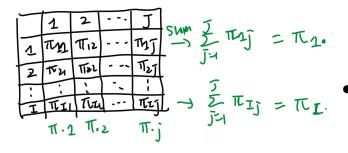
# Analysis of Variance (ANOVA)

Chapter 12 of Rice 07/27/2021



# In the previous lecture,



#### • $\chi^2$ test of independence:

- For a 2x2 table, we can use Fisher's exact test;
- For a I x J table, we assume under the null hypothesis that  $H_0: \pi_{ij} = \pi_{i.}\pi_{.j}, \ i = 1, ..., I, \ j = 1, ..., J.$

The difference between the numbers of free parameters:

$$\nu = (IJ - 1) - (I + J - 2) = (I - 1)(J - 1).$$

#### $\chi^2$ test of homogeneity:

We assume under the null hypothesis that

$$H_0: \pi_{i1} = \pi_{i2} = \cdots = \pi_{iJ}, \ \ i = 1, \ldots, I.$$

The difference between the numbers of free parameters:  $\nu = J(I-1) - (I-1) = (I-1)(J-1)$ .

#### In both case

Under H<sub>0</sub>,

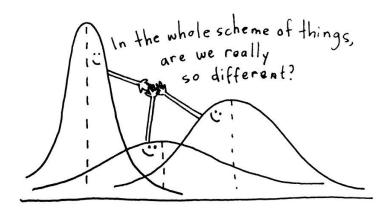
$$-2\log\lambda(\mathbf{X}_n)\stackrel{d}{
ightarrow}\chi^2_{(I-1)(J-1)} \ \ ext{as } n
ightarrow\infty.$$

#### Analysis of variance

**Example 1**. To compare the effects of three toxins and a control on the liver of a certain species of trout, researchers recorded the amounts of deterioration (in standard units) of the liver of each sacrificed fish.

Toxin 1	Toxin 2	Toxin 3	Control
28	33	18	11
23	36	21	14
14	34	20	11
27	29	22	<b>16</b>
	<b>3</b> 1	24	
	34		





ANOVA: Comparing the means of several populations via analyzing variances.

#### One-way vs Two-way ANOVA

The one-way layout involves **one factor** in the experimental design:

Treatments						
1	2	3		$\boldsymbol{k}$		
$y_{11}$	$y_{21}$	$\overline{y}_{31}$	•••	$\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ $		
$y_{12}$	$y_{22}$	$y_{32}$	• • •	$y_{k2}$		
	:	:		$y_{k3}$		
		$y_{3n_3}$		:		
$y_{1n_1}$				•		
	$y_{2n_2}$			$y_{kn_k}$		

The two-way layout involves **two factors** in the experimental design:

	1	2		J	< ☐ 2nd Factor
1	$y_{111},y_{112},\ \cdots,y_{11n_{11}}$		• • •	$y_{1J1},y_{1J2},\ \cdots,y_{1Jn_{1J}}$	
2	$y_{211},y_{212},\ \cdots,y_{21n_{21}}$		• • •	$y_{2J1},y_{2J2},\ \cdots,y_{2Jn_{2J}}$	
:	•	•	٠.,	•	
I					
1st Factor	or	$y_{ijk},$	k=1,	$\cdots,n_{ij}.$	

Main interest: difference in means

*Main interest*: difference in means + interrelationship of the two factors

### Multivariate analysis of variance (MANOVA)

The one-way layout involves **one factor** in the experimental design:

	Tre	atmen	ts	_
1	2	3		$\boldsymbol{k}$
$\mathbf{y}_{11}$	$\mathbf{y}_{21}$	$\mathbf{y}_{31}$	•••	$\overline{\;\mathbf{y}_{k1}\;}$
$\widecheck{\mathbf{y}_{12}}$	$\mathbf{y}_{22}$	$\mathbf{y}_{32}$	• • •	$\mathbf{y}_{k2}$
	:	:		$\mathbf{y}_{k3}$
		$\mathbf{y}_{3n_3}$		:
$\mathbf{y}_{1n_1}$				•
	$\mathbf{y}_{2n_2}$			$\mathbf{y}_{kn_k}$

$$\mathbf{y} = ig(y^1, \ \cdots, \ y^pig)$$

The two-way layout involves **two factors** in the experimental design:

	1	2		J	← 2nd Factor
1		$\mathbf{y}_{121},  \mathbf{y}_{122}, \\ \cdots,  \mathbf{y}_{12n_{12}}$	• • •	$\mathbf{y}_{1J1},\mathbf{y}_{1J2},\ \cdots,\mathbf{y}_{1Jn_{1J}}$	
2		$\mathbf{y}_{221},  \mathbf{y}_{222}, \\ \cdots,  \mathbf{y}_{22n_{22}}$	• • •	$\mathbf{y}_{2J1},\mathbf{y}_{2J2},\ \cdots,\mathbf{y}_{2Jn_{2J}}$	
:	:	•	٠	:	
I					
st Fact	or	$\mathbf{y}_{ijk}$	,k=1,	$,\cdots,n_{ij}$	

# One-way ANOVA (univariate)

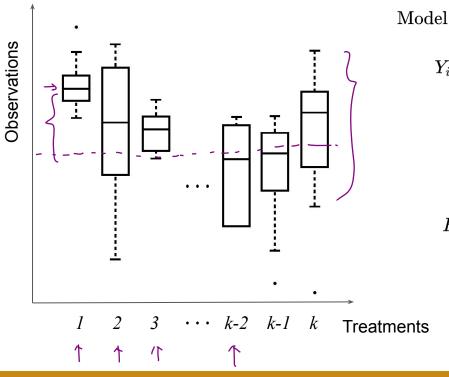
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### One-way ANOVA: model assumption

 $H_0$ : All population means are the same.



Model assumption  $(j = 1, \dots, n_i, i = 1, \dots, k)$ :

$$Y_{ij} = \underbrace{\frac{\iota}{\mu}}_{ ext{common mean level}} + \underbrace{\frac{\alpha_i}{ ext{unique effect due to treatment }i}}_{ ext{Note } \sum_{i=1}^k \alpha_i = 0.} + \underbrace{\frac{\epsilon_{ij}}{ ext{iid}}}_{ ext{N}(0, \, \sigma^2)}$$

$$H_0: \, lpha_1 = \cdots = \underbrace{lpha_k = 0}_{} \, ext{ versus } \, H_1: lpha_i 
eq lpha_j ext{ for some } i 
eq j$$

#### One-way ANOVA: LRT

**Example 2**. Assume  $Y_{ij}=\mu+\alpha_i+\epsilon_{ij}$ , where  $\epsilon_{ij}\overset{\mathrm{iid}}{\sim}N(0,\,\sigma^2)$ . We can derive the LRT for the hypotheses:  $H_0: \, lpha_1 = \cdots = lpha_k \;\; ext{versus} \;\; H_1: lpha_i = lpha_j \; ext{for some} \; i 
eq j.$ 

$$H_{0}: \alpha_{1} = \cdots = \alpha_{k} \text{ versus } H_{1}: \alpha_{i} = \alpha_{j} \text{ for some } i \neq j.$$

$$Solvation. \quad \bigoplus_{b} = \begin{cases} A_{1} = \cdots = A_{k} = 0, \quad M \in \mathbb{R}^{2}, \\ A_{1} = \cdots = A_{k} = 0, \quad M \in \mathbb{R}^{2}, \\ A_{1} = \cdots = A_{k} = 0, \quad M \in \mathbb{R}^{2}, \\ A_{1} = \cdots = A_{k} = 0, \quad M \in \mathbb{R}^{2}, \\ A_{1} = \cdots = A_{k} = 0, \quad M \in \mathbb{R}^{2}, \\ A_{1} = \cdots = A_{k} = 0, \quad M \in \mathbb{R}^{2}, \\ A_{1} = \cdots = A_{k} = 0, \quad M \in \mathbb{R}^{2}, \\ A_{1} = \cdots = A_{k} = 0, \quad M \in \mathbb{R}^{2}, \\ A_{1} = \cdots = A_{k} = 0, \quad M \in \mathbb{R}^{2}, \\ A_{1} = \cdots = A_{k} = 0, \quad M \in \mathbb{R}^{2}, \\ A_{2} = \cdots = A_{k} = 0, \quad M \in \mathbb{R}^{2}, \\ A_{1} = \cdots = A_{k} = 0, \quad M \in \mathbb{R}^{2}, \\ A_{2} = \cdots = A_{k} = 0, \quad M \in \mathbb{R}^{2}, \\ A_{1} = \cdots = A_{k} = 0, \quad M \in \mathbb{R}^{2}, \\ A_{2} = \cdots = A_{k} = 0, \quad M \in \mathbb{R}^{2}, \\ A_{1} = \cdots = A_{k} = 0, \quad M \in \mathbb{R}^{2}, \\ A_{2} = \cdots = A_{k} = 0, \quad M \in \mathbb{R}^{2}, \\ A_{2} = \cdots = A_{k} = 0, \quad M \in \mathbb{R}^{2}, \\ A_{2} = \cdots = A_{k} = 0, \quad M \in \mathbb{R}^{2}, \\ A_{2} = \cdots = A_{k} = 0, \quad M \in \mathbb{R}^{2}, \\ A_{2} = \cdots = A_{k} = 0, \quad M \in \mathbb{R}^{2}, \\ A_{2} = \cdots = A_{k} = 0, \quad M \in \mathbb{R}^{2}, \\ A_{2} = \cdots = A_{k} = 0, \quad M \in \mathbb{R}^{2}, \\ A_{2} = \cdots = A_{k} = 0, \quad M \in \mathbb{R}^{2}, \\ A_{2} = \cdots = A_{k} = 0, \quad M \in \mathbb{R}^{2}, \\ A_{3} = \cdots = A_{k} = 0, \quad M \in \mathbb{R}^{2}, \\ A_{4} = \cdots = A_{k} = 0, \quad M \in \mathbb{R}^{2}, \\ A_{4} = \cdots = A_{k} = 0, \quad M \in \mathbb{R}^{2}, \\ A_{4} = \cdots = A_{k} = 0, \quad M \in \mathbb{R}^{2}, \\ A_{4} = \cdots = A_{k} = 0, \quad M \in \mathbb{R}^{2}, \\ A_{4} = \cdots = A_{k} = 0, \quad M \in \mathbb{R}^{2}, \\ A_{4} = \cdots = A_{k} = 0, \quad M \in \mathbb{R}^{2}, \\ A_{4} = \cdots = A_{k} = 0, \quad M \in \mathbb{R}^{2}, \\ A_{4} = \cdots = A_{k} = 0, \quad M \in \mathbb{R}^{2}, \\ A_{4} = \cdots = A_{k} = 0, \quad M \in \mathbb{R}^{2}, \\ A_{4} = \cdots = A_{k} = 0, \quad M \in \mathbb{R}^{2}, \\ A_{4} = \cdots = A_{k} = 0, \quad M \in \mathbb{R}^{2}, \\ A_{4} = \cdots = A_{k} = 0, \quad M \in \mathbb{R}^{2}, \\ A_{4} = \cdots = A_{k} = 0, \quad M \in \mathbb{R}^{2}, \\ A_{4} = \cdots = A_{k} = 0, \quad M \in \mathbb{R}^{2}, \\ A_{5} = \cdots = A_{k} = 0, \quad M \in \mathbb{R}^{2}, \\ A_{5} = \cdots = A_{k} = 0, \quad M \in \mathbb{R}^{2}, \\ A_{5} = \cdots = A_{k} = 0, \quad M \in \mathbb{R}^{2}, \\ A_{5} = \cdots = A_{k} = 0, \quad M \in \mathbb{R}^{2}, \\ A_{5} = \cdots = A_{k} = 0, \quad M \in \mathbb{R}^{2}, \\ A_{5} = \cdots = A_{k} = 0, \quad M \in \mathbb{R}^{2}, \\ A_{5} = \cdots = A_{k} = 0, \quad M \in \mathbb{R}^{2}, \\ A_{5} = \cdots = A$$

### One-way ANOVA: LRT

Solution contid. Sup 
$$L(M_1, \alpha_1, -\alpha_k, b^2 | T_{ij}) = \sup_{j \in \mathbb{N}} \left(\frac{1}{\sqrt{L_1 t_0}}\right)^n e^{-\frac{1}{2b^2} \sum_{i=1}^k \sum_{j=1}^{N_i} \left(T_{ij} - M - \alpha_i\right)^2} e^{-\frac{1}{2b^2} \sum_{i=1}^k \sum_{j=1}^{N_i} \left(T_{ij} - M - \alpha_i\right)^2}$$

population mean for k+h treatment

One-way ANOVA: LRT

Solution contid. which means 
$$\frac{N_{k}}{N_{k}} = \frac{N_{k}}{N_{k}} =$$

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### One-way ANOVA: LRT

$$P = \left\{ \lambda(\mathbf{I}_{n}) \leq C \right\} = \left\{ \frac{6n^{2}}{6r^{2}} \right\}^{\frac{n}{2}} \leq C \right\} = \left\{ \frac{SSw}{SS + st} \leq C^{\frac{2}{n}} \right\}$$

**Lemma A**. The LRT rejection region is solely based on the following identity:

$$\sum_{i=1}^{k} \sum_{j=1}^{n_i} (Y_{ij} - \bar{Y}_{..})^2 = \sum_{i=1}^{k} \sum_{j=1}^{n_i} (Y_{ij} - \bar{Y}_{i.})^2 + \sum_{i=1}^{k} n_i (\bar{Y}_{i.} - \bar{Y}_{..})^2.$$
Total sum of squares

SS within groups

SS between groups

Total sum of squares

Proof. 
$$6^{2} - 6^{2} = \sum_{i=1}^{k} \sum_{j=1}^{k} (Y_{ij} - Y_{i.})^{2} - \sum_{i=1}^{k} \sum_{j=1}^{k} (Y_{ij} - Y_{i.})^{2}$$

$$= \sum_{i=1}^{k} \sum_{j=1}^{k} (Y_{ij}^{2} + Y_{i.}^{2} - 2Y_{ij}^{2} Y_{i.}) = (Y_{ij}^{2} + Y_{i.}^{2} - 2Y_{ij}^{2} Y_{i.})$$

$$= \sum_{i=1}^{k} \sum_{j=1}^{k} (Y_{ii}^{2} - 2Y_{ij}^{2} Y_{i.}) - Y_{i.}^{2} + 2Y_{ij}^{2} Y_{i.})$$

$$= \sum_{i=1}^{k} (N_{i} Y_{i.}^{2} - 2Y_{i.} Y_{ij}^{2}) - N_{i} Y_{i.}^{2} + 2Y_{i.}^{2} Y_{ij}^{2}$$

$$= N_{i} Y_{i.}^{2} - 2Y_{i.} Y_{i.} - Y_{i.}^{2} + 2Y_{i.}^{2}$$

$$= N_{i} Y_{i.}^{2} - 2Y_{i.} Y_{i.} - Y_{i.}^{2} + 2Y_{i.}^{2}$$

$$= \sum_{i=1}^{k} N_{i} [Y_{i.}^{2} - 2Y_{i.} Y_{i.} - Y_{i.}^{2} + 2Y_{i.}^{2}]$$

$$= \sum_{i=1}^{k} N_{i} [Y_{i.}^{2} - 2Y_{i.} Y_{i.} - Y_{i.}^{2} + 2Y_{i.}^{2}]$$

$$= \sum_{i=1}^{k} N_{i} [Y_{i.}^{2} - 2Y_{i.} Y_{i.} - Y_{i.}^{2}]$$

$$\chi_n^2 + \chi_m^2 = \chi_{n+m}^2$$

### One-way ANOVA: LRT

Proposition A. Under the one-way ANOVA model assumption,

$$rac{SS_W}{\sigma^2} \sim \chi^2_{n-k}, ext{ and it's independent of each $ar{Y}_{i\cdot}$, $i=1,\ldots,k$.} \quad lefootnotesize$$

Furthermore, under  $H_0$ ,  $\frac{SS_B}{\sigma^2} \sim \chi^2_{k-1}$ , and it's independent of  $SS_W$ .

Proof\*. 
$$\frac{1}{b^{2}} \frac{N}{j+1} (Y_{1j} - \overline{Y_{1}})^{2} \sim \chi_{n_{k-1}}^{2} \qquad \prod_{j=1}^{n_{k}} (Y_{kj} - \overline{Y_{k}})^{2} \sim \chi_{n_{k-1}}^{2} \qquad \prod_{j=1}^{n_{k}} (Y_{kj} - \overline{Y_{k}})^{2} \sim \chi_{n_{k-1}}^{2} \qquad \prod_{j=1}^{n_{k}} (Y_{ij} - \overline{Y_{i}})^{2} \sim \chi_{n_{k-1}}^{2} \qquad \prod_{j=1}^{n_{k}} (X_{ij} - \overline{Y_{i}})^{2} \sim \chi_{n_{k-1}}^{2} \qquad \chi_$$

1:

# One-way ANOVA: sampling distribution under $H_0$

ALIN) = { SSB SSW > C' {

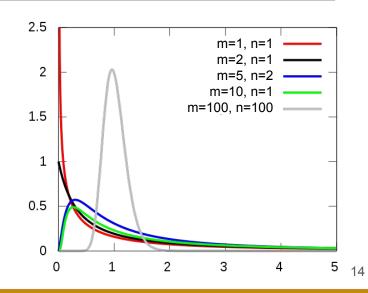
**Definition**. Let  $U \sim \chi_m^2$ ,  $V \sim \chi_n^2$  and  $U \perp \!\!\! \perp V$ . Then

$$rac{U/m}{V/n} \sim F_{m,n},$$

which is called a *F* distribution with *m* and *n* degrees of freedom.

$$f(w) = \frac{\Gamma[(m+n)/2]}{\Gamma(m/2)\Gamma(n/2)} \left(\frac{m}{n}\right)^{m/2} w^{m/2-1} \left(1 + \frac{m}{n}w\right)^{-(m+n)/2}, \qquad w \ge 0$$

$$\frac{1}{\sqrt{N}} = \frac{1}{\sqrt{N}} \left( \frac{1}{\sqrt{N}} + \frac{1}{\sqrt{N}} \right) = \frac{1}{\sqrt{N}} \left( \frac{1}{\sqrt{N}} \right) = \frac{1}{\sqrt{$$



## One-way ANOVA: sampling distribution under $H_0$

**Theorem A**. Under the one-way ANOVA model assumption, the LRT rejection region is equivalent to

$$R = \left\{ rac{SS_{B/(k-1)}}{SS_{W/(n-k)}}c'' 
ight\}.$$

Under  $H_0$ ,  $rac{SS_B/(k-1)}{SS_W/(n-k)}\sim F_{k-1,\,n-k}$ .

Proof. See previous page.



$$C'' = 9f(\alpha, df1 = k+1, df2 = N-k, |ower. +all = FALSE)$$

### One-way ANOVA: summary table

F statistic = 
$$\frac{SS_B/(r_H)}{SS_W/(n_K)}$$
 =

Source	df	Sum Sq	Mean Sq	F value	p-value
Between group (or treatment)	k-1	$SS_B = \sum_{i=1}^k n_i (ar{Y}_{i\cdot} - ar{Y}_{\cdot\cdot})^2$	$MS_B = SS_B / (k-1)$	$MS_B/MS_W$	<pre>pf(MS_B/MS_W, k-1, n-k, lower.tail = FALSE)</pre>
Within group (or residuals)	n-k	$SS_W^{}=\sum_{i=1}^k\sum_{j=1}^{n_i}\left(Y_{ij}-ar{Y}_{i\cdot} ight)^2$	$MS_W = SS_W/(n-k)$		
Total	n-1	$SS_{Total} = \sum_{i=1}^{k} \sum_{j=1}^{n_i} \left(Y_{ij} - ar{Y}_{\cdot\cdot} ight)^2$			

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 $\epsilon$ 

#### One-way ANOVA: implementation

```
t_{mp} = 1 \text{ ist } \left( ((1, 2), ((2, 3, 4)) \right)
t_{mp}
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((2
```

**Example 1**. To compare the effects of three toxins and a control on the liver of a certain species of trout, researchers recorded the amounts of deterioration (in standard units) of the liver of each sacrificed fish.

```
# F statistic
SS_B <- sum(unlist(S_B))
SS_B
[1] 995.9035

SS_W <- sum(unlist(S_W))
SS_W
[1] 190.8333

{SS_B/(k-1)}/{SS_W/(n-k)}
[1] 26.09354

# Critical value
qf(0.95, k-1, n-k, lower.tail = FALSE)
[1] 0.1149046</pre>
```

```
# p-value
pf(26.09354, k-1, n-k, lower.tail = FALSE)
[1] 3.347973e-06
```

```
group1 <- c(28, 23, 14, 27)
group2 <- c(33, 36, 34, 29, 31, 34)
group3 <- c(18, 21, 20, 22, 24)
group4 <- c(11, 14, 11, 16)
#Combine into a list
Observations <- list(group1, group2, group3, group4)
k <- length(Observations); n <- length(unlist(Observations)) #bookkeeping
```

```
# Squares within groups
S_W <- lapply(Observations, function(vec) sum((vec-mean(vec))^2))
print(unlist(S_W))
[1] 122.000 30.833 20.000 18.000

# Squares between groups
tot_mean <- mean(unlist(Observations))
S_B <- lapply(Observations, function(vec) length(vec)*(mean(vec)-tot_mean)^2)
print(unlist(S_B))
[1] 0.898 525.618 30.596 438.792</pre>
```

#### One-way ANOVA: implementation

**Example 1**. To compare the effects of three toxins and a control on the liver of a certain species of trout, researchers recorded the amounts of deterioration (in standard units) of the liver of each sacrificed fish.

$$Y_{ij} = \underbrace{\mu + lpha_i}_{ ext{linear population}} + \epsilon_{ij}$$

```
linear model
                                                                      group_ind <- c('toxin1', 'toxin2', 'toxin3', 'control'
  fit <- lm(values ~ ind, data = input)
                                                                      input <- stack(setNames(Observations, group_ind))
> anova(fit)
                                                                      head(input, 6)
Analysis of Variance Table
                                                                      values
                                                                                ind
                                                                          28 toxin1
Response: values
                                                                          23 toxin1
         Df Sum Sq Mean Sq F value
                                     Pr(>F)
                                                                          14 toxin1
          3 995.90 331.97 26.093 3.348e-06 ***
                                                                          27 toxin1
Residuals 15 190.83 12.72
                                                                          33 toxin2
Signif, codes: 0 (***, 0.001 (**, 0.01 (*) 0.05 (.)
                                                                          36 toxin2
```

# One-way ANOVA (univariate)

Simultaneous estimates of contrasts

07/27/2021



#### Silly null hypothesis

**Example 1**. To compare the effects of three toxins and a control on the liver of a certain species of trout, researchers recorded the amounts of deterioration (in standard units) of the liver of each sacrificed fish.

$$H_0: \alpha_1 = \cdots = \alpha_k = 0.$$

Toxin 1	Toxin 2	Toxin 3	Control
28	33	18	11
23	36	21	14
14	34	20	11
<b>27</b>	29	22	<b>16</b>
	<b>3</b> 1	24	
	34		

The ANOVA test gives no information about **how** they differ, in particular about **which pairs** are significantly different.

```
# p-value
pf(26.09354, k-1, n-k, lower.tail = FALSE)
[1] 3.347973e-06
```

#### Simultaneous Bonferroni Cls

**Theorem B**. Under the one-way ANOVA model assumptions,

$$rac{\sqrt{n_i}ig(ar{Y}_{i\cdot}-\mu-lpha_iig)}{S_i}\sim t_{n_i-1}, ext{ for any } i=1,\;\ldots,\;k.$$

If one establishes m confidence intervals, and wishes to have an overall confidence level of  $1-\alpha$ , each individual confidence interval can be adjusted to the level of  $1-\frac{\alpha}{m}$ .



Simultaneous  $(1-\alpha) imes 100\%$  CIs for population means :  $ar{Y}_{i\cdot} \pm t_{n_i-1} \left( lpha'/2 \right) rac{S_i}{\sqrt{n_i}} \; ext{for any} \; i=1,\; \ldots,\; k,$  where  $lpha' = rac{2lpha/[k(k-1)]}{\kappa}.$ 

```
get_bound <- function(vec, k, alpha = 0.05){
  center = mean(vec)
  n = length(vec)
  halfwidth = qt(1 - (alpha/2)/k, df = n - 1)*sd(vec)/sqrt(n)
  return(c(center - halfwidth, center + halfwidth))
}</pre>
```

#### Simultaneous inference statements

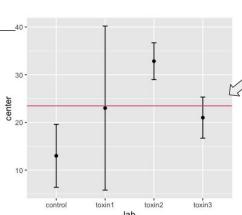
**Corollary B.** We can utilize the duality between the CIs and the HTs to perform testings on

$$H_0^i: lpha_i = egin{array}{c} \mathcal{M}^i &: \mathcal{M}^i : lpha_i = 0 \end{array} ext{ versus } H_1^i: lpha_i 
eq 0.$$

The conclusions we draw about each test hold **simultaneously**.

auxillary orgunert

Toxin 1	Toxin 2	Toxin 3	Control		
28	33	18	11		$\qquad \qquad \Rightarrow \qquad \qquad \\$
23	36	21	14		
14	34	20	11		
27	29	22	16		
	31	24			
	34			L	
			4	Ī	



```
> CIs <- sapply(Observations, get_bound, k=k, alpha=0.05)
> CIs

[,1] [,2] [,3] [,4]
[1,] 5.807657 28.97077 16.68534 6.396238
[2,] 40.192343 36.69589 25.31466 19.603762
```

as an approximation of 1

#### Tomorrow ...

- Compute Tukey Honest Significant Differences (HSD);
- The Kruskal-Wallis test;
- Two-way ANOVA.