

Multivariate Analysis Lecture 7: Hotelling's T^2

Zhaoxia Yu
Professor, Department of Statistics

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Outline of Lecture 07

- Review of Wishart and the Hotelling's T^2 distribution for one-sample problems
- Examples of one-sample Hotelling's T^2
- Two-sample Hotelling's T^2
- Examples of two-sample Hotelling's T^2
- The multivariate normality (MVN) assumption

Section 1

Review

Subsection 1

Wishart Distribution

Definition of Wishart Distribution

- A Wishart distribution can be defined in the following way
- Let \mathbf{W} be a $p \times p$ random matrix. We say \mathbf{W} follows $Wishart_p(k, \Sigma)$ if \mathbf{W} can be written as $\mathbf{W} = \mathbf{X}^T \mathbf{X}$ where \mathbf{X} denotes the random matrix formed by a random sample of size k from $MVN N(\mathbf{0}, \Sigma)$.
- The definition indicates that if we have a random sample $\mathbf{X}_1, \dots, \mathbf{X}_k$ from $N(\mathbf{0}, \Sigma)$, then $\mathbf{X}^T \mathbf{X} = \sum_{i=1}^k \mathbf{X}_i \mathbf{X}_i^T \sim Wishart_p(k, \Sigma)$.
- Remark: $E[\mathbf{W}] = k\Sigma$.

Wishart vs Chi-squared

- **Wishart:** If $\mathbf{X}_1, \dots, \mathbf{X}_k \stackrel{iid}{\sim} N(\mathbf{0}, \Sigma)$, then

$$\mathbf{X}^T \mathbf{X} = \sum_{i=1}^k \mathbf{X}_i \mathbf{X}_i^T \sim \text{Wishart}_p(k, \Sigma), \text{ where } \mathbf{X}_{k \times p} = \begin{pmatrix} X_1^T \\ \vdots \\ X_k^T \end{pmatrix}$$

- **Chi-squared:** If $X_1, \dots, X_k \stackrel{iid}{\sim} N(0, 1)$, then

$$\mathbf{X}^T \mathbf{X} = \sum_{i=1}^k X_i^2 \sim \chi_k^2, \text{ where } \mathbf{X}_{k \times 1} = \begin{pmatrix} X_1 \\ \vdots \\ X_k \end{pmatrix}$$

Wishart vs Chi-squared (continued)

- When $p = 1$,

$$W = \sum_{i=1}^k X_i^2 = \sigma^2 \sum_{i=1}^k \left(\frac{X_i}{\sigma} \right)^2 \sim \sigma^2 \chi_k^2$$

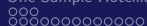
The Sample Covariance Matrix

- Let $\mathbf{X}_1, \dots, \mathbf{X}_n$ be a random sample from $N(\boldsymbol{\mu}, \boldsymbol{\Sigma})$. The $\mathbf{X}_{n \times p}$ follows a matrix normal distribution:

$$\mathbf{X} \sim N(\mathbf{1}_n \otimes \boldsymbol{\mu}^T, \boldsymbol{\Sigma}, \mathbf{I}_n)$$

- We have shown that

$$(n-1)\mathbf{S} \sim \text{Wishart}_p(n-1, \boldsymbol{\Sigma})$$



Subsection 2

Hotelling's T^2

Definition of Hotelling's T^2

- Hotelling generalized the student's t, which is for univariate, to Hotelling's T^2 , which is the multivariate version
- Definition.** We say a random variable follows Hotelling's $T^2_{p,\nu}$ if the random variable can be written as $\mathbf{Z}^T \left(\frac{\mathbf{W}}{\nu} \right)^{-1} \mathbf{Z}$ where
 - $\mathbf{Z} \sim N(\mathbf{0}, \mathbf{\Sigma})$
 - $\mathbf{W} \sim W_p(\nu, \mathbf{\Sigma})$
 - $\mathbf{Z} \perp \mathbf{W}$

Section 2

One-Sample Hotelling T^2

One-Sample Hotelling T^2

- Let $\mathbf{X}_1, \mathbf{X}_2, \dots, \mathbf{X}_n$ be a random sample from a multivariate normal distribution with mean vector $\boldsymbol{\mu}$ and covariance matrix $\boldsymbol{\Sigma}$.
- The sample mean vector and sample covariance matrix are denoted by $\bar{\mathbf{X}}$ and \mathbf{S} , respectively.
- The null hypothesis of interest $H_0 : \boldsymbol{\mu} = \boldsymbol{\mu}_0$
- The one-sample Hotelling T^2 is defined as

$$T^2 = (\hat{\boldsymbol{\mu}} - \boldsymbol{\mu}_0)^T (\text{Cov}(\hat{\boldsymbol{\mu}}))^{-1} (\hat{\boldsymbol{\mu}} - \boldsymbol{\mu}_0)$$

- We have shown that $T^2 \sim T_{p, n-1}^2$ when $H_0 : \boldsymbol{\mu} = \boldsymbol{\mu}_0$.

Hotelling's T^2 Distribution vs F Distribution

Hotelling's T^2

Claim: $T_{p,\nu}^2 \sim \frac{\nu p}{\nu+1-p} F_{p,\nu+1-p}$.

For the T^2 statistic, we have $T^2 \stackrel{H_0}{\sim} \frac{(n-1)p}{n-p} F_{p,n-p}$. We reject H_0 at significance level α when $T^2 > \frac{(n-1)p}{n-p} F_{p,n-p,1-\alpha}$.

Corollary.

$$\frac{n-p}{p} (\bar{X} - \mu_0)^T (\hat{\Sigma})^{-1} (\bar{X} - \mu_0) \stackrel{H_0}{\sim} F_{p,n-p}$$

where $\hat{\Sigma} = \frac{1}{n} X^T H X = \frac{1}{n} \sum_{i=1}^n (X_i - \bar{X})(X_i - \bar{X})^T = \frac{(n-1)S}{n}$.

Subsection 1

A Simulation Study

Understand the Wishart Distribution

- Recall that if $W \sim \text{Wishart}_p(k, \Sigma)$, then $E[\mathbf{W}] = k\Sigma$.

```
library(MASS)
p=2; n=5; B=1000; rho=0.7
Sigma=diag(1+rho, p, p) - matrix(rho, p, p)
wmat.array=array(0, c(B, p, p)) #wishart-distributed
for(b in 1:B){
  X=mvrnorm(n, rep(0,p), Sigma)
  wmat.array[b,,]=cov(X)}
apply(wmat.array, c(2,3), mean)
```

```
##           [,1]      [,2]
## [1,]  0.9583646 -0.6909337
## [2,] -0.6909337  1.0107182
```

```
Sigma*(n-1)
```

```
##           [,1] [,2]
## [1,]  4.0 -2.8
## [2,] -2.8  4.0
```

Write an R function to conduct Hotelling's T^2

- There is no R base function for conducting Hotelling's T^2 test
- We will write an R function

```
#Hotelling's T^2 for testing H0: mu=mu0 vs mu != mu0
Hotelling.T2.1sample=function(X, mu0)
{
  n=dim(X)[1]
  p=dim(X)[2]
  X.bar=colMeans(X)
  X.S=cov(X)
  T2=n*t(X.bar-mu0)%*%solve(X.S)%*(X.bar-mu0)
  p.value=1-pf(T2/((n-1)*p/(n-p)),p,n-p)
  return(list(X.bar=X.bar, X.cov=X.S, T2=T2, p.value=p.value))
}
```


Example of Multivariate One-Sample Problem: Protein Intake

- For the protein intake data, it might be more interesting to estimate the means than conducting hypothesis testing
- Suppose we are interested in estimating the means of the daily protein intake from different sources

```
library(MASS) #the library "MASS" is required
my.cov=4*(diag(4) + 0.3* rep(1,4)%o%rep(1,4))
n=60;p=4
my.mean=8*c(3,2,1,1)
eigen(my.cov) #to check whether the cov matrix is p.d.
```

```
## eigen() decomposition
## $values
## [1] 8.8 4.0 4.0 4.0
##
## $vectors
##      [,1]      [,2]      [,3]      [,4]
## [1,] -0.5  0.8660254  0.0000000  0.0000000
## [2,] -0.5 -0.2886751 -0.5773503 -0.5773503
## [3,] -0.5 -0.2886751 -0.2113249  0.7886751
## [4,] -0.5 -0.2886751  0.7886751 -0.2113249
```

Example of Multivariate One-Sample Problem: Protein Intake

- Estimate the mean vector using the sample mean vector
- Estimate covariance of the sample mean vector. Recall that

$$\text{cov}(\bar{\mathbf{X}}) = \frac{\Sigma}{n}$$

```
set.seed(1)
x=mvrnorm(n, mu=my.mean, Sigma=my.cov)
protein=as.matrix(data.frame(meat=x[,1],dairy=x[,2],
                             veg=x[,3], other=x[,4]))
colMeans(protein)
```

```
##      meat      dairy      veg      other
## 24.034032 15.928361  7.660490  7.738634
```

```
cov(protein)/n
```

```
##           meat      dairy      veg      other
## meat  0.07159404 0.013584596 0.018824131 0.009220700
## dairy 0.01358460 0.073421655 0.005829816 0.003895500
## veg   0.01882413 0.005829816 0.086176323 0.009828535
## other 0.00922070 0.003895500 0.009828535 0.075478822
```

Example of Multivariate One-Sample Problem: Protein Intake

- Use Hotelling's T^2 to quantify uncertainties. Recall that

$$T^2 = (\bar{\mathbf{X}} - \boldsymbol{\mu})^T \left(\text{Cov}(\bar{\mathbf{X}}) \right)^{-1} (\bar{\mathbf{X}} - \boldsymbol{\mu}) \sim \frac{(n-1)p}{n-p} F_{p, n-p}$$

where $\text{Cov}(\bar{\mathbf{X}}) = \frac{\mathbf{S}}{n}$.

- The result indicates that

$$Pr[(\bar{\mathbf{X}} - \boldsymbol{\mu})^T \left(\text{Cov}(\bar{\mathbf{X}}) \right)^{-1} (\bar{\mathbf{X}} - \boldsymbol{\mu}) \leq \frac{(n-1)p}{n-p} F_{p, n-p, 1-\alpha}] = 1-\alpha$$

- Thus, a $(1 - \alpha)100\%$ confidence **region** for $\boldsymbol{\mu}$ is

$$\{\boldsymbol{\mu} : (\bar{\mathbf{X}} - \boldsymbol{\mu})^T \left(\text{Cov}(\bar{\mathbf{X}}) \right)^{-1} (\bar{\mathbf{X}} - \boldsymbol{\mu}) \leq \frac{(n-1)p}{n-p} F_{p, n-p, 1-\alpha}\}$$

Example of Multivariate One-Sample Problem: Protein Intake

- Confidence intervals, which are in the form of

$$\text{estimate} \pm \text{critical value} \times \text{standard error}$$
are often preferred
- If there is only one parameter of interest, we can construct a C.I. using t-distribution, just as in univariate analysis
- Example. What is the mean protein intake? We have discussed the problem in Lecture 04.
 - Lecture 04: we constructed a large-sample C.I. by using 1.96 as the critical value. (See the protein intake example)
 - This lecture: we construct a C.I. by using $t_{n-1, 1-\frac{\alpha}{2}}$ as the critical value

$$\bar{X}_{(j)} \pm t_{n-1, 1-\frac{\alpha}{2}} \sqrt{\frac{s_{X(j)}^2}{n}} \text{ for } j = 1, \dots, p.$$

Example of Multivariate One-Sample Problem: Protein Intake

- The confidence region has exactly $(1 - \alpha)100\%$ confidence; however
- In many situations, we would like to construct confidence intervals for multiple parameters
- This is known as simultaneous intervals
- If we use the conventional method to construct individual C.I.s, we will have lower than $(1 - \alpha)100\%$ confidence to cover all the parameters simultaneously

Example of Multivariate One-Sample Problem: Protein Intake

- Some linear algebra result ensures that the following method gives $(1 - \alpha)100\%$ confidence to cover all linear combinations of the parameters (in the form of $a^T \mu$) simultaneously

$$a^T \bar{\mathbf{X}} \pm \sqrt{\frac{(n-1)p}{n-p} F_{p, n-p, 1-\alpha}} se(a^T \bar{\mathbf{X}})$$

- Example, consider the individual means $\mu_j, j = 1, \dots, 4$ in the protein intake example, the following intervals are 95% simultaneous C.I. for the mean protein intake from the four sources

Example of Multivariate One-Sample Problem: Protein Intake

```
#sample means
colMeans(protein)
```

```
##      meat      dairy      veg      other
## 24.034032 15.928361  7.660490  7.738634
```

```
#standard errors
sqrt(diag(cov(protein)/n))
```

```
##      meat      dairy      veg      other
## 0.2675706 0.2709643 0.2935580 0.2747341
```

```
#critical value based on T2
sqrt((n-1)*p/(n-p)*qf(0.95, p, n-p))
```

```
## [1] 3.269537
```

```
#lower bounds
low.bound=colMeans(protein) - sqrt((n-1)*p/(n-p)*qf(0.95, p, n-p)) *sqrt(diag(cov(protein)/n))
#upper bounds
up.bound=colMeans(protein) + sqrt((n-1)*p/(n-p)*qf(0.95, p, n-p)) *sqrt(diag(cov(protein)/n))
```

Example of Multivariate One-Sample Problem: Protein Intake

#put everything into a table

```
data.frame(lower=low.bound, mean=colMeans(protein),
            upper=up.bound)
```

##		lower	mean	upper
##	meat	23.159200	24.034032	24.908864
##	dairy	15.042433	15.928361	16.814289
##	veg	6.700691	7.660490	8.620288
##	other	6.840381	7.738634	8.636887

Example of Multivariate One-Sample Problem: Protein Intake

- Three choices of critical values
 - unadjusted: $t_{n-1, 1-\alpha/2}$. Should **NOT** be used if multiple linear functions need to be estimated
 - T^2 : $\sqrt{\frac{(n-1)p}{n-p} F_{p, n-p, 1-\alpha}}$
 - Bonferroni's correction: simply replace α with α/k where k is the total number of linear functions of the mean parameters:
 $t_{n-1, 1-\alpha/(2k)}$
- Example: the critical values for the individual means from four protein sources

Example of Multivariate One-Sample Problem: Protein Intake

```
#unadjusted, shouldn't be used when constructing simultaneous C.I.s
qt(1-0.05/2, n-1)
```

```
## [1] 2.000995
```

```
#T^2
sqrt((n-1)*p/(n-p)*qf(0.95, p, n-p))
```

```
## [1] 3.269537
```

```
#Bonferroni correction
qt(1-0.05/p/2, n-1)
```

```
## [1] 2.576588
```

Section 3

Two-Sample Hotellings T^2

One-Sample vs Two-Sample

- In the one-sample problem, the goal is to make inference of
 - univariate: a population mean (one-sample t-test problem) or
 - multivariate: a population mean vector (one-sample Hotelling T^2 problem)
- In the two-sample problem
 - univariate: compare two population means
 - multivariate: compare two population mean vectors

Univariate Two-Sample Problems

- Two independent samples
 - Sample 1 is from population 1:

$$X_{11}, \dots, X_{1,n_1} \stackrel{iid}{\sim} N(\mu_1, \sigma^2)$$

- Sample 2 is from population 2:

$$X_{21}, \dots, X_{2,n_1} \stackrel{iid}{\sim} N(\mu_2, \sigma^2)$$

- Null hypothesis: $H_0 : \mu_1 = \mu_2$

Univariate Two-Sample Problems

- Pooled sample variance

$$s_p^2 = \frac{(n_1 - 1)s_1^2 + (n_2 - 1)s_2^2}{n_1 + n_2 - 2}$$

where

$$s_i^2 = \frac{\sum_{j=1}^{n_i} X_{ij}^2 - (\sum_{j=1}^{n_i} X_{ij})^2 / n_i}{n_i - 1}$$

- Two-sample t-statistic

$$t = \frac{\bar{x}_1 - \bar{x}_2}{\sqrt{s_p^2 \left(\frac{1}{n_1} + \frac{1}{n_2} \right)}}$$

- Null distribution: $t \stackrel{H_0}{\sim} t_{n_1+n_2-2}$.

Multivariate Two-Sample Problems

- Two independent samples
 - Sample 1 is from population 1:

$$\mathbf{X}_{11}, \dots, \mathbf{X}_{1,n_1} \stackrel{iid}{\sim} N(\boldsymbol{\mu}_1, \boldsymbol{\Sigma})$$

- Sample 2 is from population 2:

$$\mathbf{X}_{21}, \dots, \mathbf{X}_{2,n_2} \stackrel{iid}{\sim} N(\boldsymbol{\mu}_2, \boldsymbol{\Sigma})$$

- Null and alternative hypotheses: $H_0 : \boldsymbol{\mu}_1 = \boldsymbol{\mu}_2$ vs $H_1 : \boldsymbol{\mu}_1 \neq \boldsymbol{\mu}_2$

Multivariate Two-Sample Problems

- SPooled sample variance

$$\mathbf{S}_p = \frac{(n_1 - 1)\mathbf{S}_1 + (n_2 - 1)\mathbf{S}_2}{n_1 + n_2 - 2}$$

where

$$\mathbf{S}_i = \frac{1}{n_i - 1} \sum_{j=1}^{n_i} (\mathbf{x}_{ij} - \bar{\mathbf{x}}_i)(\mathbf{x}_{ij} - \bar{\mathbf{x}}_i)'$$

- Two-sample Hotelling's T^2

$$T^2 = (\bar{\mathbf{X}}_1 - \bar{\mathbf{X}}_2)' \{ \mathbf{S}_p \left(\frac{1}{n_1} + \frac{1}{n_2} \right) \}^{-1} (\bar{\mathbf{X}}_1 - \bar{\mathbf{X}}_2)$$

- Null distribution:

$$T^2 \stackrel{H_0}{\sim} \frac{(n_1 + n_2 - 2)p}{n_1 + n_2 - p - 1} F_{p, n_1 + n_2 - p - 1}$$



Multivariate Two-Sample Problems: Write an R Function

- No existing base function in R.

```
Hotelling.T2.2sample=function(X, Y){
  n=dim(X)[1]; m=dim(Y)[1]; p=dim(X)[2]
  if(p!= dim(Y)[2]) return("Error: the dimensions of X and Y are not the same")
  X.bar=colMeans(X); Y.bar=colMeans(Y)
  X.S=cov(X); Y.S=cov(Y)
  pooled.S=((n-1)*X.S+(m-1)*Y.S)/(m+n-2)
  T2=t(X.bar-Y.bar)%*%solve((1/n+1/m)*pooled.S)%*(X.bar-Y.bar)
  p.value=1-pf(T2/((n+m-2)*p/(n+m-1-p)),p,n+m-1-p)
  return(list(X.bar=X.bar, Y.bar=Y.bar, T2=T2, p.value=p.value))}
```

Multivariate Two-Sample Problems: Write an R Function

- The built-in function “t.test” serves a dual function for univariate analysis
- We will write a dual function Hotelling.T2

```
Hotelling.T2=function(X, Y=NULL, mu0=NULL)
{
  if(is.null(Y) && is.null(mu0) )
    return("Error: mu0 is not specified")
  if(!is.null(X) && !is.null(mu0))
    obj=Hotelling.T2.1sample(X, mu0)
  if(!is.null(X) && !is.null(Y))
    obj=Hotelling.T2.2sample(X,Y)
  return(obj)
}
```

Multivariate Two-Sample Problems: Iris setosa vs versicolor

```
Hotelling.T2.2sample(iris[1:50,1:4], iris[51:100,1:4])
```

```
## $X.bar
## Sepal.Length Sepal.Width Petal.Length Petal.Width
##           5.006           3.428           1.462           0.246
##
## $Y.bar
## Sepal.Length Sepal.Width Petal.Length Petal.Width
##           5.936           2.770           4.260           1.326
##
## $T2
##           [,1]
## [1,] 2580.839
##
## $p.value
##           [,1]
## [1,] 0
```

Multivariate TWo-Sample Problems: Example

```
Hotelling.T2(iris[1:50,1:4], iris[51:100,1:4])
```

```
## $X.bar
## Sepal.Length Sepal.Width Petal.Length Petal.Width
##           5.006           3.428           1.462           0.246
##
## $Y.bar
## Sepal.Length Sepal.Width Petal.Length Petal.Width
##           5.936           2.770           4.260           1.326
##
## $T2
##           [,1]
## [1,] 2580.839
##
## $p.value
##           [,1]
## [1,] 0
```

Linear Functions of Differences: Iris Setosa vs Versicolor

- We might be interested in the difference between iris setosa and versicolor in the four features
- Because we are interested all the four features, we do need to construct simultaneous C.I.s for the four features. Two methods to find critical values with adjustment for multiple C.I.s:

- Method 1 - T^2 :

$$\sqrt{\frac{(n_1 + n_2 - 2)p}{n_1 + n_2 - p - 1} F_{p, n_1 + n_2 - p - 1, 1 - \alpha}}$$

- Method 2- Bonferroni's correction by replacing α with α/k , i.e., use the following critical value

$$t_{n_1 + n_2 - 2, 1 - \alpha / (2k)}$$



Linear Functions of Differences: Iris Setosa vs Versicolor

```
n1=n2=50; p=4
mean1=matrix(colMeans(iris[1:50,1:p]), p, 1)
mean2=matrix(colMeans(iris[51:100,1:p]), p, 1)
mean.diff = mean1-mean2
S1=cov(iris[1:50,1:p]); S2=cov(iris[51:100,1:p]);
Sp=( (n1-1)*S1+(n2-1)*S2 )/ (n1+n2-2)
```



Linear Functions of Differences: Iris Setosa vs Versicolor

• Method 1: T^2

```
cv=sqrt((n1+n2-2)*p/(n1+n2-p-1)*qf(1-0.05, p, n1+n2-p-1 ))
round(data.frame(diff=mean.diff, se=sqrt(diag((1/n1+1/n2)*Sp) ),
CI.lower=mean1-mean2-qt(1-0.05/(2*p), n1+n2-2)*sqrt(diag((1/n1+1/n2)*Sp) ),
CI.upper=mean1-mean2+qt(1-0.05/(2*p), n1+n2-2)*sqrt(diag((1/n1+1/n2)*Sp) ) ), 3)
```

##		diff	se	CI.lower	CI.upper
##	Sepal.Length	-0.930	0.088	-1.155	-0.705
##	Sepal.Width	0.658	0.070	0.481	0.835
##	Petal.Length	-2.798	0.071	-2.978	-2.618
##	Petal.Width	-1.080	0.032	-1.161	-0.999

Linear Functions of Differences: Iris Setosa vs Versicolor

• Method 1 Bonferroni

```
cv=sqrt((n1+n2-2)*p/(n1+n2-p-1)*qf(1-0.05, p, n1+n2-p-1 ))
round(data.frame(diff=mean.diff, se=sqrt(diag((1/n1+1/n2)*Sp) ),
CI.lower=mean1-mean2-qt(1-0.05/(2*p), n1+n2-2)*sqrt(diag((1/n1+1/n2)*Sp) ),
CI.upper=mean1-mean2+qt(1-0.05/(2*p), n1+n2-2)*sqrt(diag((1/n1+1/n2)*Sp) ) ), 3)
```

##		diff	se	CI.lower	CI.upper
##	Sepal.Length	-0.930	0.088	-1.155	-0.705
##	Sepal.Width	0.658	0.070	0.481	0.835
##	Petal.Length	-2.798	0.071	-2.978	-2.618
##	Petal.Width	-1.080	0.032	-1.161	-0.999

Section 4

Assess MVN

The assumption of MVN

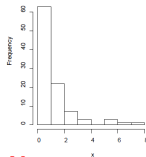
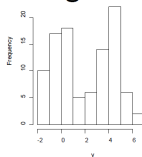
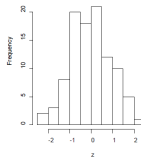
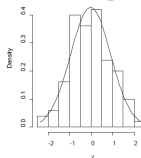
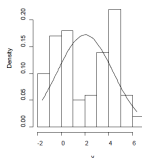
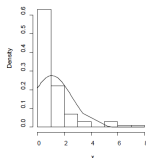
- We assume each observation \mathbf{X}_i follows a MVN
- Assessing the assumption of multivariate normality is more difficult than assessing the assumption of normality (univariate)
- This is because univariate normality does not guarantee multivariate normality. Typically, we look at the following two items:
- It is difficult to examine joint normality in more than 2d. In practice, we do 1d and 2d
 - Marginal normality
 - Are pairs of variables show elliptical contours?
- Are there outliers in the data?

Assess Marignal Normality

- Useful visual tools:
 - histogram
 - QQ plot
 - scatter plot
- Less useful tools (formal tests)
 - Kolmogorov-Smirnov test
 - Shapiro-Wilk test (correlation coefficient between data and normal scores)

Histograms

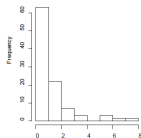
Assessing Marginal Normality: Histogram

**X****X****✓**



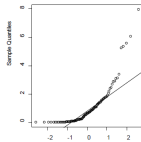
QQ plots

Assessing Marginal Normality: Q-Q Plots

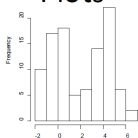


X

Normal Q-Q Plot

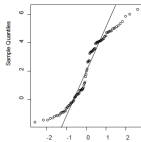


Theoretical Quantiles

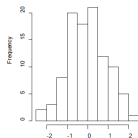


X

Normal Q-Q Plot

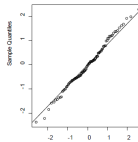


Theoretical Quantiles



✓

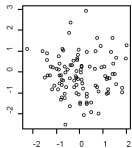
Normal Q-Q Plot



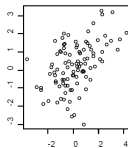
Theoretical Quantiles

Bivariate Scatter Plots

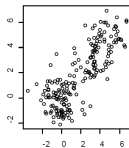
Assessing Bivariate Normality



✓



✓



✗

Large-Sample Results

- Multivariate CLT

$$\sqrt{n}(\bar{\mathbf{X}} - \boldsymbol{\mu}) \xrightarrow{D} N(\mathbf{0}, \boldsymbol{\Sigma})$$

$$\Rightarrow n(\bar{\mathbf{X}} - \boldsymbol{\mu})^T \mathbf{S}^{-1}(\bar{\mathbf{X}} - \boldsymbol{\mu}) \rightarrow \chi_p^2$$

- When $n - p$ is large, we replace $\frac{(n-1)p}{n-p} F_{p, n-p}$ with χ_p^2
- When $n_1 - p$ and $n_2 - p$ are large, we replace $\frac{(n_1+n_2-2)p}{n_1+n_2-p-1} F_{p, n_1+n_2-p-1}$ with χ_p^2

Assignment 2: Due on Monday, May 1st

- **Problem 1:** Choose a 3 – by – 3 covariance matrices with non-zero covariances. For each covariance matrix, simulate 1,000 data sets from a trivariate normal distribution.
 - ① Hints:
 - Hint 1: the R library MASS provides a function to generate a random sample from a multivariate normal distribution.
 - Hint 2: Make sure that the covariance matrix you choose is positive definite. You can compute the eigenvalues by the “eigen” function in R and check whether all the eigenvalues are positive.
 - ① Try to make sense of the covariance matrix by examining the pairwise scatter plots using the data you simulate.
 - ② During the simulation, you will generate 1,000 Wishart distributed random matrices. Calculate the trace for each of them. Explain what distribution the traces should follow and examine their histogram.
- **Problem 2:** Find a good data example to conduct a