Multiple Comparisons

David M. Rocke

November 7, 2023

David M. Rocke

Multiple Comparisons

November 7, 2023

э

Generally speaking, *multiple comparisons* involves statistical techniques for investigating the properties of multiple hypothesis tests considered as a group. We will consider two commonly encountered cases:

- multiple hypothesis tests on a list of responses or on a list of covariates;
- a group of hypotheses on a levels of a factor usually hypothesizing equality of the coefficients of several levels or more generally that a linear function of the coefficients is zero.

The Bottomly et al. mouse gene expression data contains gene expression by RNA-Seq for brain tissue in two strains of mice, 10 from the C57BL/6J strain and 11 from the DBA/2J strain. Fragments from the RNA were mapped to mouse genes, resulting in counts for 11,870 genes. If we conduct tests for difference between the counts or relative counts for the two strains for each of the genes, we have potentially 11,870 tests, though this could be reduced by eliminating genes whose total count was so small that there was little information

If we conduct 11.870 tests at the 5% level, and all of the null hypotheses are true, then the expected number of false positives is $11870 \times 0.05 = 593.5$, which will cause considerable trouble in interpretation. A common proposal for adjusting the p-values of tests uses the Bonferroni inequality, in which when conducting khypothesis tests at level α , the chance of at least one false positive is less than or equal to $k\alpha$. If we conduct the hypothesis tests each at level 0.05/k, then the chance of any false positive is less than or equal to 0.05.

What kind of effects could be detected with $\alpha = 0.05/11870 = 4.2 \times 10^{-6}$? This would require (under normality with 11 in each group) that the means would be separated by 3.13 standard deviations, which would eliminate any real possibility of detecting an effect. Tests with p = 0.00001 would not be rejected! This would be difficult for researcher to accept, and so a different approach has come to be common in these areas of investigation.

If group 1 had mean 10 and standard deviation 1, and group 2 had mean 13.13 with standard deviation 1, then the denominator of the two sample t-test would be $\sqrt{s_1^2/11 + s_2^2/11} \approx \sqrt{2/11} = 0.426$ and the expected value of the difference of the means would be 3.13, so a typical z-score when the difference would be detected would be 7.34!

Requiring zero false positives in 11,870 test would be widely considered unreasonable. So how many false positives should we allow?

Instead of trying to control the false positive number, we might instead choose to control the false discovery rate (FDR), which is the fraction of tests in a group of tests that are false positives. The most commonly used such procedure is that of Benjamini and Hochberg (1995). To use this, we can run all the hypothesis tests in the usual way and construct the vector of p-values, then apply the R function p.adjust.

```
p.adjust(p. method = p.adjust.methods, n = length(p))
p.adjust.methods
# c("holm", "hochberg", "hommel", "bonferroni", "BH", "BY",
  "fdr", "none")
#
Arguments
р
numeric vector of p-values (possibly with NAs). Any other R object is coerced
  by as.numeric.
method
correction method, a character string. Can be abbreviated.
n
number of comparisons, must be at least length(p);
  only set this (to non-default) when you know what you are doing!
```

3

8/35

Note that declaring significant any test with FDR-adjusted p-value less than 0.05 is conceptually completely different from using the 0.05 threshold on an unadjusted p-value. It seems completely reasonable to set a higher threshold such as 0.10.

Any time you conduct hypothesis tests, some of the "significant" ones may not be truly different, and 5 or 10 percent seems a modest penalty to wade through. The Bonferroni method tries to limit the false positives to zero, which reduces the power to a large extent. The other kind of multiple comparison adjustment occurs especially when we have a factor with multiple levels in a linear predictor. Suppose we have three disease types, "ALL", "AML-High", and "AML-Low" with estimates of the log hazard ratio of AML-High vs. ALL and of the log hazard ratio of AML-Low vs. ALL. The coefficient table has hypothesis tests for whether these each are zero, but not of the comparison of AML-High and AML-Low.

If we have a factor describing the type of burn as chemical, scald, electric, and flame, there are six distinct pairwise comparisons, and well as possibly other linear hypotheses, and if we conduct lots of tests on the three coefficients in the table, we may have false positives. Of course a test of whether all the rates are equal is obtainable by a LR test of the models with and without that factor. Note that Wald tests of any linear hypothesis can be conducted for any type of regression model for which asymptotically valid covariance matrices can be derived.

A linear hypothesis on a vector of coefficients β of length p with estimates $\hat{\beta}$ is of the form

$$H_0: L^\top \beta = k,$$

where *L* is a vector of numbers of length *p*; often *L* is a contrast meaning that the sum of the entries is zero and *k* is also often zero. If $\hat{\beta}$ has estimated covariance matrix \hat{V} , then the estimated variance of $L^{\top}\hat{\beta}$ is $L^{\top}\hat{V}L$ and an approximate z-statistic for the hypothesis as stated is

$$z = \frac{L^{\top}\hat{\beta} - k}{\sqrt{L^{\top}\hat{V}L}}.$$

Comparison with a Control

recovery {multcomp}
Recovery time after surgery.

This data frame contains the following variables

blanket blanket type, a factor at four levels: b0, b1, b2, and b3.

minutes response variable: recovery time after a surgical procedure.

Details

A company developed specialized heating blankets designed to help the body heat following a surgical procedure. Four types of blankets were tried on surgical patients with the aim of comparing the recovery time of patients. One of the blanket was a standard blanket that had been in use already in various hospitals.

Source

P. H. Westfall, R. D. Tobias, D. Rom, R. D. Wolfinger, Y. Hochberg (1999). Multiple Comparisons and Multiple Tests Using the SAS System. Cary, NC: SAS Institute Inc., page 66.

```
> library(multcomp)
> data(recovery)
> recovery.lm <- lm(minutes~blanket,data=recovery)</pre>
> summary(recovery.lm)
Call:
lm(formula = minutes ~ blanket, data = recovery)
Residuals
  Min 10 Median 30 Max
-6.133 -1.800 0.200 2.200 4.867
Coefficients:
           Estimate Std. Error t value Pr(>|t|)
(Intercept) 14.8000 0.5792 25.552 < 2e-16 ***
blanketb1 -2.1333 1.6038 -1.330 0.1916
blanketb2 -7.4667 1.6038 -4.656 4.07e-05 ***
blanketb3 -1.6667 0.8848 -1.884 0.0675.
___
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
Residual standard error: 2.59 on 37 degrees of freedom
Multiple R-squared: 0.3797, Adjusted R-squared: 0.3294
F-statistic: 7.55 on 3 and 37 DF, p-value: 0.0004619
                                                 ▲□▶ ▲□▶ ▲三▶ ▲三▶  三  のへで
```

It looks like blanket b2 is better than b0, but we did conduct three hypothesis tests to obtain that finding. The F-test shows that not all the blankets are the same. so it might be reasonable to attribute that only to b2, but we can test that allowing for the multiple comparisons and the correlations between the tests using the Dunnett procedure and also obtain confidence intervals adjusted for multiple comparisons. This is based on the multivariate t distribution of the coefficients and is implemented in the glht() command in the R package multcomp.

> recovery.mc <- glht(recovery.lm,linfct=mcp(blanket="Dunnett"))</pre> > summary(recovery.mc)

Simultaneous Tests for General Linear Hypotheses Multiple Comparisons of Means: Dunnett Contrasts

```
Fit: lm(formula = minutes ~ blanket, data = recovery)
```

```
Linear Hypotheses:
           Estimate Std. Error t value Pr(>|t|)
b1 - b0 == 0 -2.1333 1.6038 -1.330 0.456
b2 - b0 == 0 -7.4667 1.6038 -4.656 <0.001 ***
b3 - b0 == 0 -1.6667 0.8848 -1.884 0.182
___
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
(Adjusted p values reported -- single-step method)
```

```
> names(recovery.mc)
[1] "model" "linfct" "rhs" "coef" "vcov" "df"
[7] "alternative" "type" "focus"
```

```
> recovery.mc$linfct
```

	(Intercept)	blanketb1	blanketb2	blanketb3
b1 - b0	0	1	0	0
b2 - b0	0	0	1	0
b3 - b0	0	0	0	1
attr(,"1 [1] "Dur				
> recove	ery.mc\$rhs			
[1] 0 0	0			
> recove	ery.mc\$focus			
[1] "bla	anket"			

Some attributes of an object have extractor functions, including coef and vcov. All the components can be accessed as attributes of the object. The three linear hypotheses require the linear vectors L and the right-hand sides k.

This lists the types of pre-specified contrasts. Any set of linear hypotheses can also be specified just as a matrix linfct and right-hand side vector rhs. A base level can be given for Dunnett comparisons, which for general hypotheses is the focus attribute.

recovery.lm Coefficients	5:		
	Estimate Std. Erro	or t value Pr(>	t)
(Intercept)	14.8000 0.579	92 25.552 < 2e	-16 ***
blanketb1	-2.1333 1.603	38 -1.330 0.1	916
blanketb2	-7.4667 1.603	38 -4.656 4.07e	-05 ***
blanketb3	-1.6667 0.884	48 -1.884 0.0	675 .
recovery.mc			
Linear Hypot	theses:		
	Estimate Std. Er	ror t value Pr(>	t)
b1 - b0 == () -2.1333 1.60	038 -1.330 0	.456
b2 - b0 == (0 -7.4667 1.60	038 -4.656 <0	.001 ***
b3 - b0 == (0.88	848 -1.884 0	.182

Note that the t-scores are the same, but the p-values are adjusted for multiple comparisons so that the chance that one or more is significant at level α in the null case is less than or equal to α

> summary(recovery.mc,test = adjusted(type="bonferroni"))

```
Simultaneous Tests for General Linear Hypotheses
Multiple Comparisons of Means: Dunnett Contrasts
```

```
Fit: lm(formula = minutes ~ blanket, data = recovery)
```

```
Linear Hypotheses:
            Estimate Std. Error t value Pr(>|t|)
b1 - b0 == 0 -2.1333 1.6038 -1.330 0.574796
b2 - b0 == 0 -7.4667 1.6038 -4.656 0.000122 ***
b3 - b0 == 0 -1.6667 0.8848 -1.884 0.202439
___
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
(Adjusted p values reported -- bonferroni method)
```

Coefficients:

(Intercept) blanketb1 blanketb2 blanketb3	14.8000 -2.1333 -7.4667	1.6038 1.6038	25.552 -1.330 -4.656	< 2e-16 0.1916 4.07e-05	***	lm
Linear Hypot	heses:					
	Estimate	Std. Error	t value	Pr(> t)		
b1 - b0 == 0	-2.1333	1.6038	-1.330	0.456		Dunnett
b2 - b0 == 0	-7.4667	1.6038	-4.656	<0.001	***	
b3 - b0 == 0	-1.6667	0.8848	-1.884	0.182		
Linear Hypot	heses:					
	Estimate	Std. Error	t value	Pr(> t)		
b1 - b0 == 0	-2.1333	1.6038	-1.330	0.574796		Bonferroni
b2 - b0 == 0	-7.4667	1.6038	-4.656	0.000122	***	
b3 - b0 == 0	-1.6667	0.8848	-1.884	0.202439		

Both Dunnett and Bonferroni protect the familywise error rate, but Dunnett has smaller p-values because it uses the correlations of the tests. > confint(recovery.mc)

```
Simultaneous Confidence Intervals
```

```
Multiple Comparisons of Means: Dunnett Contrasts
```

```
Fit: lm(formula = minutes ~ blanket, data = recovery)
```

```
Quantile = 2.489
95% family-wise confidence level
```

```
Linear Hypotheses:

Estimate lwr upr

b1 - b0 == 0 -2.1333 -6.1251 1.8584

b2 - b0 == 0 -7.4667 -11.4584 -3.4749

b3 - b0 == 0 -1.6667 -3.8688 0.5355
```

There is at least a 95% chance that all the true values of the contrasts lie in their stated intervals.

22 / 35

> confint(recovery.lm)

	2.5 %	97.5 %
(Intercept)	13.626389	15.9736107
blanketb1	-5.382914	1.1162474
blanketb2	-10.716247	-4.2170859
blanketb3	-3.459387	0.1260532

Linear Hypotheses:

Estimate lwr upr b1 - b0 == 0 -2.1333 -6.1251 1.8584 b2 - b0 == 0 -7.4667 -11.4584 -3.4749 b3 - b0 == 0 -1.6667 -3.8688 0.5355

The confidence intervals from 1m are individually valid, but if we consider them to be independent the chance that at least one does not contain the true value is $1 - (0.95)^3 = 0.14$. We could use Bonferroni confidence intervals at 98.3% confidence, but the Dunnett ones will be narrower because they use the correlations of the variables.

David M. Rocke

All Pairs Comparisons

immer {MASS}
Yields from a Barley Field Trial
Description
The immer data frame has 30 rows and 4 columns. Five varieties of barley were
grown in six locations in each of 1931 and 1932.

This data frame contains the following columns:

Loc The location.

Var The variety of barley ("manchuria", "svansota", "velvet", "trebi" and "peatland").

Y1 Yield in 1931.

Y2 Yield in 1932.

イロト イヨト イヨト ・

- > library(MASS)
- > data(immer)
- > immer1 <- data.frame(immer,Yield = (immer\$Y1+immer\$Y2))</pre>
- > summary(immer.lm)

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)					
(Intercept)	204.403	12.156	16.815	2.88e-13	***				
VarP	16.300	12.156	1.341	0.194983					
VarS	-6.517	12.156	-0.536	0.597810					
VarT	47.617	12.156	3.917	0.000854	***				
VarV	9.583	12.156	0.788	0.439728					
LocD	-52.120	13.316	-3.914	0.000860	***				
LocGR	-56.680	13.316	-4.256	0.000386	***				
LocM	-7.180	13.316	-0.539	0.595705					
LocUF	-32.020	13.316	-2.405	0.025996	*				
LocW	54.280	13.316	4.076	0.000589	***				
Signif. cod	es: 0'**	**' 0.001 ' [;]	**' 0.01	'*' 0.05	'.'	0.1	٢	,	1

Residual standard error: 21.05 on 20 degrees of freedom Multiple R-squared: 0.8568, Adjusted R-squared: 0.7924 F-statistic: 13.3 on 9 and 20 DF, p-value: 1.216e-06

イロト 不得 トイヨト イヨト

3

```
> drop1(immer.lm,test="F")
Single term deletions
Model:
Yield ~ Var + Loc
      Df Sum of Sa RSS
                            AIC F value Pr(>F)
                    8866 190.66
<none>
Var
       4 10620 19486 206.29 5.9891 0.002453 **
Loc 5 42442 51308 233.33 19.1480 5.212e-07 ***
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
> tapply(immer1$Yield,immer1$Var,mean)
       м
               Р
                        S
                                 т
                                          V
188,7833 205,0833 182,2667 236,4000 198,3667
> sort(tapply(immer1$Yield,immer1$Var,mean))
       S
               М
                        v
                                 Ρ
                                          т
182,2667 188,7833 198,3667 205,0833 236,4000
```

Both variety and location are significant, but it is not clear which pairs of varieties are shown to differ.

S M V P T 182.2667 188.7833 198.3667 205.0833 236.4000

> immer.mc <- glht(immer.lm,linfct=mcp(Var = "Tukey"))
> summary(immer.mc)

Simultaneous Tests for General Linear Hypotheses

Multiple Comparisons of Means: Tukey Contrasts

Fit: lm(formula = Yield ~ Var + Loc, data = immer1)

Linear hypo	Juneses.				
	Estimate	Std. Error	t value	Pr(> t)	
P - M == 0	16.300	12.156	1.341	0.67008	
S - M == 0	-6.517	12.156	-0.536	0.98242	
T - M == 0	47.617	12.156	3.917	0.00675	**
V - M == 0	9.583	12.156	0.788	0.93102	
S - P == 0	-22.817	12.156	-1.877	0.36064	
T - P == 0	31.317	12.156	2.576	0.11336	
V - P == 0	-6.717	12.156	-0.553	0.98035	
T - S == 0	54.133	12.156	4.453	0.00201	**
V - S == 0	16.100	12.156	1.324	0.67981	
V - T == 0	-38.033	12.156	-3.129	0.03773	*

Lincor Wymothogog

3

< ロ > < 同 > < 回 > < 回 > < 回 > < 回 > < 回 > < 回 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 > < 0 >

```
> confint(immer.mc)
```

Simultaneous Confidence Intervals

Multiple Comparisons of Means: Tukey Contrasts

```
Fit: lm(formula = Yield ~ Var + Loc, data = immer1)
```

```
Quantile = 2.9932
95% family-wise confidence level
```

Linear Hypotheses: Estimate lwr upr P - M == 0 16.3000 -20.0850 52.6850 C M -- 0 C E1C7 40 001C 00 0000

ъ	-	M	==	υ	-0.510/	-42.9010	29.0003
Т	-	М	==	0	47.6167	11.2317	84.0016
V	-	М	==	0	9.5833	-26.8016	45.9683
S	-	Ρ	==	0	-22.8167	-59.2016	13.5683
Т	-	Ρ	==	0	31.3167	-5.0683	67.7016
V	-	Ρ	==	0	-6.7167	-43.1016	29.6683
Т	-	S	==	0	54.1333	17.7484	90.5183
V	-	S	==	0	16.1000	-20.2850	52.4850
V	-	Т	==	0	-38.0333	-74.4183	-1.6484

The confidence intervals and tests that result from uncorrected 1m and other regression models are often called *Least Significant Difference* = *LSD* tests and intervals. When there are many levels of a factor, this can result in false positives. One possible intermediate choice is to use the LSD tests and intervals, but only if the anova test for the factor is significant. This method is sometimes called the *Protected LSD*. This protects against the case where all the levels have equal effect, but not against partial equalities. However, for some applications this may be enough.

Another Example

> summary(burn1\$BurnT	ype)			
Chemical	Scald Ele	ctric	Flame		
9	18	11	116		
<pre>> summary(coxph(burn1.surv~Treatment+BurnType,data=burn1))</pre>					

	coef	exp(coef)	se(coef)	Z	Pr(> z)
TreatmentCleansing	-0.5958	0.5511	0.2968	-2.008	0.0447 *
BurnTypeScald	1.1328	3.1044	1.0828	1.046	0.2955
BurnTypeElectric	2.2660	9.6407	1.0837	2.091	0.0365 *
BurnTypeFlame	0.9888	2.6879	1.0160	0.973	0.3305

> drop1(coxph(burn1.surv~Treatment+BurnType,data=burn1),test="Chisq") Df ATC LRT Pr(>Chi) <none> 435.03 Treatment 1 437.14 4.1021 0.04283 * BurnType 3 436.84 7.8095 0.05012 .

Image: A matrix

э

Simultaneous Tests for General Linear Hypotheses

Multiple Comparisons of Means: Tukey Contrasts

Fit: coxph(formula = burn1.surv ~ Treatment + BurnType, data = burn1)

Linear Hypotheses:

	Estimate	Std. Error	z value	$\Pr(z)$
Scald - Chemical == 0	1.1328	1.0828	1.046	0.7013
Electric - Chemical == 0	2.2660	1.0837	2.091	0.1406
Flame - Chemical == 0	0.9888	1.0160	0.973	0.7460
Electric - Scald == 0	1.1332	0.5902	1.920	0.1999
Flame - Scald == 0	-0.1441	0.4456	-0.323	0.9870
Flame - Electric == 0	-1.2772	0.4521	-2.825	0.0212

*

3

> confint(burntype.mc)

Simultaneous Confidence Intervals

Multiple Comparisons of Means: Tukey Contrasts

```
Fit: coxph(formula = burn1.surv ~ Treatment + BurnType, data = burn1)
```

```
Quantile = 2.5176
95% family-wise confidence level
```

Linear Hypotheses:

	Estimate	lwr	upr
Scald - Chemical == 0	1.1328	-1.5931	3.8587
Electric - Chemical == 0	2.2660	-0.4622	4.9942
Flame - Chemical == 0	0.9888	-1.5691	3.5466
Electric - Scald == 0	1.1332	-0.3527	2.6190
Flame - Scald == 0	-0.1441	-1.2658	0.9777
Flame - Electric == 0	-1.2772	-2.4153	-0.1391

글 에 에 글 어

Image: A matrix

3

Scheffé Tests and Intervals

In the last example, allowing for the fact that six tests were conducted, one of them was still significant and yet the anova test for the type factor was not (quite). One reason might be that the LR test and the Wald test are only asymptotically equivalent. But another is that the hypothesis that a factor has no effect means that any linear combination of levels has no associated effect. because the effect associated with any factor level is zero. Tests and intervals can be based on this idea. that we need to be protected from false positives in any (linear) test suggested by the results of an analysis.

Suppose we have a factor with r levels and an effect μ_i associated with each level. This could be coefficients in a regression in which the coefficient for level *i* is already a comparison between level *i* and level 1. The assertion that the factor has no effect in either case is the hypothesis that $\mu_1 = \mu_2 = \cdots = \mu_r$. In the coefficient case, $\mu_1 = 0$ so then all the values of $\mu_i = 0$, but in any case, if we have a contrast L, then $L^{\top}M = 0$, where M is the vector $(\mu_1, \mu_2, \ldots, \mu_r)$. We have the (infinite) collection of contrasts and we want a test/interval such that when the total null hypothesis on the factor is true, then the chance that any test will be significant is less than or equal to α .

The method uses the estimated value of the contrast and the standard error, but instead using the t-statistic, one uses instead $\hat{C} \pm s_{\hat{C}} \sqrt{(r-1) F_{\alpha;r-1;df}}$, where df is the residual degrees of freedom. So with six types of barley in an experiment with 30 data points, the multipier is $\sqrt{5F_{.05,5,20}} = 3.68$ instead of $t_{20} = 2.086$. Generally, this level of protection is achieved at too high a cost. If differences are the inferential target, the Tukey HSD is better (with multiplier 2.518).