

Resampling Techniques and their Application

-Class 12-

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Example: Liver Weights of Wistar Rats

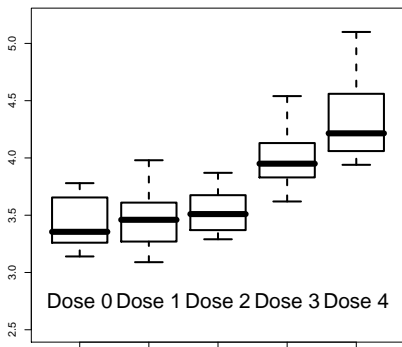
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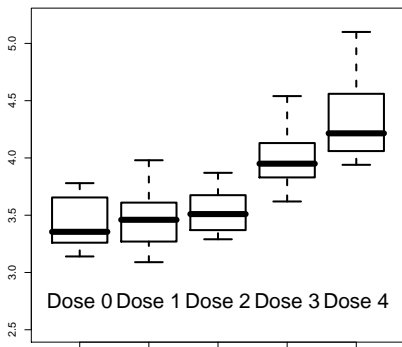
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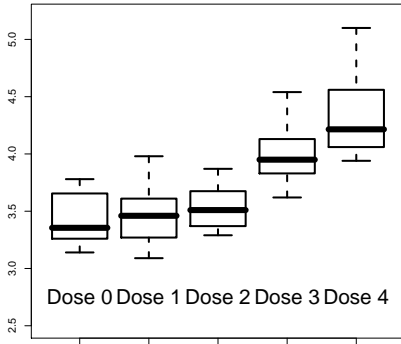
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x3 = c(3.71, 3.36, 3.38, 3.64, 3.41, 3.29, 3.61, 3.87)
x4 = c(3.86, 3.80, 4.14, 3.62, 3.95, 4.12, 4.54)
x5 = c(4.19, 4.16, 3.94, 4.26, 4.86, 3.96, 4.24, 5.10)
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- Toxicity trial: 40 rats were randomized into 5 dose groups (Dose 0 - Dose 4)
- After treatment: relative liver weight of each animal
- Question: Which dose(s) differ from control? Trend?



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- **Multiple hypotheses**

General Contrasts

- In general

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- The contrast matrix \mathbf{C} is nothing but the pattern of the alternative H_1
- In general, \mathbf{C} is a $q \times a$ matrix. Each row vector is a contrast.

$$\mathbf{C} = \begin{pmatrix} \mathbf{c}'_1 \\ \vdots \\ \mathbf{c}'_q \end{pmatrix} = \begin{pmatrix} \mu_1 & \mu_2 & \cdots & \mu_a \\ c_{11} & c_{12} & \cdots & c_{1a} \\ c_{21} & c_{22} & \cdots & c_{2a} \\ \vdots & \vdots & \vdots & \vdots \\ c_{q1} & c_{q2} & \cdots & c_{qa} \end{pmatrix}; \sum_{i=1}^a c_{\ell i} = 0, \ell = 1, \dots, q$$

General Contrasts

- Example 1: Many-to-one comparisons (Dunnett):

$$H_1 : \begin{cases} \mu_1 \neq \mu_2 \\ \mu_1 \neq \mu_3 \\ \vdots \\ \mu_1 \neq \mu_a \end{cases} \Leftrightarrow \mathbf{C} = \begin{pmatrix} -1 & 1 & 0 & \cdots & 0 \\ -1 & 0 & 1 & \cdots & 0 \\ \vdots & \vdots & \vdots & \vdots & \vdots \\ -1 & 0 & \cdots & \cdots & -1 \end{pmatrix}$$

General Contrasts (II)

- Example 2: Trend (Williams)

$$H_1 : \left\{ \begin{array}{l} \mu_1 \neq \mu_a \\ \mu_1 \neq \mu_{a-1} = \mu_a \\ \vdots \\ \mu_1 \neq \mu_2 = \dots = \mu_a \end{array} \right. \Leftrightarrow \mathbf{C} = \begin{pmatrix} -1 & 0 & 0 & \dots & 1 \\ -1 & 0 & 0 & \frac{n_{a-1}}{n_{a-1}+n_a} & \frac{n_a}{n_{a-1}+n_a} \\ \vdots & \vdots & \vdots & \vdots & \vdots \\ -1 & \frac{n_2}{n_2+\dots+n_a} & \dots & \dots & \frac{n_a}{n_2+\dots+n_a} \end{pmatrix}$$

General Contrasts (III)

- Example 3: All-pairs (Tukey):

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- And many more
- See *contrMat* function in *multcomp* package

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- Reject H_0 , if any $H_0^{(\ell)}$ is rejected

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- Variance of contrasts in means

$$\mathbf{S} = \text{Cov}(\bar{\mathbf{X}}) = \text{diag} \left(\frac{\sigma_1^2}{n_1}, \dots, \frac{\sigma_a^2}{n_a} \right)$$

$$\mathbf{\Gamma} = \text{Cov}(\mathbf{C}\bar{\mathbf{X}}) = \mathbf{CSC}' = \mathbf{C} \text{diag} \left(\frac{\sigma_1^2}{n_1}, \dots, \frac{\sigma_a^2}{n_a} \right) \mathbf{C}'$$

$$\sigma_\ell^2 = \text{Var}(\mathbf{c}_\ell' \bar{\mathbf{X}}) = \sum_{i=1}^a \sigma_i^2 \frac{c_{\ell i}^2}{n_i} = \mathbf{c}_\ell' \mathbf{S} \mathbf{c}_\ell$$

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$$\hat{\mathbf{S}} = \text{diag} \left(\frac{s_1^2}{n_1}, \dots, \frac{s_a^2}{n_a} \right)$$

$$\hat{\mathbf{\Gamma}} = \mathbf{C} \hat{\mathbf{S}} \mathbf{C}' = \mathbf{C} \text{diag} \left(\frac{s_1^2}{n_1}, \dots, \frac{s_a^2}{n_a} \right) \mathbf{C}'$$

$$\hat{\sigma}_\ell^2 = \mathbf{c}_\ell' \hat{\mathbf{S}} \mathbf{c}_\ell$$

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```
library(multcomp)
C <- contrMat(rep(1,5), "Dunnett")
X<-c(x1,x2,x3,x4,x5)
n<-c(8,7,8,7,8)
N<-sum(n)
grp<-factor(c(rep(1:5,n)))
a<-5
Dat<-data.frame(X=X,grp=grp)
Xbar<-aggregate(X~grp,data=Dat,mean)[,2]
si2 <-aggregate(X~grp,data=Dat,var)[,2]

Shat <- diag(si2/n)
Gammahat<-C%*%Shat%*%t(C)
```

Multiple Comparisons

- For $H_0^{(\ell)} : \mathbf{c}'_\ell \boldsymbol{\mu} = 0$

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```
diff <- C %*% Xbar
Tl <- diff / sqrt(c(diag(Gammahat)))
```

```
nul = sapply(1:nrow(C), function(arg) {
  c(t(C[arg,]) %*% Shat %*% C[arg,])^2 /
  sum(C[arg,]^4 * si2^2 / (n^2 * (n-1))))})
```

```
T0 <- max(abs(Tl))
```

Multiple Contrast Test Procedures (MCTP)

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- Covariance of $\mathbf{c}'_{\ell}\bar{\mathbf{X}}_{\cdot}$ and $\mathbf{c}'_m\bar{\mathbf{X}}_{\cdot}$:

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- Or, compute adjusted p-values using the $T(\mathbf{0}, \nu, \hat{\mathbf{R}})$ distribution

```
library(multcomp)
```

```
nu=round(min(nul))
```

```
Rhat<-cov2cor(Gammahat)
```

```
set.seed(1)
```

```
tmax=qmvt(0.95,tail="both",corr=Rhat,  
df=nu)$quantile
```

```
T0>=tmax
```

```
$
```

```
pv<-sapply(1:4,function(j)
```

```
1-pmvt(-abs(Tl[j]),abs(Tl[j]),df=nu,  
delta=rep(0,4),corr=Rhat)[1])
```

Properties

- Method is a multiple t-test
- In case of small samples, method might be liberal or conservative
- Resampling methods to improve the approximation /method
- Goal: Approximate the distribution of the maximum

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2. Generate resampling variables $\mathbf{X}^* = (X_{11}^*, \dots, X_{an_a}^*)'$

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8. Reject H_0 , if the p-value

$$\frac{1}{n_{boot}} \sum_{s=1}^{n_{boot}} \mathcal{I}(A_s^* \geq T_0) < \alpha$$

A Parametric Bootstrap Approach

- Many different ways of generating \mathbf{X}^* are possible

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Al<-c()
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s2vec<-rep(si2,n)
for(h in 1:nboot){
  XB <- rnorm(N,0,sqrt(s2vec))
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