Contrasts

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1 Constructing orthogonal contrasts of interest

1.1 Example from plant physiology

> In previous discussion, we've treated each treatment group on an equal footing, and have performed an ANOVA + F-test, and then carried out pairwise comparisons, either doing pairwise t-tests or the more stringent Tukey tests.
>
> In this situation, there are comparisons between specific treatments known *a priori* that are of special interest.

In such situations, we can produce orthogonal contrasts, so that each contrast represents a particular aspect of the differences amongst treatment effects.

These orthogonal contrasts should be constructed **BEFORE** examination of the data. If done afterwards, it may bias conclusions.

An initial impression of the data can be seen by looking at the ANOVA table, and a table of means.

```
In [37]: length <- c(75, 67, 70, 75, 65, 71, 67, 67, 76, 68,
                     57, 58, 60, 59, 62, 60, 60, 57, 59, 61,
                     58, 61, 56, 58, 57, 56, 61, 60, 57, 58,
                     58, 59, 58, 61, 57, 56, 58, 57, 57, 59,
                     62, 66, 65, 63, 64, 62, 65, 65, 62, 67)
```

```
In [38]: #ăimportant to code these as FACTORS!
         sugar <- factor(rep(1:5, rep(10,5)))
```

```
In [39]: growth <- data.frame(length, sugar)

         # a quick top 10, showing two of the ten values per treatment group
         growth[c(1:2,11:12,21:22,31:32,41:42),]
```

	length	sugar
1	75	1
2	67	1
11	57	2
12	58	2
21	58	3
22	61	3
31	58	4
32	59	4
41	62	5
42	66	5

1.2 ANOVA

```
In [40]: growth.aov <- aov(length ~ sugar, data=growth)

         summary(growth.aov)
```

```
            Df Sum Sq Mean Sq F value   Pr(>F)
sugar        4 1077.3  269.33   49.37 6.74e-16 ***
Residuals   45  245.5    5.46
---
Signif. codes:  0 *** 0.001 ** 0.01 * 0.05 . 0.1   1
```

1.2.1 F-test

Can see from the F-statistic, that there is evidence at the 0.1% significance level to reject the null hypothesis that the treatment means between the five treatment groups are all the same.

$SS_{Treatments}$ is associated with $a - 1 = 4$ degrees of freedom

SS_R is associated with $N - a$ degrees of freedom

Clearly, $a = 5$ (5 treatment groups) and $N = 50$ (50 observations in total)

$MS_R = s^2 = \frac{SS_R}{N-a}$ represents the **pooled estimate of the error variance**

$$F_{a-1,N-a} = \frac{MS_{Treatments}}{MS_R}$$

```
In [41]: pf(49.37, 4, 45, lower.tail=FALSE)
```

6.73254485225133e-16

1.3 Table of Means

Grand mean is the overall sample mean, $\bar{y}_{..}$

Other means are the sample treatment means (**not effects**), $\bar{y}_{i.}$

```
In [46]: model.tables(growth.aov, type = 'means')
```

```
Tables of means
Grand mean

61.94

 sugar
sugar
   1    2    3    4    5
70.1 59.3 58.2 58.0 64.1
```

1.4 Adding contrasts into the mix!

R has inbuilt functions to deal with contrasts.

Recall a contrast, ψ, is defined by a linear combination of the treatment **effects**:

$\psi = \sum_{i=1}^{a} c_i \tau_i$,

where:

$\sum_{i=1}^{a} c_i = 0$.

Sets of contrasts are specified by matrices in R. Each column represents the set of linear coefficients of a single contrast (i.e. a vector of length a, containing $\mathbf{c} = [c_1 c_2 ... c_a]^T$.

There are some built-in functions:

- `contr.helmert`
- `contr.sum`
- `contr.treatment`

For `contr.helmert`, if the number of observations is the same for each treatment (i.e. $n_i = n, i = 1, 2, ..., a$), then contrasts are mutually orthogonal.

The our dataset, we've got $a = 5$ treatment groups. We know that we'll get as many orthogonal contrasts as we have treatment degrees of freedom - the number of degrees of freedom associated with $SS_{Treatments}$. This is $a - 1$, therefore we'll get $a - 1 = 4$ orthogonal contrasts, and hence, we'll get a 5×4 matrix, 5 rows (the length of the contrast coefficient vectors) and 4 columns (each column representing vector of contrast coefficients).

The `contr.helmert` set of contrasts successfully compares **the effect of each treatment Vs the average of the previous ones**.

The `contr.sum` set of contrasts compares **the final treatment with each of the others**. These contrasts are not mutually orthogonal.

```
In [47]: contr.treatment(5)
```

2	3	4	5
0	0	0	0
1	0	0	0
0	1	0	0
0	0	1	0
0	0	0	1

```
In [48]: contr.sum(5)
```

1	0	0	0
0	1	0	0
0	0	1	0
0	0	0	1
-1	-1	-1	-1

```
In [49]: contr.helmert(5)
```

-1	-1	-1	-1
1	-1	-1	-1
0	2	-1	-1
0	0	3	-1
0	0	0	4

1.5 Constructing our own set of contrasts.

(If we didn't do this, then `contr.treatment` - the default - would be used).

We want to contruct 4 vectors: $\mathbf{c_1}, \mathbf{c_2}, \mathbf{c_3}, \mathbf{c_4}$.

Each vector will have 5 elements.

In our example, we have the same number of observations in each treatment group, so $n_i = n, i = 1, 2, ..., a$.

This means our orthogonality condition of:

$\sum_{i=1}^{a} \frac{c_i d_i}{n_i} = 0$ becomes $\sum_{i=1}^{a} c_i d_i = 0$.

1.5.1 Contrasts

1) The first is a contrast of the control against the sugars.
2) The second is a contrast of sucrose against glucose and fructose.
3) The third is a simple comparison of glucose and fructose.
4) The fourth contrast is a measure of interaction between glucose and fructose.

Remember: $\sum_{i=1}^{a} c_i = 0$ **ALL OF YOUR ELEMENTS IN THE COEFFICIENT VECTORS MUST SUM TO 0.**

```
In [57]: # contrast between control, and the sugars
         c1 <- c(4,-1,-1,-1,-1)
```

```
In [101]: # contrast between sucrose (position 5) against glucse and fructose (positions 2,3,4
          c2 <- c(0, -1, -1, -1, 3)
```

```
In [102]: # comparison between glucose (position 2) and fructose (position 3)
          c3 <- c(0, 1, -1, 0, 0)
```

```
In [103]: # measure of interaction between glucose and fructose: glucose is position (2), fruc
          # and the glucose/fructose half and half combo is position (4)
          c4 <- c(0, -1, -1, 2, 0)
```

```
In [113]: ctr <- matrix(c(c1,c2,c3,c4), nrow=5)
          #ctr <- contr.helmert(5)

          ctr
```

4	0	0	0
-1	-1	1	-1
-1	-1	-1	-1
-1	-1	0	2
-1	3	0	0

We now set the contrasts specified above, "to be associated with the factor sugar", using the `contrasts()` function, **AND REPEAT THE ANOVA**.

Standard ANOVA results DO NOT CHANGE

Must dig into the split of the ANOVA where we see what each of our contrasts, each with a degree of freedom, looks like

Means table looks the same

```
In [114]: contrasts(growth$sugar) <- ctr
```

```
In [115]: growth.aov <- aov(length ~ sugar, data=growth)

          summary(growth.aov, split = list(sugar = list("control v sugars" = 1,
                                                        "sucrose v gl,fr" = 2,
                                                        "gl v fr" = 3,
                                                        "gl,fr interaction" = 4)))
```

```
                            Df Sum Sq Mean Sq F value   Pr(>F)    
sugar                        4 1077.3   269.3  49.368 6.74e-16 ***
  sugar: control v sugars    1  832.3   832.3 152.564 4.68e-16 ***
  sugar: sucrose v gl,fr     1  235.2   235.2  43.112 4.50e-08 ***
  sugar: gl v fr             1    6.1     6.1   1.109    0.298    
  sugar: gl,fr interaction   1    3.7     3.7   0.687    0.411    
Residuals                   45  245.5     5.5                     
---
Signif. codes:  0 *** 0.001 ** 0.01 * 0.05 . 0.1   1
```

This shows strong evidence that the presence of sugars reduces growth, and that glucose and fructose reduce growth more than sucrose.

> CG Note: I think the directionality of reduce / increase growth is inferred from the means table, rather than coming out of the ANOVA summary.

No evidence that there are differences in effects between glucose and fructose, or that there's significant interaction between glucose and fructose.

```
In [118]: model.tables(growth.aov, type = 'means')
```

```
Tables of means
Grand mean

61.94

 sugar
sugar
   1    2    3    4    5
70.1 59.3 58.2 58.0 64.1
```

1.6 Finally, can see the contrast estimated values: $\frac{\hat{\psi}}{\sum c_i^2}$

```
In [119]: coef(growth.aov)
```

(Intercept) 61.94 **sugar1** 2.04 **sugar2** 1.4 **sugar3** 0.55 **sugar4** -0.25

```
In [ ]:
```