STAT 3690 Lecture Note

Part IV: Inference on the mean vector

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Inference on $\boldsymbol{\mu}$ (under the normality assumption)

Likelihood ratio test (LRT)

- Minimize the type II error rate subject to a capped type I error rate (under certain classical circumstances)
- Test statistic
$$\lambda(\mathcal{X}) = \frac{L(\hat{\boldsymbol{\theta}}_0; \mathcal{X})}{L(\hat{\boldsymbol{\theta}}; \mathcal{X})}$$
  - $\mathcal{X}$: all the observations/the entire dataset
  - L: the likelihood function
  - $\boldsymbol{\theta}$: the unknown parameter(s)
  - $\hat{\boldsymbol{\theta}}_0$: ML estimator for $\boldsymbol{\theta}$ under H_0
  - $\hat{\boldsymbol{\theta}}$: ML estimator for $\boldsymbol{\theta}$
- (Asymptotic) level α rejection region (with respect to $\lambda(\mathcal{X})$)
$$R_\alpha = \{\lambda(\mathcal{X}) : -2\ln\lambda(\mathcal{X}) \geq \chi^2_{1-\alpha,\nu}\}$$
  - I.e., reject H_0 when $-2\ln\lambda(\mathcal{X}) \geq \chi^2_{1-\alpha,\nu}$
  - $\chi^2_{1-\alpha,\nu}$ is the $(1-\alpha)$-quantile of $\chi^2(\nu)$
  - ν: the difference in numbers of free parameters without/with H_0
- (Asymptotic) p-value
$$p(\mathcal{X}) = 1 - F_{\chi^2(\nu)}\{-2\ln\lambda(\mathcal{X})\}$$
  - $F_{\chi^2(\nu)}(\cdot)$ is the cdf of $\chi^2(\nu)$

Testing $\boldsymbol{\mu}$ (J&W Sec. 5.2 & 5.3)

- Sample $\boldsymbol{X}_1, \ldots, \boldsymbol{X}_n \overset{\text{iid}}{\sim} \text{MVN}_p(\boldsymbol{\mu}, \boldsymbol{\Sigma})$, $n > p$
  - $\mathcal{X} = \{\boldsymbol{X}_1, \ldots, \boldsymbol{X}_n\}$, the set of all the data
- $H_0 : \boldsymbol{\mu} = \boldsymbol{\mu}_0$ v.s. $H_1 : \boldsymbol{\mu} \neq \boldsymbol{\mu}_0$
- Recall the univariate case ($p = 1$)
  - The model reduces to $X_1, \ldots, X_n \overset{\text{iid}}{\sim} \mathcal{N}(\mu, \sigma^2)$
  - Hypotheses reduces to $H_0 : \mu = \mu_0$ v.s. $H_1 : \mu \neq \mu_0$
  - $\bar{X}$ and s^2 are sample mean and sample variance, respectively
  - Known σ^2
    * Name of approach: Z-test (equiv. LRT)

    - $*$ Test statistic: $T(\mathcal{X}) = \sqrt{n}(\bar{X} - \mu_0)/\sigma$ ($\sim \mathcal{N}(0,1)$ under H_0)
    - $*$ Level α Rejection region (with respect to $T(\mathcal{X})$): $R_\alpha = \{T(\mathcal{X}) : |T(\mathcal{X})| \geq \Phi^{-1}_{1-\alpha/2}\}$, i.e., reject H_0 if $|T(\mathcal{X})| \geq \Phi^{-1}_{1-\alpha/2}$
      - · Critical point: $\Phi^{-1}_{1-\alpha/2}$, the $(1-\alpha/2)$-quantile of $\mathcal{N}(0,1)$
  - Unknown σ^2
    - $*$ Name of approach: t-test (equiv. LRT)
    - $*$ Test statistic: $T = \sqrt{n}(\bar{X} - \mu_0)/s$ ($\sim t(n-1)$ under H_0)
    - $*$ Level α rejection region (with respect to $T(\mathcal{X})$): $R_\alpha = \{T(\mathcal{X}) : |T(\mathcal{X})| \geq t_{1-\alpha/2,n-1}\}$, i.e., reject H_0 if $|T(\mathcal{X})| \geq t_{1-\alpha/2,n-1}$
      - · Critical point: $t_{1-\alpha/2,n-1}$, the $(1-\alpha/2)$-quantile of $t(n-1)$

- Multivariate case (with known $\boldsymbol{\Sigma}$)
  - Name of approach: LRT
  - Test statistic: $T(\mathcal{X}) = n(\bar{\boldsymbol{X}} - \boldsymbol{\mu}_0)^\top \boldsymbol{\Sigma}^{-1}(\bar{\boldsymbol{X}} - \boldsymbol{\mu}_0)$ ($\sim \chi^2(p)$ under H_0)
  - Level α rejection region (with respect to $T(\mathcal{X})$): $R_\alpha = \{T(\mathcal{X}) : T(\mathcal{X}) \geq \chi^2_{1-\alpha,p}\}$, i.e., reject H_0 if $T(\mathcal{X}) \geq \chi^2_{1-\alpha,p}$
    - $*$ Critical point: $\chi^2_{1-\alpha,p}$, the $(1-\alpha)$-quantile of $\chi^2(p)$
  - p-value: $p(\mathcal{X}) = 1 - F_{\chi^2(p)}(T(\mathcal{X}))$
    - $*$ $F_{\chi^2(p)}(\cdot)$: the cdf of $\chi^2(p)$

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

# Assume we know Sigma
Sigma <- matrix(c(555, -170, 30,
                  -170, 65, -10,
                  30, -10, 2), ncol = 3)

(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(Sigma) %*% (mu_hat - mu_0)
))
test.stat >= qchisq(0.95, df=p)
(p.val = 1-pchisq(test.stat, df=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 450477 as the value of test statistic and $[7.815, \infty)$ as the corresponding level .05 rejection region. In addition, the p-value was around 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 $[25, 50, 3]^\top$.

- Multivariate case (with unknown $\boldsymbol{\Sigma}$)
  - Name of approach: LRT
  - Test statistic: $T(\mathcal{X}) = n(\bar{\boldsymbol{X}} - \boldsymbol{\mu}_0)^\top \mathbf{S}^{-1}(\bar{\boldsymbol{X}} - \boldsymbol{\mu}_0)$ ($\sim T^2(p, n-1) = \frac{(n-1)p}{n-p} F(p, n-p)$ under H_0)
  - Level α 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 $F(p, n-p)$

```r
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)

- $\Pr\{(1-\alpha) \times 100\%$ 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 α 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
  - $= \{\boldsymbol{\mu} : n(\bar{\boldsymbol{x}} - \boldsymbol{\mu})^\top \boldsymbol{\Sigma}^{-1}(\bar{\boldsymbol{x}} - \boldsymbol{\mu}) < \chi^2_{1-\alpha,p}\}$ if $\boldsymbol{\Sigma}$ is known
  - $= \{\boldsymbol{\mu} : \frac{n(n-p)}{p(n-1)}(\bar{\boldsymbol{x}} - \boldsymbol{\mu})^\top \mathbf{S}^{-1}(\bar{\boldsymbol{x}} - \boldsymbol{\mu}) < F_{1-\alpha,p,n-p}\}$ if $\boldsymbol{\Sigma}$ is not known

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

- $\mathbf{A}$ is of $q \times p$ and $\mathrm{rk}(\mathbf{A}) = q$, i.e., $\mathbf{A}\boldsymbol{\Sigma}\mathbf{A}^\top > 0$

- Known: iid $\mathbf{A}\boldsymbol{X}_i \sim \mathrm{MVN}_q(\mathbf{A}\boldsymbol{\mu}, \mathbf{A}\Sigma\mathbf{A}^\top)$.
- 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: $T(\mathcal{X}) = n(\mathbf{A}\bar{\boldsymbol{X}} - \boldsymbol{\nu}_0)^\top(\mathbf{A}\mathbf{S}\mathbf{A}^\top)^{-1}(\mathbf{A}\bar{\boldsymbol{X}} - \boldsymbol{\nu}_0)$ ($\sim T^2(q, n-1) = \frac{(n-1)q}{n-q}F(q, n-q)$ under H_0)
  - Level α 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 $H_0 : \mu_1 = \cdots = \mu_p$ v.s. H_1 : Not all entries of $\boldsymbol{\mu}$ are equal.
    - μ_k: the kth 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

---

```r
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 $\boldsymbol{\nu}=\mathbf{A}\boldsymbol{\mu}$

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

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

    - E.g., when $\mathbf{A}=[1,0,\ldots,0]$, it is the CI for the first entry of $\boldsymbol{\mu}$, say μ_1
- Checking the coverage probability of the previous CI for each μ_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 $(1-\alpha_k)\times 100\%$ CIs for scalars $\boldsymbol{a}_k^\top\boldsymbol{\mu}$, say CR_k, $k=1,\ldots,m$, simultaneously
- Make sure $\Pr(\bigcap_k\{\boldsymbol{a}_k^\top\boldsymbol{\mu}\in\text{CR}_k\})\geq 1-\alpha$
- Bonferroni correction
  - Bonferroni inequality (optional) :

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

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

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

    - Appropriate for small m

- Scheffé's method
    - Let $\mathrm{CI}_{\boldsymbol{a}} = (\boldsymbol{a}^\top\bar{\boldsymbol{x}} - c\sqrt{\boldsymbol{a}^\top\mathbf{S}\boldsymbol{a}/n}, \boldsymbol{a}^\top\bar{\boldsymbol{x}} + c\sqrt{\boldsymbol{a}^\top\mathbf{S}\boldsymbol{a}/n})$ for all $\boldsymbol{a} \in \mathbb{R}^p$. 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): $\{\boldsymbol{a}^\top(\bar{\boldsymbol{x}}-\boldsymbol{\mu})\}^2 = [(\mathbf{S}^{1/2}\boldsymbol{a})^\top\{\mathbf{S}^{-1/2}(\bar{\boldsymbol{x}}-\boldsymbol{\mu})\}]^2 \le \{(\boldsymbol{a}^\top\mathbf{S}\boldsymbol{a})^\top/n\}\{n(\bar{\boldsymbol{x}}-\boldsymbol{\mu})^\top\mathbf{S}^{-1}(\bar{\boldsymbol{x}}-\boldsymbol{\mu})\} \Rightarrow$

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

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

```r
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, the resulting CIs (21.82, 29.82) and (69.92, 72.70) cover the mean infant mortality and mean life expectancy, simultaneously, with probability at least 95%.

The confidence region for $\boldsymbol{\mu} = [\mu_1, \ldots, \mu_p]^\top$ vs. simultaneous confidence intervals for $\mu_1, \ldots, \mu_p$

- $\boldsymbol{X}_1, \ldots, \boldsymbol{X}_n \overset{\text{iid}}{\sim} \text{MVN}_p(\boldsymbol{\mu}, \boldsymbol{\Sigma})$ with known $\boldsymbol{\Sigma}$ and $n > p$
- $(1-\alpha) \times 100\%$ CR for $\boldsymbol{\mu}$: $\{\boldsymbol{\mu} : n(\bar{\boldsymbol{x}} - \boldsymbol{\mu})^\top \mathbf{S}^{-1}(\bar{\boldsymbol{x}} - \boldsymbol{\mu}) < \frac{p(n-1)}{n-p} F_{1-\alpha,p,n-p}\}$
  - CR covering $\boldsymbol{\mu}$ with a probability at least $1-\alpha$
  - With a coverage probability closer to $(1-\alpha) \times 100\%$
- $(1-\alpha) \times 100\%$ simultaneous CI$_k$ for μ_k: $\left(\bar{x}_k - c\sqrt{S_{kk}/n}, \quad \bar{x}_k + c\sqrt{S_{kk}/n}\right)$ with $\bar{x}_k$ the kth entry of $\bar{\boldsymbol{x}}$ and S_{kk} the (k,k)-th entry of $\mathbf{S}$
  - $c = \sqrt{\frac{p(n-1)}{n-p} F_{1-\alpha,p,n-p}}$ (Scheffé) and $t_{1-\alpha/(2m),n-1}$ (Bonferroni)
    - $m = p$ in this case since one interval for each entry of $\boldsymbol{\mu}$
  - CI$_1 \times \cdots \times$ CI$_p$ covering $\boldsymbol{\mu}$ with a probability at least $1-\alpha$
  - Clearly indicating the range for each μ_k

```
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) # entries of interest
A = rbind(a1, a2)
(mu_hat <- colMeans(dataset))
(sample_cov <- cov(dataset))
c = sqrt(p*(n-1)/(n-p) * qf(1-alpha, p, n-p))

# Plot the CR for the population mean vector mu
car::ellipse(center = mu_hat, shape = sample_cov/n, radius = c, add = F,
             xlab = "infant_mortality", ylab = "life_expectancy")

# Plot the simultaneous CIs with Scheffe correction
(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)
))
```

```r
abline(v = Scheffe[1,1], col="red")
abline(v = Scheffe[1,2], col="red")
abline(h = Scheffe[2,1], col="red")
abline(h = Scheffe[2,2], col="red")

# Plot the simultaneous CIs with Bonferroni correction
(Bonferroni <- cbind(
    A %*% mu_hat - qt(1-alpha/2/nrow(A), n-1) * sqrt(diag(A %*% sample_cov %*% t(A))/n),
    A %*% mu_hat + qt(1-alpha/2/nrow(A), n-1) * sqrt(diag(A %*% sample_cov %*% t(A))/n)
))
abline(v = Bonferroni[1,1], col="green")
abline(v = Bonferroni[1,2], col="green")
abline(h = Bonferroni[2,1], col="green")
abline(h = Bonferroni[2,2], col="green")
```