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	$\cdots$	population k
mean	μ_1	μ_2	$\cdots$	μ_k
variance	σ_1^2	σ_2^2	$\cdots$	σ_k^2

- Goal: test whether $\mu_1 = \mu_2 = \cdots = \mu_k$
- 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	$\cdots$	sample k
size	n_1	n_2	$\cdots$	n_k
sample	$Y_{11}, Y_{12}, \ldots, Y_{1n_1}$	$Y_{21}, Y_{22}, \ldots, Y_{2n_2}$	$\cdots$	$Y_{k1}, Y_{k2}, \ldots, Y_{kn_k}$
sample mean	$\bar{Y}_{1\bullet}$	$\bar{Y}_{2\bullet}$	$\cdots$	$\bar{Y}_{k\bullet}$
sample variance	s_1^2	s_2^2	$\cdots$	s_k^2

- The sample means are $\bar{Y}_{1\bullet}, \bar{Y}_{2\bullet}, \ldots, \bar{Y}_{k\bullet}$ 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 μ_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 $H_0 : \mu_1 = \mu_2 = \ldots = \mu_k$ against H_a : 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 $H_0 : \mu_1 = \mu_2 = \cdots = \mu_k$ 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 $\sim$ brand)

Analysis of Variance Table

Response: angle

	Df	Sum Sq	Mean Sq	F value	$Pr(>F)$
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 of F suggest that H_0 is false
- We reject H_0 is $F > F(\alpha, k-1, n-k)$ or if $p - value < \alpha$.
- 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-value=0.03823, we would reject H_0

Example

- 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 μ_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 : Not H_0.

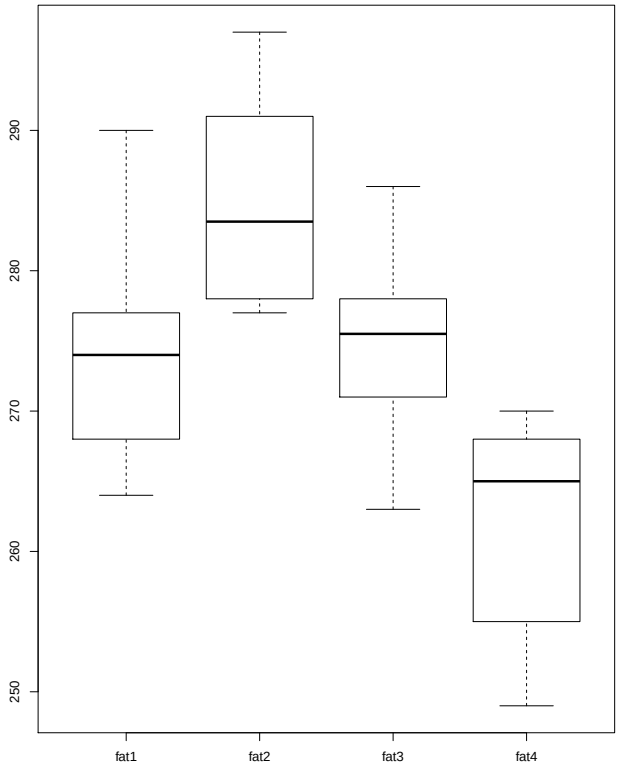
fat 1	fat 2	fat 3	fat 4
264	278	275	255
272	291	286	266
268	297	278	249
277	282	271	264
290	285	263	270
276	277	276	268

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



Example

```
> 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-value=0.0011<0.05 we reject H_0

Multiple Comparisons

- The ANOVA F-test checks whether all the population means are equal.
- Multiple comparisons are ofter 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 mehods 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 $H_0 : \mu_1 = \mu_2 = \cdots = \mu_k$. 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 $n_1 = n_2 = \cdots = n_k$

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

1. In our example $s_{spooled} = \sqrt{MSE} = \sqrt{67} = 8.18, n - k = 20$ 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.adjsut.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.

Multiple Comparisons

```
> 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	9.3×10^{-5}
3 versus 4	12.83	Yes	0.013

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

Bonferroni Comparisons

- 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 α 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"

Bonferroni Comparisons

```
> 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
```

Tukey Comparisons

- 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 of due to variation while Bonferroni is often the most conservative method
- The Bonferroni method is conservative but tend 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

Tukey Comparisons

- 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 α, 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 αth level critical value of the studentized range distribution

Tukey Comparisons

```
>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 : $\mu_i = \mu_\bullet + \alpha_i, i = 1, 2, \ldots, k$
  - Regression Model

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

  with

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

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

参数化

本质上要解决的问题就是探究分类型变量不同level下的取值对应变量的影响程度：
第一种方法：center point method
u·是所有 ui的均值。alpha（i）是每个类别与均值的差距。

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 $\hat{\alpha}_4 = -\hat{\alpha}_1 - \hat{\alpha}_2 - \hat{\alpha}_3 = -12.0834$

cell method 与center method最大的区别在于，cell method把第一类别的均值作为总体的基准项。这个就是我们最一般的哑变量相面的回归分析。

Reference cell method

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

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

with

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

- Interesting hypotheses:
  $H_0 : \mu_1 = \mu_2 = \ldots = \mu_k \Leftrightarrow H_0 : \alpha_2^* = \alpha_3^* = \ldots = \alpha_k^* = 0$ 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

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

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

-1就是不要截距项的意思，也就是说，直接计算每一个类别下的具体的参数，不设置任何基准项

```
> 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
```

Inference for a contrast of the level means

- 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

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

Inference for a contrast of the level means

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

Inference for a contrast of the level means

- 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

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

这里假定各个factor之间不相关，所以，他们的var就等于各个factor内部的var之和

This implies that

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

Inference for a contrast of the level means

- 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
```

L1 = u_a - u_b -u_c + u_d
L2 = u_a - u_d
L3 = u_b - u_c

if do three tests at the same time
\alpha will be different

compare with \alpha = 0.05/3

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

  $H_0 : \eta_1 = \eta_2 = \ldots = \eta_k$ against H_a : 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 ith 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 $KW > \chi^2_{k-1}(\alpha)$ or if $p - value < \alpha$.

```
> 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
```