Comparing Mean Vectors for Two Populations

- Data may come from
  - Two independent random samples: a sample of n_1 respondents from population 1 and a sample of n_2 respondents from population 2.
  - Randomized experiment: n_1 units are randomly allocated to treatment 1 and n_2 units are randomly allocated to treatment 2. Sample sizes need not be equal.
- Measure values for the same set of p variables (or traits) on each member of each sample.

Motivating Example: Two Processes for Manufacturing Soap

- Objective was to compare two processes for manufacturing soap. Outcome measures were $x_1 =$ lather and $x_2 =$ mildness, and $n_1 = n_2 = 50$.

- Sample statistics for process 1 are

$$\bar{\mathbf{x}}_1 = \begin{bmatrix} 8.3 \\ 4.1 \end{bmatrix}, \quad S_1 = \begin{bmatrix} 2 & 1 \\ 1 & 6 \end{bmatrix},$$

  and for process 2:

$$\bar{\mathbf{x}}_2 = \begin{bmatrix} 10.2 \\ 3.9 \end{bmatrix}, \quad S_2 = \begin{bmatrix} 2 & 1 \\ 1 & 4 \end{bmatrix}.$$

- How to formally assess a hypothesis of the form $H_0 : \boldsymbol{\mu}_1 = \boldsymbol{\mu}_2$?

- How to construct confidence intervals/regions for the mean difference $\boldsymbol{\mu}_1 - \boldsymbol{\mu}_2$?

Comparing Mean Vectors for Two Populations

- Data vectors from population 1:

$$\mathbf{x}_{1j} = \begin{bmatrix} x_{1j1} \\ x_{1j2} \\ \vdots \\ x_{1jp} \end{bmatrix} \qquad j = 1, 2, \ldots, n_1$$

- Data vectors from population 2:

$$\mathbf{x}_{2k} = \begin{bmatrix} x_{2k1} \\ x_{2k2} \\ \vdots \\ x_{2kp} \end{bmatrix} \qquad k = 1, 2, \ldots, n_2$$

- We use $\bar{\mathbf{x}}_1$ and $\bar{\mathbf{x}}_2$ to denote the sample mean vectors, and S_1 and S_2 to denote the sample covariance matrices.

Comparing Two Mean Vectors

- The following assumptions are needed to make inferences about the difference between two population mean vectors $\boldsymbol{\mu}_1 - \boldsymbol{\mu}_2$:

  1. $\mathbf{x}_{11}, \mathbf{x}_{12}, ...\mathbf{x}_{1n_1} \sim N(\boldsymbol{\mu}_1, \Sigma_1)$.
  2. $\mathbf{x}_{21}, \mathbf{x}_{22}, ..., \mathbf{x}_{2n_2} \sim N(\boldsymbol{\mu}_2, \Sigma_2)$.
  3. $\Sigma_1 = \Sigma_2$
  4. $\mathbf{x}_{11}, \mathbf{x}_{12}, ...\mathbf{x}_{1n_1}$ are independent
  5. $\mathbf{x}_{21}, \mathbf{x}_{22}, ..., \mathbf{x}_{2n_2}$ are independent.
  6. $\mathbf{x}_{11}, \mathbf{x}_{12}, ..., \mathbf{x}_{1n_1}$ are independent of $\mathbf{x}_{21}, \mathbf{x}_{22}, ..., \mathbf{x}_{2n_2}$.

Pooled Estimate of the Covariance Matrix

- If $\Sigma_1 = \Sigma_2 = \Sigma$, then

$$S_1 = \frac{1}{n_1 - 1}\sum_{j=1}^{n_1}(\mathbf{x}_{1j} - \bar{\mathbf{x}}_1)(\mathbf{x}_{1j} - \bar{\mathbf{x}}_1)', \text{ and}$$

$$S_2 = \frac{1}{n_2 - 1}\sum_{j=1}^{n_2}(\mathbf{x}_{2j} - \bar{\mathbf{x}}_2)(\mathbf{x}_{2j} - \bar{\mathbf{x}}_2)'$$

are both unbiased estimates of Σ. Then, we can pool, or average, the information from the two samples to obtain an estimate of the common covariance matrix:

$$S_{\text{pool}} = \frac{(n_1 - 1)}{(n_1 + n_2 - 2)}S_1 + \frac{(n_2 - 1)}{(n_1 + n_2 - 2)}S_2.$$

Comparing Two Mean Vectors

- Consider testing $H_0 : \boldsymbol{\mu}_1 - \boldsymbol{\mu}_2 = \boldsymbol{\delta}_0$, where $\boldsymbol{\delta}_0$ is some fixed $p \times 1$ vector. Often, $\boldsymbol{\delta}_0 = \mathbf{0}$.

- An estimate of $\boldsymbol{\mu}_1 - \boldsymbol{\mu}_2$ is $\bar{\mathbf{x}}_1 - \bar{\mathbf{x}}_2$ and

$$\text{Cov}(\bar{\mathbf{x}}_1 - \bar{\mathbf{x}}_2) = \text{Cov}(\bar{\mathbf{x}}_1) + \text{Cov}(\bar{\mathbf{x}}_2) = \frac{1}{n_1}\Sigma + \frac{1}{n_2}\Sigma,$$

  This is correct if the units from treatment 1 (or sample 1) respond independently of any unit in the sample from treatment 2.

- An estimate of the covariance matrix of the difference between the sample mean vectors is given by

$$\frac{1}{n_1}S_{\text{pool}} + \frac{1}{n_2}S_{\text{pool}} = \left(\frac{1}{n_1} + \frac{1}{n_2}\right)S_{\text{pool}}.$$

Comparing Two Mean Vectors

- We reject $H_0 : \mu_1 - \mu_2 = \delta_0$ at level α if

$$T^2 = (\bar{\mathbf{x}}_1 - \bar{\mathbf{x}}_2 - \boldsymbol{\delta}_0)' \left[\left(\frac{1}{n_1} + \frac{1}{n_2} \right) S_{\text{pool}} \right]^{-1} (\bar{\mathbf{x}}_1 - \bar{\mathbf{x}}_2 - \boldsymbol{\delta}_0) > c^2,$$

where

$$c^2 = \frac{(n_1 + n_2 - 2)p}{(n_1 + n_2 - p - 1)} F_{(p, n_1+n_2-p-1), 1-\alpha}.$$

- A $100(1-\alpha)\%$ confidence region for $\boldsymbol{\mu}_1 - \boldsymbol{\mu}_2$ is given by all values of $\boldsymbol{\mu}_1 - \boldsymbol{\mu}_2$ that satisfy

$$(\bar{\mathbf{x}}_1 - \bar{\mathbf{x}}_2 - (\boldsymbol{\mu}_1 - \boldsymbol{\mu}_2))' \left[\left(\frac{1}{n_1} + \frac{1}{n_2} \right) S_{\text{pool}} \right]^{-1} (\bar{\mathbf{x}}_1 - \bar{\mathbf{x}}_2 - (\boldsymbol{\mu}_1 - \boldsymbol{\mu}_2)) \le c^2.$$

Two Processes for Manufacturing Soap

- Objective was to compare two processes for manufacturing soap. Outcome measures were x_1 = lather and x_2 = mildness, and $n_1 = n_2 = 50$.

- Sample statistics for process 1 are

$$\bar{\mathbf{x}}_1 = \begin{bmatrix} 8.3 \\ 4.1 \end{bmatrix}, \quad S_1 = \begin{bmatrix} 2 & 1 \\ 1 & 6 \end{bmatrix},$$

  and for process 2:

$$\bar{\mathbf{x}}_2 = \begin{bmatrix} 10.2 \\ 3.9 \end{bmatrix}, \quad S_2 = \begin{bmatrix} 2 & 1 \\ 1 & 4 \end{bmatrix}.$$

- The pooled estimate of the common covariance matrix and the difference in sample mean vectors are

$$S_{\text{pool}} = \frac{49}{98} S_1 + \frac{49}{98} S_2 = \begin{bmatrix} 2 & 1 \\ 1 & 5 \end{bmatrix}, \quad \bar{\mathbf{x}}_1 - \bar{\mathbf{x}}_2 = \begin{bmatrix} -1.9 \\ 0.2 \end{bmatrix}.$$

Two Processes for Manufacturing Soap

- We reject $H_0 : \boldsymbol{\mu}_1 - \boldsymbol{\mu}_2 = \mathbf{0}$ at level $\alpha = .05$ because

$$T^2 = (\bar{\mathbf{x}}_1 - \bar{\mathbf{x}}_2 - \mathbf{0})' \left[\left(\frac{1}{n_1} + \frac{1}{n_2} \right) S_{\text{pool}} \right]^{-1} (\bar{\mathbf{x}}_1 - \bar{\mathbf{x}}_2 - \mathbf{0}) = 15.66$$

  is larger than

$$\frac{(50 + 50 - 2)(2)}{(50 + 50 - 2 - 1)} F_{(2,97),0.95} = 6.26.$$

- Eigenvalues of the pooled covariance matrix are

$$\lambda_1 = 5.303 \quad \text{and} \quad \lambda_2 = 1.697$$

- Eigenvectors the pooled covariance matrix are

$$\mathbf{e}_1 = \begin{bmatrix} 0.290 \\ 0.957 \end{bmatrix} \quad \text{and} \quad \mathbf{e}_2 = \begin{bmatrix} 0.957 \\ -0.290 \end{bmatrix}$$

Two Processes for Manufacturing Soap

- A 95% confidence ellipse for the difference between two population mean vectors is centered at $\bar{\mathbf{x}}_1 - \bar{\mathbf{x}}_2$.

- Because

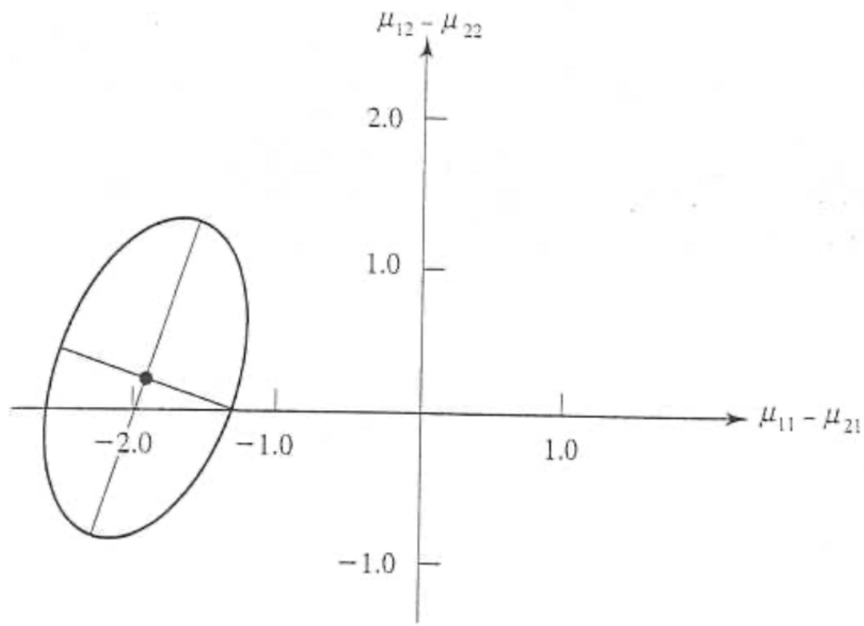
$$\left(\frac{1}{n_1}+\frac{1}{n_2}\right)c^2 = \left(\frac{1}{n_1}+\frac{1}{n_2}\right)\frac{(n_1+n_2-2)p}{(n_1+n_2-p-1)}F_{(p,n_1+n_2-p-1),1-\alpha}$$

$$= \left(\frac{1}{50}+\frac{1}{50}\right)\frac{(98)(2)}{(97)}F_{(2,97),0.95} = 0.25,$$

we know that the ellipse extends $\sqrt{5.303}\sqrt{0.25} = 1.15$ and $\sqrt{1.697}\sqrt{0.25} = 0.65$ units in the $\mathbf{e}_1$ and $\mathbf{e}_2$ directions, respectively.

Two Processes for Manufacturing Soap

- Because $\boldsymbol{\mu}_1 - \boldsymbol{\mu}_2 = \mathbf{0}$ is not inside the ellipse, we conclude that the populations of soaps produced by the two processes are centered at different mean vectors. There appears to be no big difference in mildness means for soaps made by the two processes, but soaps made with the second process produce more lather on average.



Confidence Intervals

- As before, we can obtain simultaneous confidence intervals for any linear combination of the components of $\boldsymbol{\mu}_1 - \boldsymbol{\mu}_2$.

- In the case of p variables, we might be interested in a set of p simultaneous confidence intervals:

$$
\begin{aligned}
\mathbf{a}_j'(\boldsymbol{\mu}_1 - \boldsymbol{\mu}_2) &= \begin{bmatrix} 0 & 0 & \cdots & 1 & \cdots & 0 \end{bmatrix} \begin{bmatrix} \mu_{11} - \mu_{21} \\ \mu_{12} - \mu_{22} \\ \vdots \\ \mu_{1p} - \mu_{2p} \end{bmatrix} \\
&= \mu_{1j} - \mu_{2j},
\end{aligned}
$$

  where the vector $\mathbf{a}_j$ has zeros everywhere except for the one in the jth position.

- Typically, we would be interested in m such comparisons.

Confidence Intervals

- For the j-th variable

$$(\bar{x}_{1j} - \bar{x}_{2j}) \pm \sqrt{\frac{(n_1 + n_2 - 2)p}{(n_1 + n_2 - p - 1)} F_{(p, n_1 + n_2 - p - 1), 1-\alpha}} \sqrt{\left(\frac{1}{n_1} + \frac{1}{n_2}\right) S_{\text{pool}, jj}}$$

  will simultaneously cover the true values of $\boldsymbol{\mu}_{1j} - \boldsymbol{\mu}_{2j}$ with probability of at least $(1-\alpha) \times 100\%$.
- One-at-a-time t-intervals (i.e., univariate approach) are computed as

$$(\bar{x}_{1j} - \bar{x}_{2j}) \pm t_{(n_1 + n_2 - 2), 1-\alpha/2} \sqrt{\left(\frac{1}{n_1} + \frac{1}{n_2}\right) S_{\text{pool}, jj}}$$

  and have less than $(1-\alpha)\%$ simultaneous probability of coverage unless only one comparison is made. To apply the Bonferroni method, divide α by the number of comparisons of interest, say m.

- R code demonstration

Comparing Mean Vectors for Several Populations

- Compare mean vectors for g treatments (or populations).
- Randomly assign n_ℓ units to the ℓ-th treatment (or take independent random samples from g populations)
- Measure p characteristics of each unit. Observation vectors sampled from the ℓ-th population,

$$\mathbf{x}_{\ell 1}, \mathbf{x}_{\ell 2}, ..., \mathbf{x}_{\ell n_\ell},$$

  are $p \times 1$ vectors of measurements. We use $\bar{\mathbf{x}}_\ell$ to denote the vector of sample means for the ℓth population, and S_ℓ to denote the estimated covariance matrix in the ℓth population.

- We will use n to denote the total sample size: $n = \sum_{\ell=1}^{g} n_\ell$.

Comparing Several Mean Vectors

The following conditions are all we needed for testing hypotheses:

1. Each subject responds independently of any other subject.

2. Covariance matrices are homogeneous: $\Sigma_\ell = \Sigma$ for every population.

3. Each potential observation vector sampled form the ℓ-th population, $\mathbf{x}_{\ell 1}, \mathbf{x}_{\ell 2}, ..., \mathbf{x}_{\ell n_\ell}$, has a p-variate $N(\boldsymbol{\mu}_\ell, \Sigma)$ distribution.

Pooled estimate of the covariance matrix

- If all population covariance matrices are the same, then all group-level matrices of sums of squares and cross-products estimate the same quantity.

- Then, it is reasonable to combine all the group-level covariance matrices into a single estimate by computing the weighted average of the covariance matrices. Weights are proportional to the number of units in each treatment group.

- The pooled estimate of the common covariance matrix is

$$S_{\text{pool}} = \sum_{\ell=1}^{g} \left[\frac{(n_\ell - 1)}{\sum_{j=1}^{g}(n_j - 1)} \right] S_\ell .$$

Analysis of Variance (ANOVA)

- To develop approaches to compare g multivariate means, it will be convenient to make use of the usual decomposition of the variability in the sample response vectors into two sources:

  1. Variability due to differences in treatment mean vectors (between-group variation)

  2. Variability due to measurement error or differences among units within treatment groups(within-group variation)

- We review some of these concepts in the univariate setting, when $p = 1$.

ANOVA for a Single Response

We often wish to test $H_0 : \mu_1 = \mu_2 = \cdots = \mu_g$ versus H_1 : at least two populations have different means

- Assumptions: ind. populations; equal variances $\sigma_1 = \ldots = \sigma_g$; normality; $g \geq 2$.

$$\begin{aligned} x_{11}, \ldots, x_{1n_1} &\sim N(\mu_1, \sigma_1^2) \\ x_{21}, \ldots, x_{2n_2} &\sim N(\mu_2, \sigma_2^2) \\ &\cdots \\ x_{g1}, \ldots, x_{gn_g} &\sim N(\mu_g, \sigma_g^2) \end{aligned}$$

- One-way ANOVA corresponds to the following specification: write $\mu_\ell = \mu + \tau_\ell$, and

$$x_{\ell j} = \mu + \tau_\ell + \epsilon_{\ell j}, \ell = 1, \ldots, g; j = 1, \ldots, n_\ell$$

with the constraint $\sum_\ell n_l \tau_l = 0$ and $\epsilon_{\ell j} \sim N(0, \sigma^2)$.

ANOVA for a Single Response

Source of Variation	Degrees of Freedom	Sum of Squares Squares	Mean Square	F-test
Treatment	g-1	$SS_{trt} = \sum_{\ell=1}^{g} n_\ell(\bar{x}_\ell - \bar{x})^2$	$MS_{trt} = \frac{SS_{trt}}{g-1}$	$F = \frac{MS_{trt}}{MS_{error}}$
Residuals	n-g	$SS_{error} = \sum_{\ell=1}^{g} \sum_{j} (x_{\ell j} - \bar{x}_\ell)^2$	$MS_{error} = \frac{SS_{error}}{df_{error}}$	
Cor. Total	n-1	$SS_{CT} = \sum_{\ell=1}^{g} \sum_{j=1}^{n_j} (x_{\ell j} - \bar{x})^2$		

Reject the null hypothesis if $F = \dfrac{MS_{trt}}{MS_{error}} > F_{(g-1,n-g),1-\alpha}$

MANOVA: Multivariate Analysis of Variance

- We now extend ANOVA to the case where the observations are p-dimensional vectors.
- Test the null hypothesis $H_0 : \boldsymbol{\mu}_1 = \boldsymbol{\mu}_2 = ... = \boldsymbol{\mu}_g$

  against the alternative

  H_A : at least 2 of the populations have different mean vectors

- Assumptions: See Slide 139

- One-way MANOVA model:

$$\mathbf{x}_{\ell j} = \boldsymbol{\mu} + \boldsymbol{\tau}_\ell + \boldsymbol{\epsilon}_{\ell j}, \; \ell = 1, \ldots, g; j = 1, \ldots, n_\ell$$

  with the constraint that $\sum n_\ell \boldsymbol{\tau}_\ell = \mathbf{0}$ and $\boldsymbol{\epsilon}_{\ell j} \sim N_p(\mathbf{0}, \boldsymbol{\Sigma})$.

Multivariate Analysis of Variance (MANOVA)

Source of variation	Matrix of sum of squares and cross-products (SSP)	Degrees of freedom (d.f.)
Treatment	$B = \sum_\ell n_\ell (\bar{\mathbf{x}}_\ell - \bar{\mathbf{x}})(\bar{\mathbf{x}}_\ell - \bar{\mathbf{x}})'$	$g-1$
Residual	$W = \sum_\ell \sum_j (\mathbf{x}_{\ell j} - \bar{\mathbf{x}}_\ell)(\mathbf{x}_{\ell j} - \bar{\mathbf{x}}_\ell)'$	$n-g$
Total corrected	$B + W = \sum_\ell \sum_j (\mathbf{x}_{\ell j} - \bar{\mathbf{x}})(\mathbf{x}_{\ell j} - \bar{\mathbf{x}})'$	$n-1$

Note that

$$
\begin{aligned}
W &= \sum_{\ell=1}^{g} \sum_{j=1}^{n_\ell} (x_{\ell j} - \bar{\mathbf{x}}_\ell)(x_{\ell j} - \bar{\mathbf{x}}_\ell)' \\
&= (n_1 - 1)S_1 + (n_2 - 1)S_2 + \cdots + (n_g - 1)S_g \\
&= (n - g)S_{pooled}
\end{aligned}
$$

Hypotheses Testing in MANOVA

- One test of the null hypothesis is carried out using a statistic called *Wilk's* Λ (a likelihood ratio test):

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

- If B is "small" relative to W, then Λ will be close to 1. Otherwise, Λ will be small.
- We reject the null hypothesis when Λ is small.
- SAS uses different notation. It calls the B matrix H and it calls the W matrix E, for 'hypothesis' and 'error', respectively.
- The exact distribution of Wilk's lambda is available for some special cases

Exact distribution of Wilk's Λ

No. of variables	No. of groups	Sampling distribution for multivariate normal data
$p = 1$	$g \geq 2$	$\left(\frac{n-g}{g-1}\right)\left(\frac{1-\Lambda}{\Lambda}\right) \sim F_{g-1,n-g}$
$p = 2$	$g \geq 2$	$\left(\frac{n-g-1}{g-1}\right)\left(\frac{1-\sqrt{\Lambda}}{\sqrt{\Lambda}}\right) \sim F_{2(g-1),2(n-g-1)}$
$p \geq 1$	$g = 2$	$\left(\frac{n-p-1}{p}\right)\left(\frac{1-\Lambda}{\Lambda}\right) \sim F_{p,n-p-1}$
$p \geq 1$	$g = 3$	$\left(\frac{n-p-2}{p}\right)\left(\frac{1-\sqrt{\Lambda}}{\sqrt{\Lambda}}\right) \sim F_{2p,2(n-p-2)}$

F approximation to the sampling distribution of Wilk's Criterion

When the null hypothesis of equal population mean vectors is true, the distribution of the Wilk's Lambda statistic can be approximated by an F-distribution.

$$\frac{1-\Lambda^{1/b}}{\Lambda^{1/b}} \frac{ab-c}{p(g-1)} \sim F_{(p(g-1),ab-c)}$$

where

$$\begin{aligned} a &= (n-g)-(p-g+2)/2 \\ b &= \sqrt{\frac{p^2(g-1)^2-4}{p^2+(g-1)^2-5}} \\ c &= (p(g-1)-2)/2 \end{aligned}$$

Other Tests

- Most packages (including SAS) will compute Wilk's Λ and some other statistics.
- Lawley-Hotelling trace: Reject the null hypothesis of no treatment differences at level α if

$$nT_0^2 = \text{tr}(BW^{-1})$$

  is sufficiently large.
- Pillai trace: $V = \text{tr}[B(B+W)^{-1}]$.
- Roy's maximum root: the test statistic is the largest eigenvalue of BW^{-1}. (The F-distribution used by SAS is not accurate.)
- The power of Wilk's, Lawley-Hotelling and Pillai statistics is similar. Roy's statistic has higher power only when one of the g treatments is very different from the rest.

Example: One-way MANOVA

- Populations: $g = 3$ types of students
  - (ℓ=1) Technical school students ($n_1 = 23$)
  - (ℓ=2) Architecture students ($n_2 = 38$)
  - (ℓ=3) Medical technology students ($n_3 = 21$)
- Response variables: $p = 4$ test scores
  - aptitude test
  - mathematics test
  - language test
  - general knowledge
- Test the null hypothesis that the mean vectors for the four traits are the same for all three groups of students

Example

The value of Wilks Lambda is $\frac{|W|}{|B+W|} = 0.544$

$$\begin{aligned} a &= (82-3)-(4-2+1)/2 = 77.5 \\ b &= \sqrt{\frac{4^2 2^2 - 4}{4^2+2^2-5}} = 2 \\ c &= ((4)(2)-2)/2 = 3 \end{aligned}$$

and

$$F = \left(\frac{1-\sqrt{\Lambda}}{\sqrt{\Lambda}}\right)\ \left(\frac{ab-c}{p(g-1)}\right) = 6.76$$

on $(p(g-1), ab-c) = (8, 152)$ degrees of freedom. p-value $<$ .0001

Conclude that the means scores are different for at least two groups of students for at least one the the four response variables

Bonferroni Confidence Intervals

- To construct simultaneous confidence intervals for the differences in treatment means for the i-th response variable

$$\mu_{ik} - \mu_{i\ell}$$

we need the variance of $\bar{x}_{ik} = \bar{x}_{i\ell}$:

$$\text{Var}(\bar{x}_{ik} - \bar{x}_{i\ell}) = \left(\frac{1}{n_k} + \frac{1}{n_\ell}\right)\sigma_{ii},$$

where σ_{ii} is estimated as

$$s_{pooled,ii} = \frac{w_{ii}}{n-g},$$

and w_{ii} is the ith diagonal element of the within group sum of squares and cross-products matrix W.

Bonferroni Confidence Intervals

- If we wish to carry out all pairwise comparisons, there will be $pg(g-1)/2$ of them.

- To maintain a simultaneous type I error level of no more than α we can use

$$t_{(n-g),1-\frac{\alpha}{2m}} \qquad \text{where} \qquad m = \frac{pg(g-1)}{2}.$$

- Formulas for the simultaneous confidence intervals are

$$(\bar{x}_{ik} - \bar{x}_{i\ell}) \ \pm \ t_{(n-g),1-\frac{\alpha}{2m}} \sqrt{\left(\frac{1}{n_k} + \frac{1}{n_\ell}\right) s_{pooled,ii}}$$

Bonferroni Simultaneous Intervals

- We have three groups and four variables, for a total of $4{\times}3{\times}2/2 = 12$ comparisons, three for each response variable.

- From the output:

$$w_{11} = 55036.1955 \quad w_{22} = 14588.9983$$

$$w_{33} = 4759.8655 \quad w_{44} = 7040.6248$$

with $n_1 = 23, n_2 = 38, n_3 = 21$ and $n - g = 82 - 3 = 79$.

Bonferroni Simultaneous Intervals

- A 95% confidence interval for the true difference between technical school and architecture students on mathematics is

$$\begin{aligned}
\bar{x}_{21} - \bar{x}_{22} &\pm t_{(n-g),1-\frac{\alpha}{2m}} \sqrt{\frac{w_{22}}{n-g}\left(\frac{1}{n_1} + \frac{1}{n_2}\right)} \\
47.3913 - 51.1842 &\pm t_{(79),1-0.05/24} \sqrt{\frac{14588.9983}{79}\left(\frac{1}{23} + \frac{1}{38}\right)} \\
-3.7929 &\pm 2.951\sqrt{184.671 \times 0.0698} \\
\Rightarrow & \quad (-14.388,\ 6.802).
\end{aligned}$$

Since the interval includes 0, there is insufficient evidence to reject the null hypothesis of equal mathematics means scores for technical and architecture students.

Bonferroni Simultaneous Intervals

- Similarly, we can compare mean math scores for other types of students. Compare technical school to medical technology students:

$$
\begin{aligned}
\bar{x}_{21} - \bar{x}_{32} &\pm t_{(n-g),1-\frac{\alpha}{2m}} \sqrt{\frac{w_{22}}{n-g}\left(\frac{1}{n_1} + \frac{1}{n_3}\right)} \\
47.3913 - 38.0952 &\pm t_{(79),1-(0.05/24)} \sqrt{\frac{14588.9983}{79}\left(\frac{1}{23} + \frac{1}{21}\right)} \\
9.296 &\pm 2.951\sqrt{184.671 \times 0.09110} \\
\Rightarrow & \quad (-2.808,\ 21.400).
\end{aligned}
$$

Bonferroni Simultaneous Intervals

- Confidence interval for the difference in mean math scores for architecture versus medical technology students:

$$\begin{aligned} \bar{x}_{22} - \bar{x}_{23} \quad &\pm \quad t_{(n-g),1-\frac{\alpha}{2m}} \sqrt{\frac{w_{22}}{n-g}\left(\frac{1}{n_2}+\frac{1}{n_3}\right)} \\ 13.089 \quad &\pm \quad 2.951\sqrt{184.671 \times 0.0739} \\ \Rightarrow \quad & \quad (2.185,\ 23.993). \end{aligned}$$

- Repeat these calculations for each of the other three response variables to construct 12 confidence intervals with simultaneous 95% confidence.

- R code demonstration