Comparison Among Several Sample

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- 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

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

Assumptions

To carry out the comparison, we assume that level of the factor (i.e. at each treatment), there is a probability distribution for the response and that

- Each probability distribution is normal
- These probability distribution have the same variances. That is, $\sigma_1^2 = \sigma_2^2 = \cdots = \sigma_k^2$
- The responses for each treatment is a random sample from the corresponding distribution
- These samples are independent

- 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

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

where

$$\bar{\mu}\bullet = \frac{\sum_{i=1}^{k} \mu_i}{k}.$$

Therefore when H_0 is true

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

- 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

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.

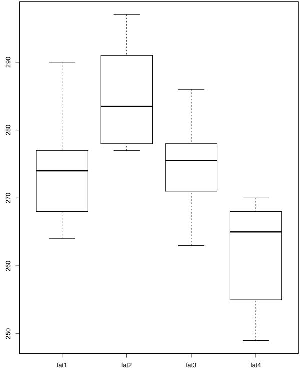
fat 1	fat 2	fat 3	fat 4
264	278	275	255
272	291	286	266
268	297	278	249
277	282	271	264
290	285	263	270
276	277	276	268

```
> 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
```

Example

> 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
```

$$SSB = 1596, \; SSW = 1328, \; MSB = 531.8, \; MSE = 66.9, F = 7.95$$

If we take $\alpha = 0.05$, we have $F(1 - 0.05, 2, 20) = 3.098391$. since $7.95 > 3.098391$ we reject H_0
Also p-value=0.0011<0.05 we reject H_0

- 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 $\bar{Y}_{j\bullet}$ need 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.

```
> 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"

```
> 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 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

```
> 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
$$\begin{bmatrix} \mu_1 \\ \mu_2 \\ \mu_3 \\ \vdots \\ \mu_{k-1} \\ \mu_k \end{bmatrix} = \begin{bmatrix} 1 & 1 & 0 & \ldots & 0 \\ 1 & 0 & 1 & \ldots & 0 \\ 1 & 0 & 0 & \ldots & 0 \\ \vdots & \vdots & \vdots & \vdots & \vdots \\ 1 & 0 & 0 & \ldots & 1 \\ 1 & -1 & -1 & \ldots & -1 \end{bmatrix} \begin{bmatrix} \mu_\bullet \\ \alpha_1 \\ \alpha_2 \\ \vdots \\ \alpha_{k-1} \end{bmatrix} = X_1\boldsymbol{\beta}$$
  - Interesting hypotheses: $H_0 : \mu_1 = \mu_2 = \ldots = \mu_k \Leftrightarrow H_0 : \alpha_1 = \alpha_2 = \ldots = \alpha_{k-1} = 0$ or $H_0 : C\boldsymbol{\beta} = \mathbf{0}$ 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: $\mu_i = \mu^* + \alpha_i^*, i = 1, 2, \ldots, k$.
- Regression model:

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

  with

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

- Interesting hypotheses:
  $H_0 : \mu_1 = \mu_2 = \ldots = \mu_k \Leftrightarrow H_0 : \alpha_2^* = \alpha_3^* = \ldots = \alpha_k^* = 0$ or $H_0 : C\boldsymbol{\beta} = \mathbf{0}$ 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 $H_0 : C\boldsymbol{\beta} = \mathbf{0}$ 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
```

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

- 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

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

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.