

# STAT 3690 Lecture Note

Week Six (Feb 13, 15, & 17, 2023)

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## Inference on $\mu$ under the normality assumption (con'd)

### Testing $\mu$ (J&W Sec. 5.2 & 5.3, con'd)

- Sample  $\mathbf{X}_1, \dots, \mathbf{X}_n \stackrel{\text{iid}}{\sim} \text{MVN}_p(\boldsymbol{\mu}, \boldsymbol{\Sigma})$ ,  $n > p$ 
  - $\mathcal{X} = \{\mathbf{X}_1, \dots, \mathbf{X}_n\}$
- $H_0 : \boldsymbol{\mu} = \boldsymbol{\mu}_0$  v.s.  $H_1 : \boldsymbol{\mu} \neq \boldsymbol{\mu}_0$
- Multivariate case (with unknown  $\boldsymbol{\Sigma}$ )
  - Name of approach: LRT
  - Test statistic:  $T(\mathcal{X}) = n(\bar{\mathbf{X}} - \boldsymbol{\mu}_0)^\top \mathbf{S}^{-1}(\bar{\mathbf{X}} - \boldsymbol{\mu}_0) (\sim T^2(p, n-1) = \frac{(n-1)p}{n-p} F(p, n-p)$  under  $H_0$ )
  - Level  $\alpha$  rejection region (with respect to  $T(\mathcal{X})$ ):  $R_\alpha = \{T(\mathcal{X}) : \frac{n-p}{p(n-1)} T(\mathcal{X}) \geq F_{1-\alpha, p, n-p}\}$ , i.e., reject  $H_0$  if  $T(\mathcal{X}) \geq \frac{p(n-1)}{n-p} F_{1-\alpha, p, n-p}$ 
    - \*  $F_{1-\alpha, p, n-p}$ : the  $(1-\alpha)$ -quantile of  $F(p, n-p)$
  - $p$ -value:  $p(\mathcal{X}) = 1 - F_{F(p, n-p)}\{\frac{n-p}{p(n-1)} T(\mathcal{X})\}$ 
    - \*  $F_{F(p, n-p)}$ : the cdf of  $F(p, n-p)$

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```
options(digits = 4)
install.packages(c("dslabs"))
library(dslabs)
data("gapminder")
dataset = as.matrix(gapminder[
  !is.na(gapminder$infant_mortality),
  c("infant_mortality", "life_expectancy", "fertility")])

(mu_hat <- colMeans(dataset))

# Test mu = mu_0
mu_0 <- c(25, 50, 3)
n = nrow(dataset)
p = ncol(dataset)
(test.stat <- drop(
  n * t(mu_hat - mu_0) %*% solve(cov(dataset)) %*% (mu_hat - mu_0)
))
(cri.point = (n-1)*p/(n-p)*qf(.95, p, n-p))
```

```
test.stat >= cri.point
(p.val = 1-pf((n-p)/(n-1)/p*test.stat, p, n-p))
```

- Report: Testing hypotheses  $H_0 : \boldsymbol{\mu} = [25, 50, 3]^\top$  v.s.  $H_1 : \boldsymbol{\mu} \neq [25, 50, 3]^\top$ , we carried on the LRT and obtained 249718 as the value of test statistic with  $[7.819, \infty)$  as the corresponding level .05 rejection region. In addition, the  $p$ -value was almost 0. So, at the .05 level, there was a strong statistical evidence implying the rejection of  $H_0$ , i.e., we believed that the population mean vector was not  $[25, 50, 3]^\top$ .

### $(1 - \alpha) \times 100\%$ confidence region (CR) for $\boldsymbol{\mu}$ (J&W Sec. 5.4)

- $\Pr\{(1 - \alpha) \times 100\% \text{ CR covers } \boldsymbol{\mu}\} \geq 1 - \alpha$ 
  - CR is a set made of observations and is hence random
  - $\boldsymbol{\mu}$  is fixed
  - $(1 - \alpha) \times 100\%$  CR covers  $\boldsymbol{\mu}$  with probability at least  $(1 - \alpha) \times 100\%$
- Inverted from the level  $\alpha$  rejection region for  $H_0 : \boldsymbol{\mu} = \boldsymbol{\mu}_0$  v.s.  $H_1 : \boldsymbol{\mu} \neq \boldsymbol{\mu}_0$ . Specifically,
  1. Take the rejection region as a function of  $\boldsymbol{\mu}_0$ ;
  2. Replace  $\boldsymbol{\mu}_0$  with  $\boldsymbol{\mu}$ ;
  3. Take the complement.
- Eventually,  $(1 - \alpha) \times 100\%$  CR
  - $= \{\boldsymbol{\mu} : n(\bar{\mathbf{x}} - \boldsymbol{\mu})^\top \boldsymbol{\Sigma}^{-1}(\bar{\mathbf{x}} - \boldsymbol{\mu}) < \chi_{1-\alpha, p}^2\}$  if  $\boldsymbol{\Sigma}$  is known
  - $= \{\boldsymbol{\mu} : \frac{n(n-p)}{p(n-1)}(\bar{\mathbf{x}} - \boldsymbol{\mu})^\top \mathbf{S}^{-1}(\bar{\mathbf{x}} - \boldsymbol{\mu}) < F_{1-\alpha, p, n-p}\}$  if  $\boldsymbol{\Sigma}$  is not known

### Testing $\mathbf{A}\boldsymbol{\mu}$ (J&W pp. 279)

- $\mathbf{A}$  is of  $q \times p$  and  $\text{rk}(\mathbf{A}) = q$ , i.e.,  $\mathbf{A}\boldsymbol{\Sigma}\mathbf{A}^\top > 0$
- Known: iid  $\mathbf{A}\mathbf{X}_i \sim \text{MVN}_q(\mathbf{A}\boldsymbol{\mu}, \mathbf{A}\boldsymbol{\Sigma}\mathbf{A}^\top)$ .
- LRT for  $H_0 : \mathbf{A}\boldsymbol{\mu} = \boldsymbol{\nu}_0$  v.s.  $H_1 : \mathbf{A}\boldsymbol{\mu} \neq \boldsymbol{\nu}_0$ 
  - Test statistic:  $T(\mathcal{X}) = n(\mathbf{A}\bar{\mathbf{X}} - \boldsymbol{\nu}_0)^\top (\mathbf{A}\boldsymbol{\Sigma}\mathbf{A}^\top)^{-1}(\mathbf{A}\bar{\mathbf{X}} - \boldsymbol{\nu}_0) (\sim T^2(q, n-1) = \frac{(n-1)q}{n-q} F(q, n-q))$  under  $H_0$
  - Level  $\alpha$  rejection region (with respect to  $T(\mathcal{X})$ ):  $R_\alpha = \{T(\mathcal{X}) : \frac{n-q}{q(n-1)} T(\mathcal{X}) \geq F_{1-\alpha, q, n-q}\}$
  - $p$ -value:  $p(\mathcal{X}) = 1 - F_{F(q, n-q)}\{\frac{n-q}{q(n-1)} T(\mathcal{X})\}$
- Multiple comparison
  - Interested in  $H_0 : \mu_1 = \dots = \mu_p$  v.s.  $H_1 : \text{Not all entries of } \boldsymbol{\mu} \text{ are equal.}$ 
    - \*  $\mu_k$ : the  $k$ th entry of  $\boldsymbol{\mu}$
  - Take

$$\boldsymbol{\nu}_0 = \mathbf{0}_{(p-1) \times 1}, \quad \mathbf{A} = \begin{bmatrix} 1 & -1 & 0 & \cdots & 0 \\ 1 & 0 & -1 & \cdots & 0 \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ 1 & 0 & 0 & \cdots & -1 \end{bmatrix}_{(p-1) \times p}.$$

- $p = 2$  (i.e.,  $\mathbf{A} = [1, -1]$ ): the case of A/B testing

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```
options(digits = 4)
install.packages(c("dslabs", "tidyverse"))
library(dslabs)
library(tidyverse)
data("gapminder")
dataset = gapminder[
  !is.na(gapminder$infant_mortality) &
  gapminder$region == 'South America' &
```

```

gapminder$year %in% 2000:2008,
c('country', 'year', "life_expectancy")] %>%
spread(year, life_expectancy)
(dataset = as.matrix(dataset[, -1]))
n = nrow(dataset); p = ncol(dataset)
(mu_hat <- colMeans(dataset))

# Test H0: A %%% mu = nu_0
(nu_0 <- as.matrix(rep(0, p-1)))
(A = cbind(rep(1, p-1), -diag(p-1)))

(test.stat <- drop(
  n * t(A %%% mu_hat - nu_0) %%%
  solve(A %%% cov(dataset) %%% t(A)) %%%
  (A %%% mu_hat - nu_0)
))
(cri.point = (n-1)*(p-1)/(n-p+1)*qf(.95, p-1, n-p+1))
test.stat >= cri.point
(p.val = 1-pf((n-p+1)/(n-1)/(p-1)*test.stat, p-1, n-p+1))

```

- Report: Testing hypotheses  $H_0$ : the average life expectancy over south american countries doesn't vary with time v.s.  $H_1$ : otherwise, we carried on the LRT and obtained 628.5 as the value of test statistic and  $[132.9, \infty)$  as the corresponding level .05 rejection region. In addition, the  $p$ -value was .002858. So, at the .05 level, there was a strong statistical evidence against  $H_0$ , i.e., we believed that the average life expectancy over south american countries does vary with time.

$(1 - \alpha) \times 100\%$  **CR for  $\nu = \mathbf{A}\mu$**

- $\mathbf{X}_1, \dots, \mathbf{X}_n \stackrel{\text{iid}}{\sim} \text{MVN}_p(\mu, \Sigma)$  with unknown  $\Sigma$  and  $n > p$
- $\mathbf{A}$  is of  $q \times p$  and  $\text{rk}(\mathbf{A}) = q$ , i.e.,  $\mathbf{A}\Sigma\mathbf{A}^\top > 0$
- Then iid  $\mathbf{A}\mathbf{X}_i \sim \text{MVN}_q(\nu, \mathbf{A}\Sigma\mathbf{A}^\top)$
- $(1 - \alpha) \times 100\%$  CR for  $\nu$  is  $\{\nu : \frac{n(n-q)}{q(n-1)}(\mathbf{A}\bar{\mathbf{x}} - \nu)^\top (\mathbf{A}\mathbf{S}\mathbf{A}^\top)^{-1}(\mathbf{A}\bar{\mathbf{x}} - \nu) < F_{1-\alpha, q, n-q}\}$
- Special case:  $\mathbf{A} = \mathbf{a}^\top \in \mathbb{R}^{1 \times p}$ , i.e.,  $\mathbf{A}$  is a row vector. Then
  - $(1 - \alpha) \times 100\%$  CR for scalar  $\nu = \mathbf{a}^\top \mu$  is  $\{\nu : n(\mathbf{a}^\top \bar{\mathbf{x}} - \nu)^2 / (\mathbf{a}^\top \mathbf{S} \mathbf{a}) < F_{1-\alpha, 1, n-1}\}$ , i.e.,

$$\left( \mathbf{a}^\top \bar{\mathbf{x}} - t_{1-\alpha/2, n-1} \sqrt{\mathbf{a}^\top \mathbf{S} \mathbf{a} / n}, \quad \mathbf{a}^\top \bar{\mathbf{x}} + t_{1-\alpha/2, n-1} \sqrt{\mathbf{a}^\top \mathbf{S} \mathbf{a} / n} \right)$$

\* E.g., when  $\mathbf{A} = [1, 0, \dots, 0]$ , it is the CR for the first entry of  $\mu$ , say  $\mu_1$

- Checking the coverage probability of the previous CR for each  $\mu_k$

```

options(digits = 4)
install.packages(c("MASS"))
set.seed(1)
B = 5e3L
n = 5e2L
Mu = (1:10)^2; (p = length(Mu))
(Sigma = diag(p)+.5)
alpha <- .05
(A = diag(p))
cover = matrix(0, ncol = p, nrow = B)

```

```

for (b in 1:B){
  sample = MASS::mvrnorm(n, Mu, Sigma)
  mu_hat = colMeans(sample)
  sample_cov = cov(sample)
  LB = A %%% mu_hat - qt(1-alpha/2, n-1)* sqrt(diag(A %%% sample_cov %%% t(A))/n)
  RB = A %%% mu_hat + qt(1-alpha/2, n-1)* sqrt(diag(A %%% sample_cov %%% t(A))/n)
  cover[b,] = (LB < Mu) * (Mu < RB)
}
(cover_prob_indiv = colMeans(cover))
(cover_prob_simul = mean(apply(cover, 1, prod)))

```

## Simultaneous confidence intervals

- Interested in  $(1 - \alpha_k)$  CRs for scalars  $\mathbf{a}_k^\top \boldsymbol{\mu}$ , say  $\text{CR}_k$ ,  $k = 1, \dots, m$ , simultaneously
- Make sure  $\Pr(\bigcap_k \{\mathbf{a}_k^\top \boldsymbol{\mu} \in \text{CR}_k\}) \geq 1 - \alpha$
- Bonferroni correction
  - Bonferroni inequality (optional) :

$$\Pr\left(\bigcap_{k=1}^m \{\mathbf{a}_k^\top \boldsymbol{\mu} \in \text{CR}_k\}\right) = 1 - \Pr\left(\bigcup_{k=1}^m \{\mathbf{a}_k^\top \boldsymbol{\mu} \notin \text{CR}_k\}\right) \geq 1 - \sum_{k=1}^m \Pr(\mathbf{a}_k^\top \boldsymbol{\mu} \notin \text{CR}_k) = 1 - \sum_{k=1}^m \alpha_k$$

- Taking  $\alpha_k$  such that  $\alpha = \sum_{k=1}^m \alpha_k$ , e.g.,  $\alpha_k = \alpha/m$ , i.e.,

$$(\mathbf{a}_k^\top \bar{\mathbf{x}} - t_{1-\alpha/(2m), n-1} \sqrt{\mathbf{a}_k^\top \mathbf{S} \mathbf{a}_k / n}, \quad \mathbf{a}_k^\top \bar{\mathbf{x}} + t_{1-\alpha/(2m), n-1} \sqrt{\mathbf{a}_k^\top \mathbf{S} \mathbf{a}_k / n})$$

- Appropriate for small  $m$
- Scheffé's method
  - Let  $\text{CR}_{\mathbf{a}} = (\mathbf{a}^\top \bar{\mathbf{x}} - c \sqrt{\mathbf{a}^\top \mathbf{S} \mathbf{a} / n}, \mathbf{a}^\top \bar{\mathbf{x}} + c \sqrt{\mathbf{a}^\top \mathbf{S} \mathbf{a} / n})$  for all  $\mathbf{a} \in \mathbb{R}^p$ . Then we may find that  $c = \sqrt{p(n-1)(n-p)^{-1} F_{1-\alpha, p, n-p}}$ .
  - Derivation by Cauchy-Schwarz inequality (optional):  $\{\mathbf{a}^\top (\bar{\mathbf{x}} - \boldsymbol{\mu})\}^2 = [(\mathbf{S}^{1/2} \mathbf{a})^\top \{\mathbf{S}^{-1/2} (\bar{\mathbf{x}} - \boldsymbol{\mu})\}]^2 \leq \{(\mathbf{a}^\top \mathbf{S} \mathbf{a})^\top / n\} \{n(\bar{\mathbf{x}} - \boldsymbol{\mu})^\top \mathbf{S}^{-1} (\bar{\mathbf{x}} - \boldsymbol{\mu})\} \Rightarrow$

$$\begin{aligned}
\Pr\left(\bigcap_{k=1}^m \{\mathbf{a}_k^\top \boldsymbol{\mu} \in \text{CR}_k\}\right) &\geq \Pr\left(\bigcap_{\mathbf{a} \in \mathbb{R}^p} \{\mathbf{a}^\top \boldsymbol{\mu} \in \text{CR}_{\mathbf{a}}\}\right) = 1 - \Pr\left(\bigcup_{\mathbf{a} \in \mathbb{R}^p} \{\mathbf{a}^\top \boldsymbol{\mu} \notin \text{CR}_{\mathbf{a}}\}\right) \\
&= 1 - \Pr\left(\bigcup_{\mathbf{a} \in \mathbb{R}^p} [\{\mathbf{a}^\top (\bar{\mathbf{X}} - \boldsymbol{\mu})\}^2 / \{(\mathbf{a}^\top \mathbf{S} \mathbf{a})^\top / n\} > c^2]\right) \\
&\geq 1 - \Pr(\{n(\bar{\mathbf{X}} - \boldsymbol{\mu})^\top \mathbf{S}^{-1} (\bar{\mathbf{X}} - \boldsymbol{\mu}) > c^2\})
\end{aligned}$$

- Assume  $\Pr(\{n(\bar{\mathbf{X}} - \boldsymbol{\mu})^\top \mathbf{S}^{-1} (\bar{\mathbf{X}} - \boldsymbol{\mu}) > c^2\}) = \alpha$  and obtain  $c = \sqrt{p(n-1)(n-p)^{-1} F_{1-\alpha, p, n-p}}$ .
- Appropriate for large even infinite  $m$

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```

options(digits = 4)
install.packages(c("dslabs"))
library(dslabs)
data("gapminder")
dataset = gapminder[
  !is.na(gapminder$infant_mortality) &
  gapminder$year == 2012,
  c('infant_mortality', 'life_expectancy')]

```

```

dataset = as.matrix(dataset)

n = nrow(dataset); p = ncol(dataset)

alpha <- .05
a1 = c(1,0); a2 = c(0,1)
A = rbind(a1, a2)
(mu_hat <- colMeans(dataset))
(sample_cov <- cov(dataset))

# Simultaneous CIs without correction
c = qt(1-alpha/2, n-1)
(NOcorrection <- cbind(
  A %*% mu_hat - c * sqrt(diag(A %*% sample_cov %*% t(A))/n),
  A %*% mu_hat + c * sqrt(diag(A %*% sample_cov %*% t(A))/n)
))

# Simultaneous CIs with Bonferroni correction
m = nrow(A)
c = qt(1-alpha/2/m, n-1)
(Bonferroni <- cbind(
  A %*% mu_hat - c * sqrt(diag(A %*% sample_cov %*% t(A))/n),
  A %*% mu_hat + c * sqrt(diag(A %*% sample_cov %*% t(A))/n)
))

# Simultaneous CIs with Scheffe correction
c = sqrt(p*(n-1)/(n-p) * qf(1-alpha, p, n-p))
(Scheffe <- cbind(
  A %*% mu_hat - c * sqrt(diag(A %*% sample_cov %*% t(A))/n),
  A %*% mu_hat + c * sqrt(diag(A %*% sample_cov %*% t(A))/n)
))

```

- Report: After the Bonferroni correction, resulting CRs (21.82, 29.82) and (69.92, 72.70) cover the mean infant mortality and mean life expectancy, simultaneously, with probability at least 95%.

## Comparing two multivariate means (J&W Sec. 6.3)

- Two independent samples following two distributions with equal covariance

$$\begin{aligned}
 & - \mathbf{X}_{11}, \dots, \mathbf{X}_{1n_1} \stackrel{\text{iid}}{\sim} \text{MVN}_p(\boldsymbol{\mu}_1, \boldsymbol{\Sigma}) \\
 & - \mathbf{X}_{21}, \dots, \mathbf{X}_{2n_2} \stackrel{\text{iid}}{\sim} \text{MVN}_p(\boldsymbol{\mu}_2, \boldsymbol{\Sigma})
 \end{aligned}$$

- Let  $\bar{\mathbf{X}}_i$  and  $\mathbf{S}_i$  be the sample mean and sample covariance for the  $i$ th sample,  $i = 1, 2$ .
- Hypotheses  $H_0 : \boldsymbol{\mu}_1 = \boldsymbol{\mu}_2$  v.s.  $H_1 : \boldsymbol{\mu}_1 \neq \boldsymbol{\mu}_2$
- Test statistic following LRT

$$\begin{aligned}
 T(\mathcal{X}) &= (\bar{\mathbf{X}}_1 - \bar{\mathbf{X}}_2)^\top \{ (n_1^{-1} + n_2^{-1}) \mathbf{S}_{\text{pool}} \}^{-1} (\bar{\mathbf{X}}_1 - \bar{\mathbf{X}}_2) \sim \frac{(n_1 + n_2 - 2)p}{n_1 + n_2 - p - 1} F(p, n_1 + n_2 - p - 1) \\
 \mathbf{S}_{\text{pool}} &= \frac{(n_1 - 1)\mathbf{S}_1 + (n_2 - 1)\mathbf{S}_2}{n_1 + n_2 - 2}
 \end{aligned}$$

- Level  $\alpha$  rejection region

$$\left\{ T(\mathcal{X}) : T(\mathcal{X}) \geq \frac{p(n_1 + n_2 - 2)}{n_1 + n_2 - p - 1} F_{1-\alpha, p, n_1 + n_2 - p - 1} \right\}$$

- $p$ -value

$$1 - F_{F_{1-\alpha, p, n_1+n_2-p-1}} \left[ \frac{n_1 + n_2 - p - 1}{p(n_1 + n_2 - 2)} T(\mathcal{X}) \right]$$


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- Report: Testing hypotheses  $H_0$ : in 2012 Asia and Africa shared the identical mean value in both infant mortality and life expectancy v.s.  $H_1$ : otherwise, we carried on the LRT and obtained 87.65 as the value of test statistic and  $[6.255, \infty)$  as the corresponding rejection region. In addition, the  $p$ -value was 4.952e-14. So, at the .05 level, there was a strong statistical evidence against  $H_0$ , i.e., we rejected  $H_0$  and believed that in 2012 Asia and Africa didn't share the identical mean value in either infant mortality or life expectancy.

## Testing for equality of population means (one-way multivariate analysis of variance (1-way MANOVA), J&W Sec. 6.4)

- Generalization of two-sample problem
    - Model:  $m$  independent samples, where
      - \*  $\mathbf{X}_{11}, \dots, \mathbf{X}_{1n_1} \stackrel{\text{iid}}{\sim} \text{MVN}_p(\boldsymbol{\mu}_1, \boldsymbol{\Sigma})$
      - \*  $\vdots$
      - \*  $\mathbf{X}_{m1}, \dots, \mathbf{X}_{mn_m} \stackrel{\text{iid}}{\sim} \text{MVN}_p(\boldsymbol{\mu}_m, \boldsymbol{\Sigma})$
    - Hypotheses  $H_0 : \boldsymbol{\mu}_1 = \dots = \boldsymbol{\mu}_m$  v.s.  $H_1 : \text{otherwise}$
  - Alternatively
    - Model:  $m$  independent samples, where
      - \*  $\mathbf{X}_{11}, \dots, \mathbf{X}_{1n_1} \stackrel{\text{iid}}{\sim} \text{MVN}_p(\boldsymbol{\mu} + \boldsymbol{\tau}_1, \boldsymbol{\Sigma})$
      - \*  $\vdots$
      - \*  $\mathbf{X}_{m1}, \dots, \mathbf{X}_{mn_m} \stackrel{\text{iid}}{\sim} \text{MVN}_p(\boldsymbol{\mu} + \boldsymbol{\tau}_m, \boldsymbol{\Sigma})$
      - Identifiability:  $\sum_i \boldsymbol{\tau}_i = \mathbf{0}$  otherwise there are infinitely many models that lead to the same data-generating mechanism.
    - Hypotheses  $H_0 : \boldsymbol{\tau}_1 = \dots = \boldsymbol{\tau}_m = \mathbf{0}$  v.s.  $H_1 : \text{otherwise}$
  - Alternatively
    - Model:  $\mathbf{X}_{ij} = \boldsymbol{\mu} + \boldsymbol{\tau}_i + \mathbf{E}_{ij}$  with  $\mathbf{E}_{ij} \stackrel{\text{iid}}{\sim} \text{MVN}_p(\mathbf{0}, \boldsymbol{\Sigma})$
    - \* Identifiability:  $\sum_i \boldsymbol{\tau}_i = \mathbf{0}$
    - Hypotheses  $H_0 : \boldsymbol{\tau}_1 = \dots = \boldsymbol{\tau}_m = \mathbf{0}$  v.s.  $H_1 : \text{otherwise}$
- 

- Sample means and sample covariances
  - Sample mean for the  $i$ th sample  $\bar{\mathbf{X}}_i = n_i^{-1} \sum_j \mathbf{X}_{ij}$
  - Sample covariance for the  $i$ th sample  $\mathbf{S}_i = (n_i - 1)^{-1} \sum_j (\mathbf{X}_{ij} - \bar{\mathbf{X}}_i)(\mathbf{X}_{ij} - \bar{\mathbf{X}}_i)^\top$
  - Grand mean  $\bar{\mathbf{X}} = \sum_i n_i \bar{\mathbf{X}}_i / \sum_i n_i = \sum_{ij} \mathbf{X}_{ij} / \sum_i n_i$
  - Sum of squares and cross products matrix (SSP)
    - \* Within-group SSP

$$\text{SSP}_w = \sum_i (n_i - 1) \mathbf{S}_i = \sum_{ij} (\mathbf{X}_{ij} - \bar{\mathbf{X}}_i)(\mathbf{X}_{ij} - \bar{\mathbf{X}}_i)^\top$$

- \* Between-group SSP

$$\text{SSP}_b = \sum_i n_i (\bar{\mathbf{X}}_i - \bar{\mathbf{X}})(\bar{\mathbf{X}}_i - \bar{\mathbf{X}})^\top$$

- \* Total (corrected) SSP

$$\text{SSP}_{\text{cor}} = \sum_{ij} (\mathbf{X}_{ij} - \bar{\mathbf{X}})(\mathbf{X}_{ij} - \bar{\mathbf{X}})^\top = \text{SSP}_w + \text{SSP}_b$$

- Exercise: verify the decomposition  $\mathbf{SSP}_{\text{cor}} = \mathbf{SSP}_{\text{w}} + \mathbf{SSP}_{\text{b}}$ .

- ML estimator of  $(\boldsymbol{\mu}_1, \dots, \boldsymbol{\mu}_m, \boldsymbol{\Sigma})$ 
  - Unconstrained
    - \*  $\hat{\boldsymbol{\mu}}_i = \bar{\mathbf{X}}_i = n_i^{-1} \sum_j \mathbf{X}_{ij}$
    - \*  $\hat{\boldsymbol{\Sigma}} = (\sum_i n_i)^{-1} \mathbf{SSP}_{\text{w}}$
  - Under  $H_0$ 
    - \*  $\hat{\boldsymbol{\mu}}_i = \bar{\mathbf{X}}$  for each  $i$
    - \*  $\hat{\boldsymbol{\Sigma}} = (\sum_i n_i)^{-1} \mathbf{SSP}_{\text{cor}}$
- Likelihood ratio

$$\lambda = \left\{ \frac{\det(\mathbf{SSP}_{\text{w}})}{\det(\mathbf{SSP}_{\text{cor}})} \right\}^{\sum_i n_i / 2}$$

monotonic with respect to the Wilk's lambda test statistic

$$\Lambda = \frac{\det(\mathbf{SSP}_{\text{w}})}{\det(\mathbf{SSP}_{\text{cor}})}$$

- Under  $H_0$ ,  $\Lambda \sim$  Wilk's lambda distribution  $\Lambda(\boldsymbol{\Sigma}, \sum_i n_i - m, m - 1)$ 
  - \* Since  $\mathbf{SSP}_{\text{w}} \sim W_p(\boldsymbol{\Sigma}, \sum_i n_i - m)$  and  $\mathbf{SSP}_{\text{b}} \sim W_p(\boldsymbol{\Sigma}, m - 1)$
  - \* When  $\sum_i n_i - m$  is large (i.e.,  $(p + m)/2 - \sum_i n_i + 1 \ll 0$ ), Bartlett's approximation

$$\{(p + m)/2 - \sum_i n_i + 1\} \ln \Lambda \approx \chi^2(p(m - 1))$$

- Level  $\alpha$  rejection region (with respect to  $\Lambda$ )

$$\begin{aligned} & \left\{ \Lambda : \{(p + m)/2 - \sum_i n_i + 1\} \ln \Lambda \geq \chi_{1-\alpha, p(m-1)}^2 \right\} \\ &= \left\{ \Lambda : \Lambda \leq \exp \left\{ \frac{\chi_{1-\alpha, p(m-1)}^2}{(p + m)/2 - \sum_i n_i + 1} \right\} \right\} \end{aligned}$$

- $p$ -value

$$1 - F_{\chi^2(p(m-1))} \left[ \{(p + m)/2 - \sum_i n_i + 1\} \ln \Lambda \right]$$

- Exercise: factors in producing plastic film (see W. J. Krzanowski (1988) *Principles of Multivariate Analysis*. A User's Perspective. Oxford UP, pp. 381.)
  - Three response variables (tear, gloss and opacity) describing measured characteristics of the resultant film
  - A total of 20 runs
  - One factor **RATE** (rate of extrusion, 2-level, low or high) in the production test
- Report: Testing hypotheses  $H_0$ : no **RATE** effect on film characteristics v.s.  $H_1$ : otherwise, we carried on the Wilk's lambda test and obtained 0.4136 as the value of test statistic and  $(-\infty, 0.6227]$  as the level .05 rejection region. In addition, the  $p$ -value was 0.002227. So, at the .05 level, there was statistical evidence against  $H_0$ , i.e., we rejected  $H_0$  and believed that there was an effect from **RATE** on film characteristics.