

# One Way Analysis of Variance

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- Completely Randomized Design (CRD) is an experimental design in which the experimental units are either randomly selected from each of the populations or are randomly assigned to one of the populations.
- A Factor is the variable of interest. It separates the experimental units into their respective populations.
- A Treatment is one level of the Factor under study. If more than one factor is of interest, then a treatment is a combination of levels of the factors.
- A One-Way Analysis of Variance (1-way ANOVA or AOV) is the statistical method for testing and comparing means from 2 or more independent populations.
- Observational Study is one in which we cannot control the type of treatment performed on the experimental units.
- Planned Experiment is one in which the type of treatment is randomly allocated or assigned to each experimental unit.

## Assumptions of the CRD:

- For observational studies, random samples are taken from each of the populations of interest.
- For planned experiments, the treatments are randomly assigned to the randomly chosen experimental units (the objects on which the experiment is to be performed). Here, the populations refer to conceptual ones in which there is one population for each of the treatments in the experiment.
- Samples are independent
- Homogeneous Variance: we shall assume that the populations of interest all have the same variability, i.e. they all have the same variance
- Approximate Normality: we assume that each population is normally distributed

- The one-way analysis of variance (ANOVA) is a generalization of the two sample t-test ( $k \geq 2$ )
- Assume the populations of interest have the following (unknown) population means and variances

	population 1	population 2	...	population k
mean	$\mu_1$	$\mu_2$	...	$\mu_k$
variance	$\sigma_1^2$	$\sigma_2^2$	...	$\sigma_k^2$

- Goal: test whether  $\mu_1 = \mu_2 = \dots = \mu_k$
- We will compare these means without assuming any parametric relationships (regression does assume such a relationship).

Example:

- Suppose we have five medical treatments and ten subjects on each treatment.
- Goal: Compare the treatments in terms of their effectiveness
- If there were two treatments, what would we use?
- We will compare means among treatment groups.
- In the context of ANOVA, we say these five treatment make one factor with five levels and each level represents a treatment.

- To answer this question, random samples from each of the  $k$ -populations (each population corresponds to a level of the factor) leading to

	sample 1	sample 2	...	sample $k$
size	$n_1$	$n_2$	...	$n_k$
sample	$Y_{11}, Y_{12}, \dots, Y_{1n_1}$	$Y_{21}, Y_{22}, \dots, Y_{2n_2}$	...	$Y_{k1}, Y_{k2}, \dots, Y_{kn_k}$
sample mean	$\bar{Y}_{1\bullet}$	$\bar{Y}_{2\bullet}$	...	$\bar{Y}_{k\bullet}$
sample variance	$s_1^2$	$s_2^2$	...	$s_k^2$

- The sample means are  $\bar{Y}_{1\bullet}, \bar{Y}_{2\bullet}, \dots, \bar{Y}_{k\bullet}$  and the average response over all the samples is

$$\bar{Y}_{\bullet\bullet} = \frac{\sum_{i=1}^k \sum_{j=1}^{n_i} Y_{ij}}{\sum_{i=1}^k n_i} = \frac{\sum_{i=1}^k n_i \bar{Y}_{i\bullet}}{n}$$

where

$$n = \sum_{i=1}^k n_i.$$

Example: A forest manager is responsible for the selection and purchase of chainsaws for her field crew. Her primary interest is worker safety. She is provided with data on chainsaw kickback values (degrees of deflection) for 4 brands of chainsaws (A, B, C, D) with  $N = 5$  observations each. The obvious null hypothesis is:

$$H_0 : \mu_A = \mu_B = \mu_C = \mu_D$$

against  $H_a$  : at least two of these means are not equal. Here  $\mu_j$  is average angle of deflection

A	B	C	D
42	28	57	29
17	50	45	40
24	44	48	22
39	32	41	34
43	61	54	30



- An F test is used to test  $H_0 : \mu_1 = \mu_2 = \dots = \mu_k$  against  $H_a : \text{Not } H_0$  (that is at least two means are not equal)
- The assumptions needed for the test are analogous to the pooled two sample t-test
- The F-test is computed from the ANOVA table which breaks the spread in the combined data SST (Total Sum of Squares) into two components (or sums of squares): within sum of squares (SSE) and the between sums of square (SSR)

$$SST = SSE + SSR$$

- The Between SS (often called the model Sum of Squares) measures the spread between the sample means

$$SSR = \sum_{i=1}^k n_i (\bar{Y}_{i\bullet} - \bar{Y}_{\bullet\bullet})^2$$

- The within SS (often called Error Sum of Squares ) is

$$SSE = \sum_{i=1}^k \sum_{j=1}^{n_i} (Y_{ij} - \bar{Y}_{i\bullet})^2$$

- Each SS has its own degrees of freedom ( $df$ )

$$df(SST) = n - 1 \quad df(SSR) = k - 1 \quad \text{and} \quad df(SSE) = n - k$$

- it is always the case that

$$df(SST) = df(SSR) + df(SSE)$$

- The mean square error for each source of variation is the corresponding SS divided by its  $df$ , that is,

$$MSR = \frac{SSR}{k - 1} \quad \text{and} \quad MSE = \frac{SSE}{n - k}$$

The sums of squares and their dfs are neatly arranged into called the ANOVA table

Source	df	SS	MS	F
Model (Between Groups)	k-1	SSR	$MSR = SSR/(k-1)$	$MSB/MSE$
Error (Within Groups)	n-k	SSE	$MSE = SSE/(n-k)$	
Between Groups (Model)	n-1	SST		

- The decision on whether to reject  $H_0 : \mu_1 = \mu_2 = \dots = \mu_k$  is based on the

$$F = \frac{MSR}{MSE}$$

- We have  $E(MSE) = \sigma^2$  and

$$E(MSR) = \sigma^2 + \frac{\sum_{i=1}^k n_i (\mu_i - \tilde{\mu}_{\bullet})^2}{k-1}$$

where

$$\tilde{\mu}_{\bullet} = \frac{\sum_{i=1}^k n_i \mu_i}{n}.$$

Therefore when  $H_0$  is true

$$\frac{E(MSR)}{E(MSE)} = 1$$

# Example

angle	brand
42	a
17	a
24	a
39	a
43	a
28	b
50	b
44	b
32	b
61	b
57	c
45	c
48	c
41	c
54	c
29	d
40	d
22	d
34	d
30	d

# Example

```
> anova(angle ~ brand)
```

## Analysis of Variance Table

Response: angle

	Df	Sum Sq	Mean Sq	F value	<i>Pr(&gt; F)</i>
brand	3	1080	360.00	3.5556	0.03823
Residuals	16	1620	101.25		

- Large values of  $F$  indicate large variability among the sample means relative to the spread of the data within the samples. That is, large values of  $F$  suggest that  $H_0$  is false
- We reject  $H_0$  if  $F > F(\alpha, k - 1, n - k)$  or if  $p\text{-value} < \alpha$ .
- For  $k = 2$ , the  $F$  test is equivalent to the pooled two-sample  $t$ -test

In the example if we take  $\alpha = 0.05$ , since the  $p\text{-value} = 0.03823$ , we would reject  $H_0$

- During cooking, doughnuts absorb fat in various amounts.
- A scientist wished to learn whether the amount absorbed depends on the type of fat.
- For each of 4 fats, 6 batches of 24 doughnuts were prepared. The data are grams of fat absorbed by batch.
- Let  $\mu_i$  = population mean of fat  $i$  absorbed per batch of 24 doughnuts.
- The Scientist wishes to test  $H_0 : \mu_1 = \mu_2 = \mu_3 = \mu_4$  against  $H_a : \text{Not } H_0$ .

fat 1	fat 2	fat 3	fat 4
264	278	275	255
272	291	286	266
268	297	278	249
277	282	271	264
290	285	263	270
276	277	276	268

## Example

```
> fat<-c(rep("fat1",6),rep("fat2",6),rep("fat3",6),rep("fat4",6))
> amount<-c(264,272,268,277,290,276,278,291,297,282,285,277,275,286,278,271,
263,276,255,266,249,264,270,268)
> data<-data.frame(fat,amount)
> summary(data[,2][data[,1]=='fat1'])
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
264.0   269.0   274.0   274.5   276.8   290.0

> summary(data[,2][data[,1]=='fat2'])
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
277.0   279.0   283.5   285.0   289.5   297.0

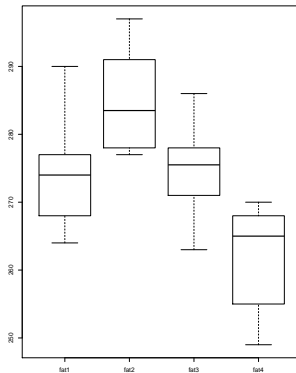
> summary(data[,2][data[,1]=='fat3'])
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
263.0   272.0   275.5   274.8   277.5   286.0

> summary(data[,2][data[,1]=='fat4'])
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
249.0   257.2   265.0   262.0   267.5   270.0
```



```
> boxplot(data[,2] data[,1])
```

Figure: Histogram and Box Plots



```
> summary(fit)
              Df Sum Sq Mean Sq F value Pr(>F)
data[, 1]      3   1596    531.8   7.948 0.0011 **
Residuals     20   1338     66.9
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

$$SSR = 1596, SSE = 1328, MSR = 531.8, MSE = 66.9, F = 7.95$$

If we take  $\alpha = 0.05$ , we have  $F(0.05, 2, 20) = 3.098391$ . since  $7.95 > 3.098391$  we reject  $H_0$

Also  $p\text{-value} = 0.0011 < 0.05$  we reject  $H_0$

- The ANOVA F-test checks whether all the population means are equal.
- Multiple comparisons are often used as a follow up to a significant ANOVA F-test to determine which population means are different.
- We will discuss Fisher's, Bonferroni's and Tukey's methods for comparing all pairs of means

Fisher's least significant difference method (LSD) is a two step process

- (1) Carry out the ANOVA F-test of  $H_0 : \mu_1 = \mu_2 = \dots = \mu_k$ . If  $H_0$  is not rejected stop and conclude that there insufficient evidence to claim differences among the population means. If  $H_0$  is rejected, go to step 2
- (2) Compare each pair of means using a pooled two sample t-test at the alpha level using  $s_{pooled} = \sqrt{MSE}$  from the ANOVA table and  $df = df(SSE)$ , that is test  $H_0 : \mu_i = \mu_j$  against  $H_a : \mu_i \neq \mu_j$  for all pair  $(i, j)$  using

$$t = \frac{\bar{Y}_{i\bullet} - \bar{Y}_{j\bullet}}{\sqrt{MSE} \sqrt{1/n_i + 1/n_j}}$$

and reject  $H_0$  if  $|t| > t_{n-k}(\alpha/2)$ . of equivalently if

$$|\bar{Y}_{i\bullet} - \bar{Y}_{j\bullet}| > t_{n-k}(\alpha/2) \sqrt{MSE} \sqrt{1/n_i + 1/n_j}$$

- (3) The minimum absolute difference between  $\bar{Y}_{i\bullet}$  and  $\bar{Y}_{j\bullet}$  needed to reject  $H_0$  is the LSD, the quantity on the right hand side of the equation above
- (4) If  $n_1 = n_2 = \dots = n_k$

$$LSD = t_{n-k}(\alpha/2) \sqrt{MSE} \sqrt{2/n_1}$$

- ① In our example  $s_{pooled} = \sqrt{MSE} = \sqrt{67} = 8.18$ ,  $n - k = 20$  and if  $\alpha = 0.05$ ,  $t_{20}(0.025) = 2.086$ . Since  $n_1 = n_2 = n_3 = n_4 = 6$ ,

$$LSD = 2.086 \times 8.18 \times \sqrt{2/6} = 9.85.$$

- ② Any two sample means that differ by at least 9.85 in magnitude are significantly different at 5%.
- ③ One way to get Fisher comparisons in R uses `pairwise.t.test()` with `p.adj=sct.method`.
- ④ The resulting summary of multiple comparisons is in terms of p-values for all pairwise two sample t-tests using the pooled standard deviation from the ANOVA using `pool.sd=TRUE`.

```
> pairwise.t.test(data[,2],data[,1],pool.sd=TRUE,p.adjust.method="none" )
```

Pairwise comparisons using t tests with pooled SD

data: data[, 2] and data[, 1]

	fat1	fat2	fat3
fat2	0.038	-	-
fat3	0.944	0.044	-
fat4	0.015	9.3e-05	0.013

P value adjustment method: none

There are  $c = 4(4 - 1)/2 = 6$  comparisons of two fats

Comparison	Absolute difference in means	Exceeds LSD	p-value
1 versus 2	10.50	Yes	0.038
1 versus 3	0.33	No	0.944
1 versus 4	12.50	Yes	0.015
2 versus 3	10.17	Yes	0.044
2 versus 4	23.00	Yes	$9.3 \times 10^{-5}$
3 versus 4	12.83	Yes	0.013

There are three groups here  $\{4\}$ ,  $\{1, 3\}$  and  $\{2\}$

- If the F-test indicates that a factor is significant, then any pair of means that differ by at least LSD are considered to be different.
- This is the least conservative of all the procedures, because no adjustment is made for multiple comparisons (so when doing lots of comparisons this makes Type I errors likely)
- The Bonferroni method controls the FER by reducing the individual comparison rate
- The FER is guaranteed to be no larger than a pre-specified amount say  $\alpha$  by setting the individual error rate for each of the  $k(k-1)/2$  comparisons of interest equal to

$$\alpha = \frac{\alpha}{k(k-1)/2}$$

- To implement the Bonferroni adjustment in R use `p.adjust.method="bonf"`



```
> pairwise.t.test(data[,2],data[,1],pool.sd=TRUE,p.adjust.method="bonf" )
```

Pairwise comparisons using t tests with pooled SD

data: data[, 2] and data[, 1]

	fat1	fat2	fat3
fat2	0.22733	-	-
fat3	1.00000	0.26241	-
fat4	0.09286	0.00056	0.07960

P value adjustment method: bonferroni

- The LSD and Bonferroni methods comprise the ends of the spectrum of multiple comparisons methods
- Among multiple comparisons procedure, the LSD method is the most likely to find differences whether real or due to variation while Bonferroni is often the most conservative method
- The Bonferroni method is conservative but tends to work well when the number of comparisons is small, say 4 or less
- For  $r > 4$ , Bonferroni starts to get much more conservative than necessary

- Another multiple comparisons procedure is Tukey's method (a.k.a. Tukey's Honest Significance Test). The function `TukeyHSD()` creates a set of confidence intervals on the differences between means with the specified family-wise probability of coverage.
- The general form is `TukeyHSD(fit, conf.level = 0.95)`. Here `fit` is a fitted model object (e.g., an `aov.fit`) and `conf.level` is the confidence level.
- Tukey's method is designed for equal sample sizes but can be used for different sample sizes too.
- The method rejects the equality of a pair of means based on the studentized range distribution. To implement this method at  $\alpha$ , reject  $H_0 : \mu_i = \mu_j$  when

$$|\bar{Y}_{i\bullet} - \bar{Y}_{j\bullet}| > \frac{q(1 - \alpha, k, n - k)}{\sqrt{2}} \sqrt{MSE} \sqrt{\frac{1}{n_i} + \frac{1}{n_j}}$$

where  $q(1 - \alpha, k, n - k)$  is the  $\alpha$ th level critical value of the studentized range distribution

```
>fit<-aov(data[,2] ~ data[,1])  
> TukeyHSD(fit)  
  Tukey multiple comparisons of means  
    95\% family-wise confidence level
```

```
Fit: aov(formula = data[, 2] ~ data[, 1], data = data)
```

```
$'data[, 1]'
```

	diff	lwr	upr	p adj
fat2-fat1	10.5000000	-2.719028	23.7190277	0.1510591
fat3-fat1	0.3333333	-12.885694	13.5523611	0.9998693
fat4-fat1	-12.5000000	-25.719028	0.7190277	0.0679493
fat3-fat2	-10.1666667	-23.385694	3.0523611	0.1709831
fat4-fat2	-23.0000000	-36.219028	-9.7809723	0.0004978
fat4-fat3	-12.8333333	-26.052361	0.3856944	0.0590077

- We discuss three different parametrizations for describing the variation in means.
- Which of these methods is used depends on what we want the resulting parameters to mean and on the nature of constraints we may wish to impose on the model
- Method 1: Factor effects method (center point method):

- let

$$\mu_{\bullet} = \frac{1}{k} \sum_{i=1}^k \mu_i \quad \text{and} \quad \alpha_i = \mu_i - \mu_{\bullet} \quad (\Rightarrow \sum_{i=1}^k \alpha_i = 0)$$

- ANOVA model :  $\mu_i = \mu_{\bullet} + \alpha_i, i = 1, 2, \dots, k$
- Regression Model

$$Y_{ij} = \mu_{\bullet} + \alpha_i + \epsilon_{ij}$$

with

$$\begin{bmatrix} \mu_1 \\ \mu_2 \\ \mu_3 \\ \vdots \\ \mu_{k-1} \\ \mu_k \end{bmatrix} = \begin{bmatrix} 1 & 1 & 0 & \dots & 0 \\ 1 & 0 & 1 & \dots & 0 \\ 1 & 0 & 0 & \dots & 0 \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ 1 & 0 & 0 & \dots & 1 \\ 1 & -1 & -1 & \dots & -1 \end{bmatrix} \begin{bmatrix} \mu_{\bullet} \\ \alpha_1 \\ \alpha_2 \\ \vdots \\ \alpha_{k-1} \end{bmatrix} = X_1 \beta$$

- Interesting hypotheses:  $H_0 : \mu_1 = \mu_2 = \dots = \mu_k \Leftrightarrow H_0 : \alpha_1 = \alpha_2 = \dots = \alpha_{k-1} = 0$   
or  $H_0 : C\beta = \mathbf{0}$  where  $C = [\mathbf{0}, I_{k-1}]$

In our example, to carry out the analysis we use the following

```
> a<-gl(4,6)    #this creates the level (4 levels repeated 6 times each)

> lm(data[,2]~ a, contrasts = list(a = "contr.sum"))    # this fit the model
Call:
lm(formula = data[, 2] ~ a, contrasts = list(a = "contr.sum"))
```

Coefficients:

(Intercept)	a1	a2	a3
274.0833	0.4167	10.9167	0.7500

```
> summary(lm(data[,2] ~ a, contrasts = list(a = "contr.sum")))
```

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	274.0833	1.6698	164.143	< 2e-16 ***
a1	0.4167	2.8922	0.144	0.88689
a2	10.9167	2.8922	3.775	0.00119 **
a3	0.7500	2.8922	0.259	0.79804

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 8.18 on 20 degrees of freedom

Multiple R-squared: 0.5438, Adjusted R-squared: 0.4754

F-statistic: 7.948 on 3 and 20 DF, p-value: 0.001104

The fitted model is

$$\hat{Y}_{ij} = 274.0833 + \hat{\alpha}_i$$

where  $\hat{\alpha}_1 = 0.4167$ ,  $\hat{\alpha}_2 = 10.9167$ ,  $\hat{\alpha}_3 = 0.7500$  and  $\hat{\alpha}_4 = -\hat{\alpha}_1 - \hat{\alpha}_2 - \hat{\alpha}_3 = -12.0834$

## Reference cell method

- Define  $\mu^* \equiv \mu_1$  (reference cell) and  $\alpha_i^* = \mu_i - \mu^*$  ( $\alpha_1^* = 0$  by definition).
- ANOVA model:  $\mu_i = \mu^* + \alpha_i^*, i = 1, 2, \dots, k$ .
- Regression model:

$$Y_{ij} = \mu^* + \alpha_i + \epsilon_{ij}$$

with

$$\begin{bmatrix} \mu_1 \\ \mu_2 \\ \mu_3 \\ \vdots \\ \mu_k \end{bmatrix} = \begin{bmatrix} 1 & 0 & 0 & \dots & 0 \\ 1 & 1 & 0 & \dots & 0 \\ 1 & 0 & 1 & \dots & 0 \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ 1 & 0 & 0 & \dots & 1 \end{bmatrix} \begin{bmatrix} \mu^* \\ \alpha_2^* \\ \alpha_3^* \\ \vdots \\ \alpha_k^* \end{bmatrix} = X_2 \beta$$

- Interesting hypotheses:

$H_0 : \mu_1 = \mu_2 = \dots = \mu_k \Leftrightarrow H_0 : \alpha_2^* = \alpha_3^* = \dots = \alpha_k^* = 0$  or  $H_0 : C\beta = \mathbf{0}$  where  $C = [\mathbf{0}, I_{k-1}]$



```
> lm(data[,2]~factor(data[,1]))
```

Call:

```
lm(formula = data[, 2] ~ factor(data[, 1]))
```

Coefficients:

(Intercept)	factor(data[, 1])fat2	factor(data[, 1])fat3
274.5000	10.5000	0.3333
factor(data[, 1])fat4		
-12.5000		

The reference mean here is the mean of fat1. The model is

$$\hat{Y} = \begin{cases} 274.5, & \text{if fat 1} \\ 274.5 + 10.5 = 285 & \text{if fat 2} \\ 274.5 + 0.3 = 274.83 & \text{if fat 3} \\ 274.5 - 12.5 = 222 & \text{if fat 4} \end{cases}$$

```
> summary(lm(data[,2]~factor(data[,1])))
```

Call:

```
lm(formula = data[, 2] ~ factor(data[, 1]))
```

Residuals:

Min	1Q	Median	3Q	Max
-13.0000	-6.6250	0.6667	4.5000	15.5000

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )	
(Intercept)	274.5000	3.3396	82.196	<2e-16	***
factor(data[, 1])fat2	10.5000	4.7229	2.223	0.0379	*
factor(data[, 1])fat3	0.3333	4.7229	0.071	0.9444	
factor(data[, 1])fat4	-12.5000	4.7229	-2.647	0.0155	*

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 8.18 on 20 degrees of freedom

Multiple R-squared: 0.5438, Adjusted R-squared: 0.4754

F-statistic: 7.948 on 3 and 20 DF, p-value: 0.001104

Cell mean method (here the cell means are the parameters)

- ANOVA model:  $\mu_i = \mu_i$ .
- Regression model:

$$Y_{ij} = \mu_i + \epsilon_{ij}$$

with

$$\begin{bmatrix} \mu_1 \\ \mu_2 \\ \mu_3 \\ \vdots \\ \mu_k \end{bmatrix} = \begin{bmatrix} 1 & 0 & 0 & \dots & 0 \\ 0 & 1 & 0 & \dots & 0 \\ 0 & 0 & 1 & \dots & 0 \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & 0 & \dots & 1 \end{bmatrix} \begin{bmatrix} \mu_1 \\ \mu_2 \\ \mu_3 \\ \vdots \\ \mu_k \end{bmatrix} = X_3 \beta$$

- Interesting hypotheses:  $H_0 : \mu_1 = \mu_2 = \dots = \mu_k \Leftrightarrow H_0 := \alpha_3^* = \dots = \alpha_k^* = 0$  or  $H_0 : C\beta = \mathbf{0}$  where  $C = I_k$

```
> lm(data[,2]~factor(data[,1])-1)
```

Call:

```
lm(formula = data[, 2] ~ factor(data[, 1]) - 1)
```

Coefficients:

factor(data[, 1])fat1	factor(data[, 1])fat2	factor(data[, 1])fat3
274.5	285.0	274.8
factor(data[, 1])fat4		
262.0		

```
> summary(lm(data[,2]~factor(data[,1])-1))
```

Call:

```
lm(formula = data[, 2] ~ factor(data[, 1]) - 1)
```

Residuals:

Min	1Q	Median	3Q	Max
-13.0000	-6.6250	0.6667	4.5000	15.5000

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
factor(data[, 1])fat1	274.50	3.34	82.20	<2e-16 ***
factor(data[, 1])fat2	285.00	3.34	85.34	<2e-16 ***
factor(data[, 1])fat3	274.83	3.34	82.30	<2e-16 ***
factor(data[, 1])fat4	262.00	3.34	78.45	<2e-16 ***

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 8.18 on 20 degrees of freedom

Multiple R-squared: 0.9993, Adjusted R-squared: 0.9991

F-statistic: 6742 on 4 and 20 DF, p-value: < 2.2e-16

- Suppose that chainsaws A & B were homeowner models and C & D were industrial grade. Now additional comparison can be made

- Homeowner vs. Industrial

$$H_0 : \mu_A + \mu_B = \mu_C + \mu_D$$

- Model A vs Model C

$$H_0 : \mu_A = \mu_C$$

- Model A vs Model C

$$H_0 : \mu_B = \mu_C$$

- In all these case,  $H_0$  can be expressed as

$$L = c_1\mu_A + c_2\mu_B + c_3\mu_C + c_4\mu_D = 0 \quad \text{where} \quad c_1 + c_2 + c_3 + c_4 = 0$$

- A contrast  $L$  is defined as a linear combination of the level means where the coefficient add up to zero. That is

$$L = \sum_{i=1}^k c_i \mu_i \quad \text{where} \quad \sum_{i=1}^k c_i = 0$$

- Examples:

- ①  $L = \mu_2 - \mu_1$
- ②  $L = \mu_3 - (\mu_1 + \mu_2)/2$
- ③  $L = (\mu_1 + \mu_2)/2 - (\mu_3 + \mu_4)/2$

- We estimate  $L = \sum_{i=1}^k c_i \mu_i$  by

$$\hat{L} = \sum_{i=1}^k c_i \bar{Y}_{i\bullet}$$

- We have

$$E(\hat{L}) = \sum_{i=1}^k c_i E(\bar{Y}_{i\bullet}) = \sum_{i=1}^k c_i \mu_i = L \quad (\hat{L} \text{ is an unbiased estimator of } L)$$

and

$$\text{Var}(\hat{L}) = \sum_{i=1}^k c_i^2 \text{Var}(\bar{Y}_{i\bullet}) = \sigma^2 \sum_{i=1}^k \frac{c_i^2}{n_i}$$

This implies that

$$SE(\hat{L}) = \sqrt{MSE} \sqrt{\sum_{i=1}^k \frac{c_i^2}{n_i}}$$



- A  $100(1 - \alpha)\%$  confidence interval for  $L$  is

$$\hat{L} \pm t_{n-k}(\alpha/2)SE(\hat{L})$$

- To test  $H_0 : L = 0$  against  $H_a : L \neq 0$ , the test statistic is

$$t = \frac{\hat{L} - 0}{SE(\hat{L})}$$

and we reject  $H_0$  is

$$|t| > t_{n-k}(\alpha/2)$$

Same technique works for linear combinations. Later we will look at multiple contrasts.

# Inference for a contrast of the level means

```
> contrasts(brand)<-cbind(c(1,-1,-1,+1), c(1,0,0, -1), c(0,1,-1,0))
> fit<-aov(angle~brand, contrasts=contrasts(brand))
> summary.lm(fit)
```

Call:

```
aov(formula = angle ~ brand, contrasts = contrasts(brand))
```

Residuals:

Min	1Q	Median	3Q	Max
-16.00	-8.25	0.00	7.25	18.00

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )	
(Intercept)	39.000	2.250	17.333	8.58e-12	***
brand1	-7.000	2.250	-3.111	0.00672	**
brand2	1.000	3.182	0.314	0.75738	
brand3	-3.000	3.182	-0.943	0.35980	

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 10.06 on 16 degrees of freedom

Multiple R-squared: 0.4, Adjusted R-squared: 0.2875

F-statistic: 3.556 on 3 and 16 DF, p-value: 0.03823

- Suppose we have  $k$  population with medians  $\eta_1, \eta_2, \dots, \eta_k$ .
- Test

$H_0 : \eta_1 = \eta_2 = \dots = \eta_k$  against  $H_a : \text{at least two of these medians are not equal}$

- We apply the Kruskal-Wallis test. And to do so we pool the responses from all groups and rank them; then we apply one way ANOVA to the ranks, not to the original observations.
- If  $R_{i\bullet}$  = sum of the ranks corresponding to the data from  $i$ th sample, the Kruskal-Wallis test statistic is

$$KW = \frac{12}{n(n+1)} \sum_{i=1}^k \frac{R_{i\bullet}^2}{n_i} - 3(n+1)$$

and we reject  $H_0$  if  $KW > \chi_{k-1}^2(\alpha)$  or if  $p\text{-value} < \alpha$ .

```
> kruskal.test(data[,2]~data[,1])
```

Kruskal-Wallis rank sum test

data: data[, 2] by data[, 1]

Kruskal-Wallis chi-squared = 13.249, df = 3, p-value = 0.004128