. The full derivation is extremely complicated because of asymptotic analysis of special functions, so we refer the reader to [Box49] for the details of the full tour-de-force story.

For motivation, consider the univariate case ($p = 1$). If $Z \sim \mathcal{N}(0,1)$ which has density $(2\pi)^{-1/2} \exp(-z^2/2)$ for all $z \in \mathbb{R}$, by change-of-variables its square Z^2 has density $\frac{(1/2)^{1/2}}{\Gamma(1/2)} x^{-1/2} e^{-x/2}$ for all $x > 0$, which is Gamma$(1/2, 1/2) = \chi^2(1)$ with rate parameterization, hence

Z^2 has moment generating function $(1 - 2t)^{-1/2}$ for all $t < 1/2$. So if $Z_1, \ldots, Z_d \overset{\text{iid}}{\sim} \mathcal{N}(0,1)$, then their squares are also independent and identitically distributed, so the sum $Z_1^2 + \cdots + Z_d^2$ has moment generating function the product $[(1-2t)^{-1/2}]^d = (1-2t)^{-d/2}$, hence the sum has distribution $\text{Gamma}(d/2, 1/2) = \chi^2(d)$. Therefore, if $Y_1, \ldots, Y_{d+1} \overset{\text{iid}}{\sim} \mathcal{N}(\mu, \sigma^2)$, then the scaled sample variance $s^2/\sigma^2 := \sum_{j=1}^{d+1} \left((Y_j - \overline{Y})/\sigma \right)^2$ has a $\chi^2(d)$ distribution, since we lose one degree of freedom due to $\overline{Y}$. The probability density function of $x > 0$ is $\frac{(1/2)^{d/2}}{\Gamma(d/2)} x^{d/2-1} e^{-x/2}$. Notice therein the occurence of the special function of Daniel Bernoulli (1729):

$$\Gamma(s) := \int_0^\infty t^{s-1} e^{-t}\, dt \quad \text{for all } s > 0,$$

where $\Gamma(n+1) = n!$. The special numbers B_n of Jacob Bernoulli (1713), where $B_0 = 1, B_1 = -1/2, B_2 = 1/6, B_3 = 0$, now occur because Stirling's approximation $n! \approx \sqrt{2\pi n}(n/e)^n$ has this generalization [Bar00].

Theorem 3.1 (Barnes 1900). *For all complex $s \in \mathbb{C}$ and small $h \in \mathbb{C}$,*

$$\log \frac{\Gamma(s+h)}{\sqrt{2\pi}} = (s + h - \tfrac{1}{2})\log s - s - \sum_{r=1}^n (-1)^r \frac{B_{r+1}(h)}{r(r+1)s^r} + \mathcal{O}(s^{-n-1})$$

where the Bernoulli function is $B_n(h) := (B+h)^n = \sum_{k=0}^n \binom{n}{k} B_{n-k} h^k$.

Now consider the multivariate case $(p \geqslant 1)$. If $Z_1, \ldots, Z_d \overset{\text{iid}}{\sim} \mathcal{N}_p(0, A)$, then the sum $\sum_{j=1}^d Z_j Z_j'$ is a $p \times p$ random matrix that by definition has the Wishart distribution $\mathcal{W}_d(A)$ where $d \geqslant p$ is the degrees of freedom. For example, our setting has $\nu_l S_l \sim \mathcal{W}_{\nu_l}(A_l)$. Its density is in [Wis28].

Theorem 3.2 (Wishart 1928). *The matrix-valued distribution $\mathcal{W}_d(A)$ has probability density function of positive definite $W \in \mathbb{R}^{p \times p}$ given by*

$$\frac{|W|^{(d-p-1)/2} \exp\left(-\operatorname{tr} A^{-1} W / 2\right)}{2^{dp/2} |A|^{d/2} \cdot \pi^{p(p-1)/4} \prod_{k=0}^{p-1} \Gamma\left(\frac{d-k}{2}\right)}.$$

Box uses these two theorems as a starting point for intricate analysis of the characteristic exponent. We only jump in to show notation of his resulting algebra. He selects the multiplier ρ so that $\alpha_1 = 0$. Here, it lies in a family of constants with a particular definition [Box49, (43)]

$$\alpha_1 := -\frac{g}{3}(3D_1\beta + 2D_2)$$

where ρ occurs in $\beta := (1 - \rho)\nu$, and $D_r := \delta_r \gamma_r$ with [Box49, (39–40)]

$$\delta_r \; := \; B_{r+1}\left(-\frac{B+p}{2}\right) - B_{r+1}\left(-\frac{B}{2}\right)$$

$$\gamma_r \; := \; g^{-1}\sum_{l=1}^{g}\left(\frac{\nu}{\nu_l}\right)^{r-1} - g^{-r}.$$

Note $\alpha_1 = 0$ iff $1 - \rho = -\frac{2D_2}{3D_1}/\nu = -\frac{2\delta_2}{3\delta_1}\frac{\gamma_2/\nu}{\gamma_1}$. Next, since $\nu = N/g$, note

$$\gamma_1 \; = \; 1 - g^{-1}$$

$$\gamma_2 \; = \; g^{-1}\sum_{l=1}^{g}\frac{\nu}{\nu_l} - g^{-2} \; = \; \nu g^{-1}\left(\sum_{l=1}^{g}\nu_l^{-1} - N^{-1}\right).$$

Now, using the aforementioned special values of the Bernoulli numbers,

$$B_2(h) \; = \; (B+h)^2 = B_2 + 2B_1 h + B_0 h^2 = \frac{1}{6} - h + h^2$$

$$B_3(h) \; = \; (B+h)^3 = B_3 + 3B_2 h + 3B_1 h^2 + B_0 h^3 = \frac{1}{2}h - \frac{3}{2}h^2 + h^3.$$

Then the formal variable "B" can be expanded to yield [Box49, (42)][1]

$$\delta_1 \; = \; 4^{-1}\left[(B-p)^2 - B^2\right] = 4^{-1}\left[-(-p) + (-p)^2\right] = 4^{-1}p(p+1)$$

$$\delta_2 \; = \; 8^{-1}\left[(B-p)^3 - B^3\right] = 8^{-1}\left[\frac{1}{2}(-p) - \frac{3}{2}(-p)^2 + (-p)^3\right]$$

$$= \; -16^{-1}p(2p^2 + 3p - 1).$$

Thus $-\frac{2\delta_2}{3\delta_1} = \frac{2p^2+3p-1}{6(p+1)}$ and $\frac{\gamma_2/\nu}{\gamma_1} = \frac{1}{g-1}\left(\sum_{l=1}^{g}\nu_l^{-1} - N^{-1}\right)$, as desired.

4. Example : weight gain in rats

In Figure 4, three treatment groups of rats' weight gains are measured in Weeks 1–4 (i.e. once-differenced timeseries) [Box50, Table D]. The Appendix has the output of an R notebook that runs `boxM()` from Michael Friendly's library `heplots`, containing a version of the rat data.

Here $p = 4$ and $g = 3$. The plot of confidence intervals of $\log|S_l|$ and $\log|S_0|$ shows large overlaps between the sample covariances of all three groups and the pooled one. The total degrees of freedom is $(p+1)(g-1)p/2 = 20$ and Box's $\chi^2(20)$-statistic is $\rho M \doteq 12.14$. The associated (right-tailed) p-value is 91.12%. Therefore, at 5% significance level, we fail to reject the null hypothesis that all three treatments have the same covariance that describes the evolution of rat weight gains.

---

[1]Our last equality of δ_2 actually yields "+1" instead of "−1", so $2p^2 + 3p + 1 = (2p+1)(p+1)$. Is this a typo carried forward in the literature and computer code?

We *can* proceed with MANOVA for this dataset. Despite $p, g < 5$, note that $n_1 = 10, n_2 = 7, n_3 = 10$ are all $\leqslant 20$ (Remark 2.6). We did not check the assumption of multivariate normality per group.

INITIAL WEIGHT AND WEEKLY GAINS IN WEIGHT FOR 27 RATS

Group 1. Control						Group 2. Thyroxin						Group 3. Thiouracil					
Rat	y_0	y_1	y_2	y_3	y_4	Rat	y_0	y_1	y_2	y_3	y_4	Rat	y_0	y_1	y_2	y_3	y_4
1	57	29	28	25	33	11	59	26	36	35	35	18	61	25	23	11	9
2	60	33	30	23	31	12	54	17	19	20	28	19	59	21	21	10	11
3	52	25	34	33	41	13	56	19	33	43	38	20	53	26	21	6	27
4	49	18	33	29	35	14	59	26	31	32	29	21	59	29	12	11	11
5	56	25	23	17	30	15	57	15	25	23	24	22	51	24	26	22	17
6	46	24	32	29	22	16	52	21	24	19	24	23	51	24	17	8	19
7	51	20	23	16	31	17	52	18	35	33	33	24	56	22	17	8	5
8	63	28	21	18	24							25	58	11	24	21	24
9	49	18	23	22	28							26	46	15	17	12	17
10	57	25	28	29	30							27	53	19	17	15	18

y_0 represents initial weight of rat y_2 gain in 2nd week
y_1 gain in 1st week y_3 gain in 3rd week
                                                y_4 gain in 4th week

FIGURE 4.1. weight gains of rats per treatment group

5. EXAMPLE : EGYPTIAN SKULLS

Five epochs of ancient human skulls in Egypt were obtained, and according to Figure 5 the following four measurements were made.
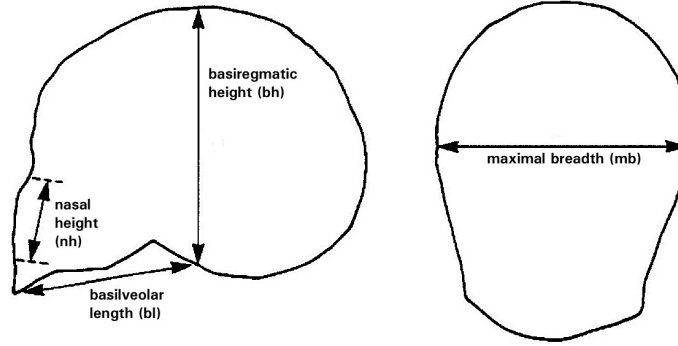

FIGURE 5.1. four types of skull measurements

Here $p = 4$ and $g = 5$. The plot of confidence intervals of $\log |S_l|$ and $\log |S_0|$ shows large overlaps between the the latter three sample covariances, with extremal shifts of the earliest two epochs, and the pooled one still overlaps the five epochs but has a much smaller range. The total degrees of freedom is $(p+1)(g-1)p/2 = 40$ and Box's $\chi^2(40)$-statistic is $\rho M \doteq 45.67$. The associated (right-tailed) p-value is 24.83%.

Therefore, at 5% significance level, we fail to reject the null hypothesis that all five epochs have the same covariance that describes shifts in cranial measurements over time. We *can* proceed with MANOVA for this dataset. Despite $p < 5$ and $n_1 = n_2 = n_3 = n_4 = n_5 = 30 > 20$, note that $g \geqslant 5$ (Remark 2.6). We did not check the assumption of multivariate normality per group.

6. Example : wine cultivars

Wine from three cultivars in the same region in Italy were obtained, and thirteen measurements of chemical composition were made.

Here $p = 13$ and $g = 3$. The plot of confidence intervals of $\log|S_l|$ and $\log|S_0|$ shows large overlaps between the cultivars barbera and barolo, whereas grignolino was completely separate, which has a minor overlap with the small range of the the pooled one. The total degrees of freedom is $(p+1)(g-1)p/2 = 182$ and Box's $\chi^2(182)$-statistic is $\rho M \doteq 684$. The associated (right-tailed) p-value is 2.2×10^{-16}. Therefore, at 5% significance level, we do reject the null hypothesis that all three cultivars have the same covariance that describes chemical composition of their wines. We *cannot* proceed with MANOVA for this dataset. Despite $g < 5$ and $n_1 = 48, n_2 = 59, n_3 = 71$ all > 20, note that $p \geqslant 5$ (Remark 2.6). We did not check the assumption of multivariate normality per group.

References

[And03] Theodore W Anderson. *An introduction to multivariate statistical analysis.* Wiley Series in Probability and Statistics. Wiley-Interscience [John Wiley & Sons], Hoboken, NJ, third edition, 2003.

[Bar00] Ernest W Barnes. The theory of the Gamma function. *Messenger Math.*, 29:64–128, 1900. URL: http://resolver.sub.uni-goettingen.de/purl?PPN599484047_0029.

[Bar37] Maurice S Bartlett. Properties of sufficiency and statistical tests. *Proc. R. Soc. Lond. A*, 160:268–282, 1937. doi:10.1098/rspa.1937.0109.

[Box49] George E P Box. A general distribution theory for a class of likelihood criteria. *Biometrika*, 36:317–346, 1949. doi:10.1093/biomet/36.3-4.317.

[Box50] George E P Box. Problems in the analysis of growth and wear curves. *Biometrics*, 6(4):362–389, 1950. doi:10.2307/3001781.

[Bro39] George W Brown. On the power of the L_1 test for equality of several variances. *Ann. Math. Statist.*, 10(2):119–128, 1939. doi:10.1214/aoms/1177732210.

[Dud03] Richard M Dudley. Wilks' theorem; a likelihood ratio test for nested composite hypotheses, 2003. OpenCourseWare lecture note from Mathematical Statistics (18.466). URL: https://math.mit.edu/~rmd/650/wilks.pdf.

[Har40] Herman O Hartley. Testing the homogeneity of a set of variances. *Biometrika*, 31:249–255, 1940. doi:10.1093/biomet/31.3-4.249.

[JW07]   Richard A Johnson and Dean W Wichern. *Applied multivariate statistical analysis*. Pearson Prentice Hall, Upper Saddle River, NJ, sixth edition, 2007.

[NP28]   Jerzy Neyman and Egon S Pearson. On the use and interpretation of certain test criteria for purposes of statistical inference: Part I. *Biometrika*, 20A(1–2):175—240, 1928. `doi:10.2307/2331945`.

[NP33]   Jerzy Neyman and Egon S Pearson. On the problem of the most efficient tests of statistical hypotheses. *Philos. Trans. Roy. Soc. London Ser. A*, 231:289–337, 1933. `doi:10.1098/rsta.1933.0009`.

[Per80] Michael D Perlman. Unbiasedness of the likelihood ratio tests for equality of several covariance matrices and equality of several multivariate normal populations. *Ann. Statist.*, 8(2):247–263, 1980. `doi:10.1214/aos/1176344951`.

[Wil38] Samuel S Wilks. The large-sample distribution of the likelihood ratio for testing composite hypotheses. *Ann. Math. Statist.*, 9(1):60–62, 1938. `doi:10.1214/aoms/1177732360`.

[Wis28] John Wishart. The generalised product moment distribution in samples from a normal multivariate population. *Biometrika*, 20A(1–2):32–52, 1928. `doi:10.1093/biomet/20A.1-2.32`.

Email address: `qayum@uchicago.edu`

APPENDIX : Examples of Application of Box's M-test

Qayum Khan (qayum@uchicago.edu (mailto:qayum@uchicago.edu))

2023-05-01

Example 1 : Rat Weights - a once-differenced timeseries

Figure D of Box's 1950 article is already a datafile.

```
data( RatWeight )
RatGain <- data.frame( group = RatWeight$trt,
                       gain1 = RatWeight$wt1-RatWeight$wt0,
                       gain2 = RatWeight$wt2-RatWeight$wt1,
                       gain3 = RatWeight$wt3-RatWeight$wt2,
                       gain4 = RatWeight$wt4-RatWeight$wt3 )
table(RatGain$group)
```

```
##
##    Control Thiouracil   Thyroxin
##         10         10          7
```

```
RatFormula <- as.formula( cbind(gain1,gain2,gain3,gain4) ~ group )
RatModel <- lm( RatFormula, data=RatGain )
heplot( RatModel )
```
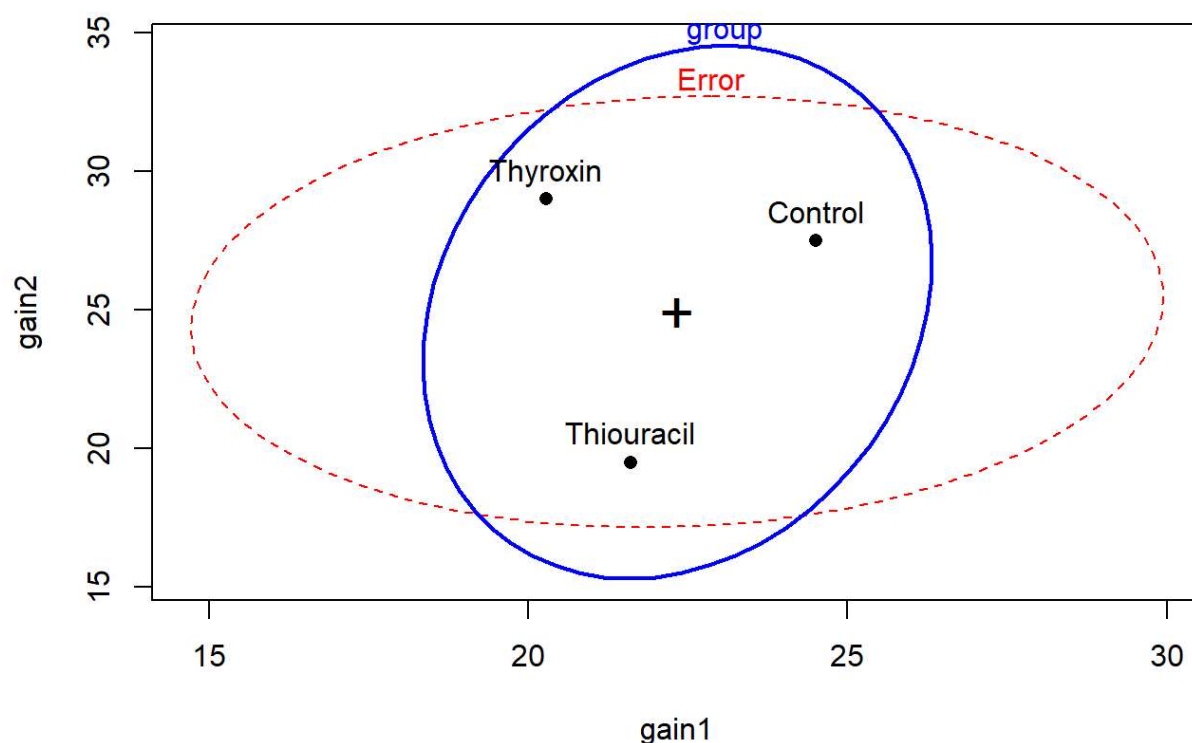


```
RatTest <- boxM( RatFormula, data=RatGain )
plot( RatTest ) # 95% confidence intervals, determined by Cai--Liang--Zhou (2015)
```
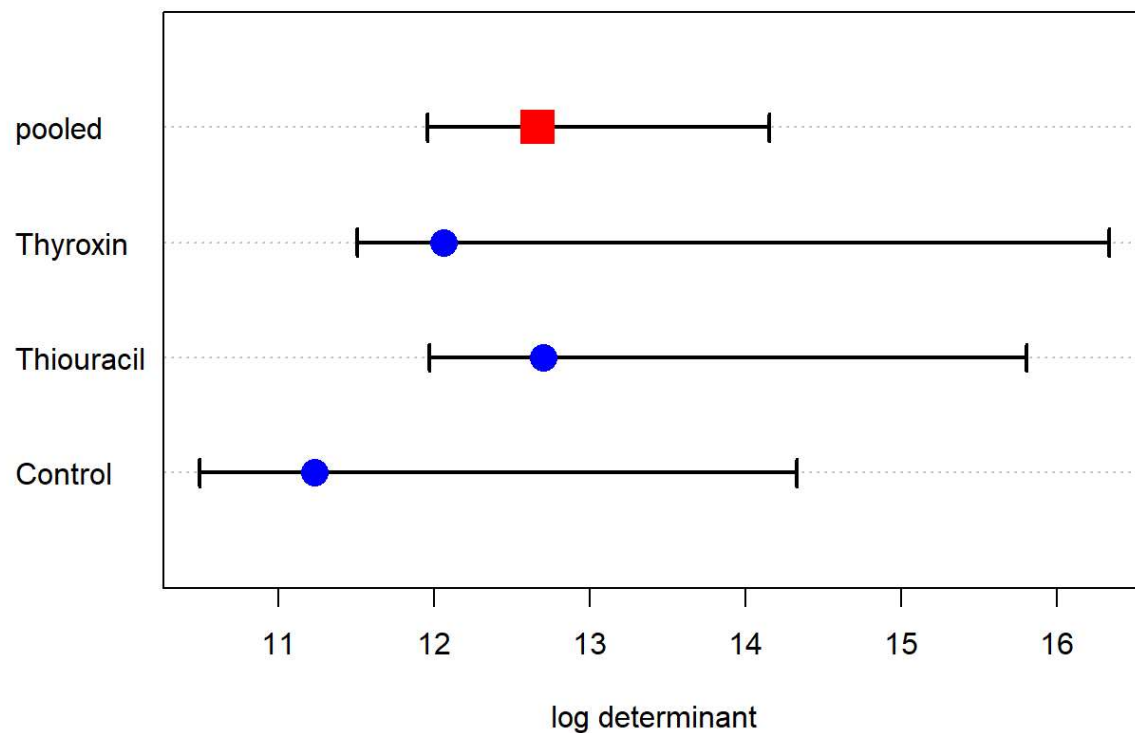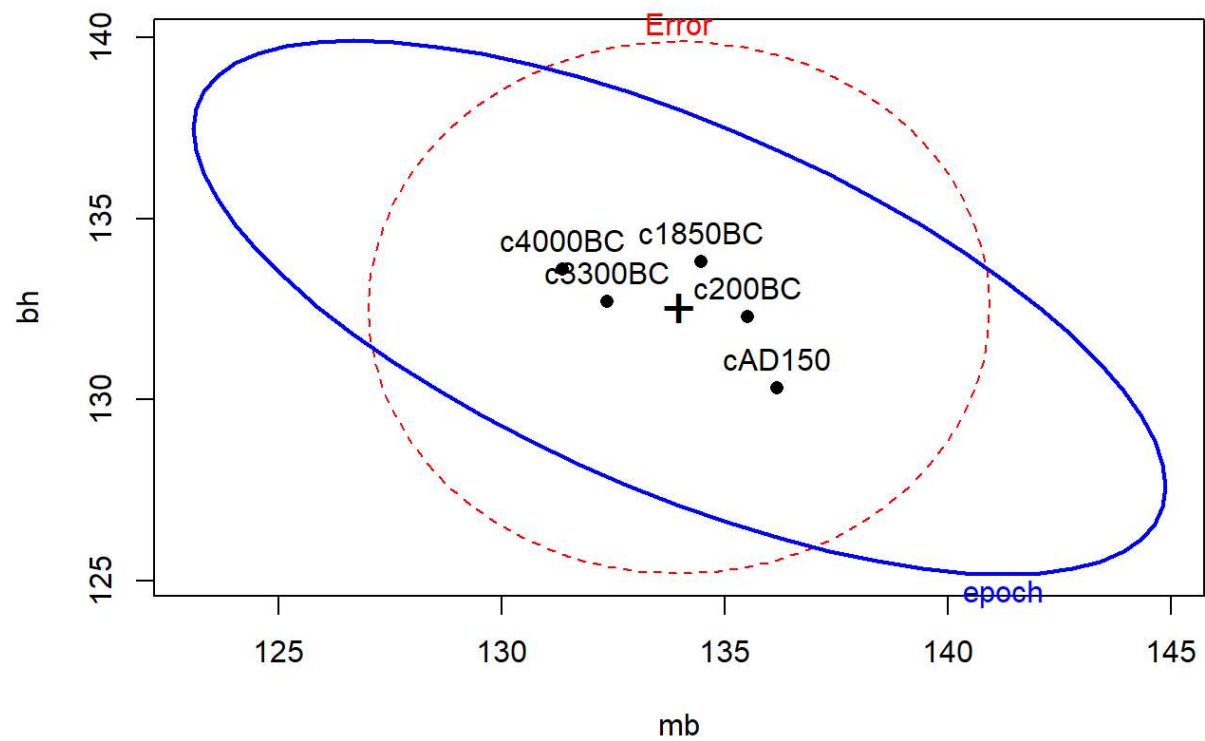
```
summary( RatTest, cov=F )
```

```
## Summary for Box's M-test of Equality of Covariance Matrices
##
## Chi-Sq:   12.1383
## df:   20
## p-value: 0.9112
##
## log of Covariance determinants:
##     Control Thiouracil   Thyroxin      pooled
##    11.22898   12.70088   12.05800   12.66151
##
## Eigenvalues:
##       Control Thiouracil   Thyroxin     pooled
## 1 63.392798   63.824832 121.423002 72.468683
## 2 23.940349   31.837288  26.826905 25.210030
## 3 19.244905   17.826403   7.931672 22.118624
## 4  2.577504    9.055921   6.675563  7.804448
##
## Statistics based on eigenvalues:
##                  Control   Thiouracil    Thyroxin       pooled
## product    75281.014845 3.280364e+05 1.724742e+05 3.153727e+05
## sum          109.155556 1.225444e+02 1.628571e+02 1.276018e+02
## precision      2.010134 4.681667e+00 3.111498e+00 4.409003e+00
## max           63.392798 6.382483e+01 1.214230e+02 7.246868e+01
```

Example 2 : Skull Measurements
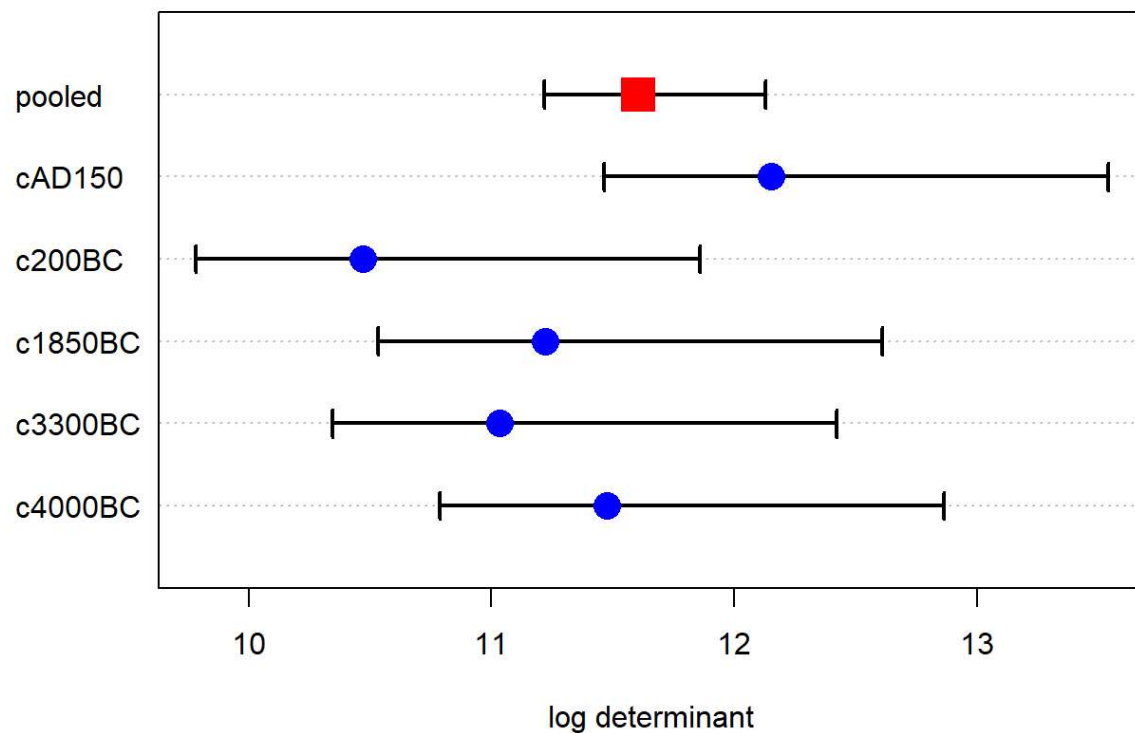
```
data( Skulls )
table( Skulls$epoch )
```

```
##
## c4000BC c3300BC c1850BC  c200BC  cAD150
##      30      30      30      30      30
```

```
SkullFormula <- as.formula( cbind(mb,bh,bl,nh) ~ epoch )
SkullModel <- lm( SkullFormula, data=Skulls )
heplot( SkullModel )
```



```
SkullTest <- boxM( SkullFormula, data=Skulls )
plot( SkullTest ) # 95% confidence intervals, determined by Cai--Liang--Zhou (2015)
```
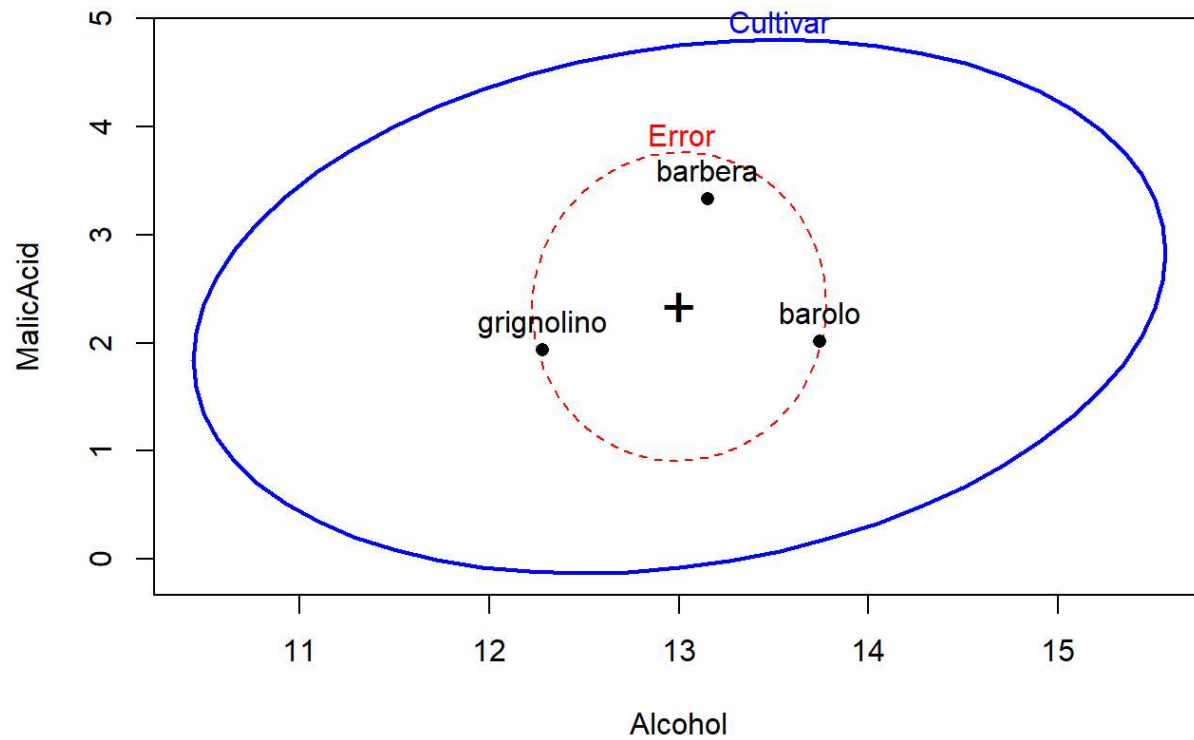
```
summary( SkullTest, cov=F )
```

```
## Summary for Box's M-test of Equality of Covariance Matrices
##
## Chi-Sq:   45.66723
## df:    40
## p-value: 0.2483
##
## log of Covariance determinants:
##   c4000BC  c3300BC  c1850BC   c200BC   cAD150   pooled
## 11.47659 11.03211 11.22162 10.46913 12.15302 11.60530
##
## Eigenvalues:
##      c4000BC  c3300BC  c1850BC   c200BC   cAD150   pooled
## 1 34.823361 28.39920 26.93111 35.906372 37.33170 29.461507
## 2 30.333915 22.03058 19.07469 16.955955 28.59993 21.440705
## 3 18.435832 15.59589 13.20735 13.675102 14.79973 18.778959
## 4  4.951721  6.33640 11.01443  4.229238 12.00313  9.245956
##
## Statistics based on eigenvalues:
##                    c4000BC        c3300BC        c1850BC        c200BC        cAD150
## product   96431.295985 61827.946165 74729.072524 35211.657580 1.896666e+05
## sum          88.544828    72.362069    70.227586    70.766667 9.273448e+01
## precision     3.145891     3.305332     3.905294     2.522696 4.702951e+00
## max          34.823361    28.399195    26.931111    35.906372 3.733170e+01
##                   pooled
## product   1.096775e+05
## sum       7.892713e+01
## precision 4.132414e+00
## max       2.946151e+01
```

Example 3 : Chemical Composition of Wine
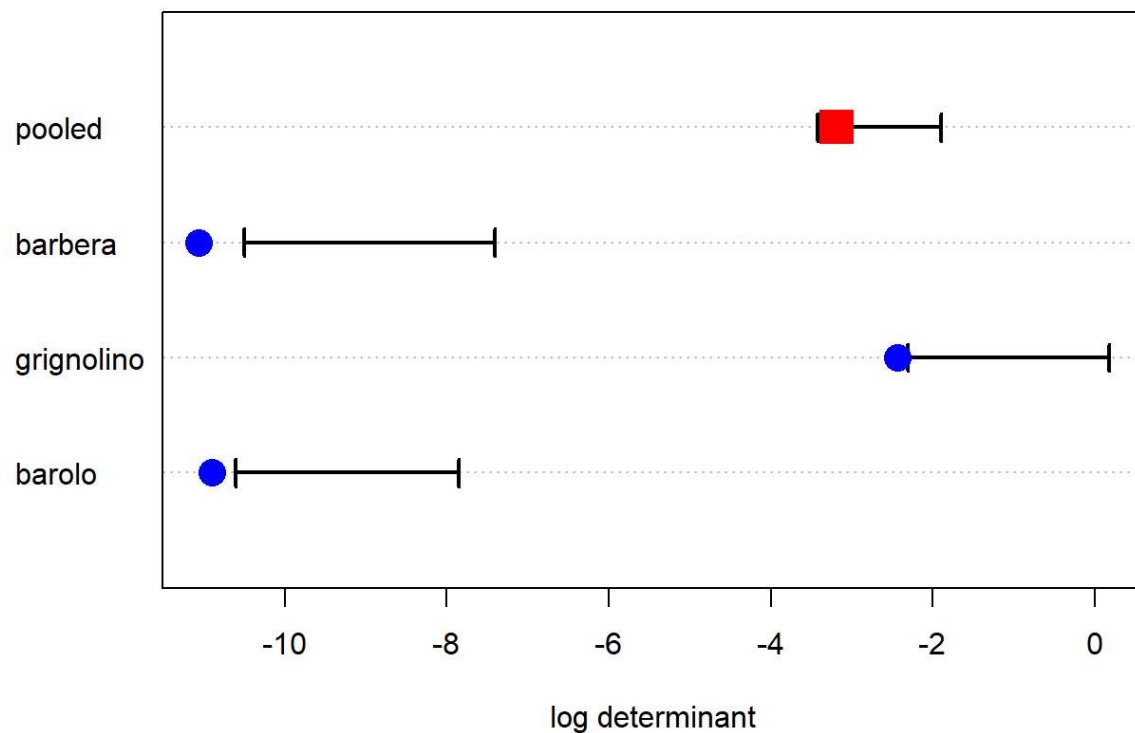
```
data( Wine )
table( Wine$Cultivar )
```

```
##
##      barolo grignolino     barbera
##         59          71          48
```

```
WineFormula <- as.formula( cbind(Alcohol, MalicAcid, Ash, AlcAsh, Mg, Phenols, Flav, NonFlavPhenols, Proa, Color, Hue, OD, P
roline) ~ Cultivar )
WineModel <- lm( WineFormula, data=Wine )
heplot( WineModel )
```



```
WineTest <- boxM( WineFormula, data=Wine )
plot( WineTest ) # 95% confidence intervals, determined by Cai--Liang--Zhou (2015)
```

```
summary( WineTest, cov=F )
```

```
## Summary for Box's M-test of Equality of Covariance Matrices
##
## Chi-Sq:   684.2031
## df:    182
## p-value: < 2.2e-16
##
## log of Covariance determinants:
##      barolo grignolino    barbera     pooled
## -10.902255  -2.443270 -11.055300  -3.189442
##
## Eigenvalues:
##          barolo  grignolino    barbera     pooled
## 1  4.907464e+04 2.478610e+04 1.325179e+04 2.971561e+04
## 2  1.083042e+02 2.100615e+02 1.145923e+02 1.730817e+02
## 3  6.199478e+00 1.143357e+01 6.052432e+00 7.951330e+00
## 4  9.329764e-01 1.130294e+00 4.306843e+00 2.257991e+00
## 5  4.120210e-01 9.589978e-01 1.091765e+00 8.197491e-01
## 6  1.816698e-01 6.395512e-01 2.362204e-01 4.260405e-01
## 7  1.117702e-01 2.543443e-01 1.278753e-01 2.295385e-01
## 8  9.972618e-02 1.814558e-01 8.229714e-02 1.451121e-01
## 9  7.915028e-02 1.155837e-01 3.304591e-02 1.117280e-01
## 10 3.052211e-02 5.564865e-02 2.379950e-02 6.357011e-02
## 11 2.033566e-02 3.259644e-02 9.232194e-03 3.446343e-02
## 12 6.754625e-03 2.952448e-02 6.517815e-03 1.961628e-02
## 13 2.163809e-03 7.368581e-03 3.108240e-03 7.986643e-03
##
## Statistics based on eigenvalues:
##                 barolo  grignolino     barbera       pooled
## product   1.841667e-05 8.687630e-02 1.580318e-05 4.119487e-02
## sum       4.919102e+04 2.501101e+04 1.337835e+04 2.990076e+04
## precision 1.364415e-03 4.168275e-03 1.467840e-03 4.077078e-03
## max       4.907464e+04 2.478610e+04 1.325179e+04 2.971561e+04
```