Statistical Methods

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1 Kruskal-Wallis Test for I Population Means μ_1,μ_2,\ldots,μ_I



Objectives:

• Carry out a Kruskal-Wallis test for *I* population means.



Kruskal-Wallis Test for I Population Means

 $\mu_1, \mu_2, \ldots, \mu_I$

 The *Kruskal-Wallis test* is a nonparametric alternative to the one-factor ANOVA F test for comparing I population means μ₁, μ₂,..., μ_I.

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- The *Kruskal-Wallis test* is a nonparametric alternative to the one-factor ANOVA F test for comparing I population means μ₁, μ₂,..., μ_I.
- We assume that we have *independent* random samples from *I* continuous populations that all have the **same** shape but possibly different means μ₁, μ₂,..., μ_I.

Kruskal-Wallis Test for I Population Means

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- The *Kruskal-Wallis test* is a nonparametric alternative to the one-factor ANOVA F test for comparing I population means μ₁, μ₂,..., μ_I.
- We assume that we have *independent* random samples from *I* continuous populations that all have the **same** shape but possibly different means μ₁, μ₂,..., μ_I.

 The null hypothesis is that there are no differences among the population means μ₁, μ₂, ..., μ_I:

Null Hypothesis:

$$H_0:\mu_1 = \mu_2 = \cdots = \mu_I$$

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• The **alternative hypothesis** is that there's *at least one difference* among the set of means:

Alternative Hypothesis: The alternative hypothesis will be

 H_a : At least two of the μ_i 's are different

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These are the same hypotheses as the ones tested in a *one-factor ANOVA* F *test*.

Notation:

- *I* = The number of populations from which samples are taken.
- Y_{ij} = The *j*th observation in the *i*th sample.
- $J_1, J_2, \ldots J_I$ = The sample sizes (not necessarily equal).
- N = The total number of observations (in the *I* samples combined), i.e.

$$N = \sum_{i} J_i.$$

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• (cont'd)

Now consider **combining** the *I* samples and and **ranking** the observations from smallest (rank = 1) to largest (rank = N).

- $R_{ij} =$ The rank of Y_{ij} .
- \bar{R}_i = The average of the ranks of the observations from the *i*th sample.

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 $\bar{\boldsymbol{R}}$ = The overall average of all N ranks.

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 \bar{R} = The overall average of all N ranks.

For **ties**, use the **average** of the **ranks** that would've been assigned if there weren't any ties.

Proposition

The overall average of all N ranks is

$$\bar{R} = \frac{N+1}{2}$$

because the sum of the ranks is

$$1 + 2 + \dots + N = \frac{N(N+1)}{2}$$



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Kruskal-Wallis Test Statistic: $K = \frac{12}{N(N+1)} \sum_{i=1}^{I} J_i \left(\bar{R}_i - \bar{R} \right)^2.$

 K is the sum of (J_i-weighted) squares of the mean ranks away from the overall mean rank, multiplied by the constant 12/N(N+1) (explained later).

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It's analogous to the **treatment sum of squares SSTr** in **one-factor ANOVA**.

• *K* will be **small** when the **mean ranks** $\bar{R}_1, \bar{R}_2, \ldots, \bar{R}_I$ are approximately **equal**, i.e. if the combined, sorted samples "intermingle", as would be the case if $\mu_1, \mu_2, \ldots, \mu_I$ were equal.

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K will be **large** when the **mean ranks** $\bar{R}_1, \bar{R}_2, \ldots, \bar{R}_I$ **differ**, i.e. if the combined, sorted samples "segregate", as would be the case if there were differences among $\mu_1, \mu_2, \ldots, \mu_I$

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Large values of K provide evidence against H_0 in favor of H_a : At least two of the μ_i 's are different.

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• Now suppose the sample sizes J_1, J_2, \ldots, J_I are all *large*.

Now suppose the sample sizes J₁, J₂,..., J_I are all *large*.
In this case, the sampling distribution of the test statistic is as follows.

Sampling Distribution of the Test Statistic Under H_0 : If *K* is the Kruskal-Wallis test statistic, then when

$$H_0: \mu_1 = \mu_2 = \cdots = \mu_I$$

is true,

$$K \sim \chi^2 (I-1)$$

(approximately), a chi-squared distribution with $\left(I-1\right)$ degrees of freedom.

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 - The *rejection region* as the extreme largest 100α% of K values.
 - The *p-value* as the tail area to the right of the observed *K* value.

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• **Comment**: The degrees of freedom is I - 1 because the I (J_i -weighted) deviations $J_i(\bar{R}_i - \bar{R})$ sum to zero, so only I - 1 of them are "free to vary".

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- **Comment**: The degrees of freedom is I 1 because the I (J_i -weighted) deviations $J_i(\bar{R}_i \bar{R})$ sum to zero, so only I 1 of them are "free to vary".
- **Comment**: The constant 12/N(N+1) "rescales" the sum $\sum_i J_i (\bar{R}_i \bar{R})^2$ just enough to force K to follow a $\chi^2(I-1)$ distribution (under H_0).

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Example

An agricultural experiment was carried out to examine the effects of **four** soil **treatments** on the soil **phosphorus** levels.

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An agricultural experiment was carried out to examine the effects of **four** soil **treatments** on the soil **phosphorus** levels.

Twenty plots of land were randomly assigned to receive one of the **four treatments**, with **five** plots per treatment.

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The phosphorus concentrations (mg/g) in the topsoils of the plots are shown on the next slide.

	Treatment I	Treatment II	Treatment III	Treatment IV		
-	20.2	23.0	23.6	23.0		
	15.8	21.8	27.8	33.0		
	18.0	24.2	25.8	28.4		
	20.0	20.6	24.6	24.6		
	22.0	23.8	25.0	27.7		

Side-by-side **boxplots** of the data are on the next slide.



Because the four sample sizes are small, it is difficult to ascertain from plots alone whether the data are normally distributed.

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Because the four sample sizes are small, it is difficult to ascertain from plots alone whether the data are normally distributed.

Suppose we're unwilling to assume normality because previous studies have shown that soil phosphorus concentrations follow **right skewed** distributions.

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We'll carry out a Kruskal-Wallis test of

$$H_0: \qquad \mu_1 = \mu_2 = \cdots = \mu_I$$

 H_a : At least two of the μ_i 's are different

to decide if there are *any* significant **differences** in the mean **phosphorus** concentrations for the **four treatments**.

Here are the samples combined, sorted, and ranked.

Observation	15.8	18.0	20.0	20.2	20.6	21.8	22.0	23.0	23.0	23.6
Sample	I	1	I	I	11	11	I	Ш	IV	III
Rank	1	2	3	4	5	6	7	8.5	8.5	10
Observation	23.8	24.2	24.6	24.6	25.0	25.8	27.7	27.8	28.4	33.0
Sample	II	11	111	IV	111	111	IV	111	IV	IV
Rank	11	12	13.5	13.5	15	16	17	18	19	20

The I = 4 sample sizes are all the same:

$$J_1 = J_2 = J_3 = J_4 = 5.$$

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The overall sample size is N = 20.

The group mean ranks are:

$$\bar{R}_{1} = \frac{1+2+3+4+7}{5} = 3.4.$$
$$\bar{R}_{2} = \frac{5+6+8.5+11+12}{5} = 8.5.$$
$$\bar{R}_{3} = \frac{10+13.5+15+16+18}{5} = 14.5.$$
$$\bar{R}_{4} = \frac{8.5+13.5+17+19+20}{5} = 15.6.$$

The overall mean rank is:

$$\bar{R} = \frac{20+1}{2} = 10.5.$$

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The test statistic is:

$$K = \frac{12}{N(N+1)} \sum_{i=1}^{I} J_i \left(\bar{R}_i - \bar{R} \right)^2$$

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= $\frac{12}{20(20+1)} \left[5 \left(3.4 - 10.5\right)^2 + 5 \left(8.5 - 10.5\right)^2 + 5 \left(14.5 - 10.5\right)^2 + 5 \left(15.6 - 10.5\right)^2 \right]$

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= **13.75**.

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From Table A11 (the chi-squared distribution table) with I - 1 = 3 df, the p-value is between than 0.001 and 0.005.

From Table A11 (the chi-squared distribution table) with I - 1 = 3 df, the p-value is between than 0.001 and 0.005.

Using $\alpha = 0.05$, we **reject** H_0 . There are differences among the phosphorus levels for the four treatments.