

Unbalanced Designs

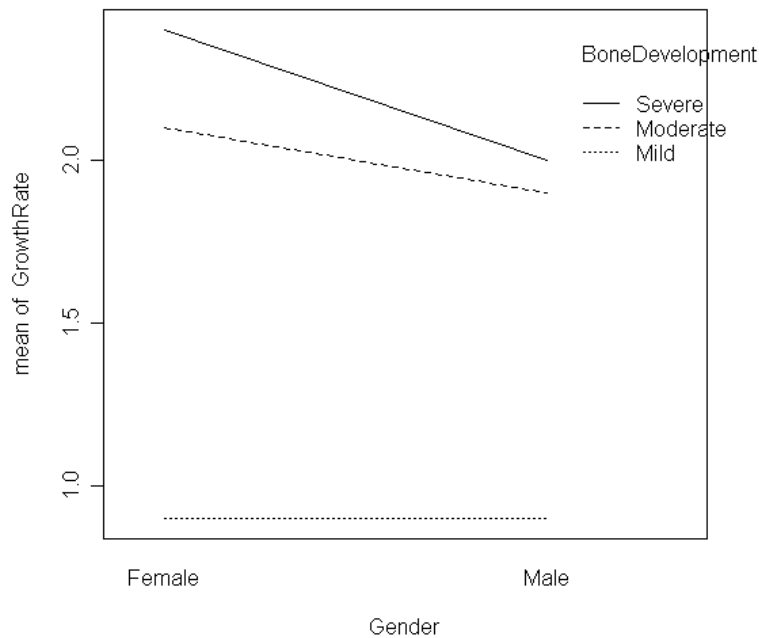
Growth Deficiency in Children

Measure percent difference in growth rate from before to after administering a synthetic growth hormone in children. Factor A=Gender (Male,Female) and Factor B=Classification of Lack of Bone Development (Severe, Moderate, Mild)

```
> gd=read.table("growthdef.txt",header=TRUE)
> gd$Treatment=as.factor(gd$Treatment)
> gd
```

	GrowthRate	Gender	BoneDevelopment	Treatment
1	1.4	Male	Severe	1
2	2.4	Male	Severe	1
3	2.2	Male	Severe	1
4	2.1	Male	Moderate	2
5	1.7	Male	Moderate	2
6	0.7	Male	Mild	3
7	1.1	Male	Mild	3
8	2.4	Female	Severe	4
9	2.5	Female	Moderate	5
10	1.8	Female	Moderate	5
11	2.0	Female	Moderate	5
12	0.5	Female	Mild	6
13	0.9	Female	Mild	6
14	1.3	Female	Mild	6

```
> attach(gd)
```



```
> a=aov(GrowthRate~Gender+BoneDevelopment+Gender:BoneDevelopment)
> anova(a) #NOTE: Only interaction SS is correct
Analysis of Variance Table
```

Response: GrowthRate

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Gender	1	0.0029	0.0029	0.0176	0.897785
BoneDevelopment	2	4.3960	2.1980	13.5262	0.002713 **
Gender:BoneDevelopment	2	0.0754	0.0377	0.2321	0.798034
Residuals	8	1.3000	0.1625		

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

```
> #Create dummy variables to run as regression
```

```
> x1=ifelse(Gender=="Male",1,-1)
```

```
> x2=ifelse(BoneDevelopment=="Severe",1,ifelse(BoneDevelopment=="Mild",-1,0))
```

```
> x3=ifelse(BoneDevelopment=="Moderate",1,ifelse(BoneDevelopment=="Mild",-1,0))
```

```
> x12=x1*x2
```

```
> x13=x1*x3
```

```
> data.frame(gd,x1,x2,x3,x12,x13)
```

	GrowthRate	Gender	BoneDevelopment	Treatment	x1	x2	x3	x12	x13	
1	1.4	Male	Severe		1	1	1	0	1	0
2	2.4	Male	Severe		1	1	1	0	1	0
3	2.2	Male	Severe		1	1	1	0	1	0
4	2.1	Male	Moderate		2	1	0	1	0	1
5	1.7	Male	Moderate		2	1	0	1	0	1
6	0.7	Male	Mild		3	1	-1	-1	-1	-1
7	1.1	Male	Mild		3	1	-1	-1	-1	-1
8	2.4	Female	Severe		4	-1	1	0	-1	0
9	2.5	Female	Moderate		5	-1	0	1	0	-1
10	1.8	Female	Moderate		5	-1	0	1	0	-1
11	2.0	Female	Moderate		5	-1	0	1	0	-1
12	0.5	Female	Mild		6	-1	-1	-1	1	1
13	0.9	Female	Mild		6	-1	-1	-1	1	1
14	1.3	Female	Mild		6	-1	-1	-1	1	1

```
> bdreg=lm(GrowthRate~x1+x2+x3+x12+x13) #full model again (same as above aov command)
```

```
> anova(bdreg)
```

Analysis of Variance Table

Response: GrowthRate

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
x1	1	0.0029	0.0029	0.0176	0.897785
x2	1	3.6509	3.6509	22.4668	0.001464 **
x3	1	0.7451	0.7451	4.5855	0.064638 .
x12	1	0.0754	0.0754	0.4642	0.514913
x13	1	2.045e-33	2.045e-33	1.259e-32	1.000000
Residuals	8	1.3000	0.1625		

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

```
> F=(.0754+2.045e-33)/2/.1625
```

```
> F
```

```
[1] 0.232
```

```
> 1-pf(F,2,8)
```

```
[1] 0.7981
```

```
> # same result as in original anova table since interaction term was last
```

```
> bdreg=lm(GrowthRate~x2+x3+x12+x13+x1) #test for Gender main effects (put x1 last)
> anova(bdreg)
Analysis of Variance Table
```

```
Response: GrowthRate
      Df Sum Sq Mean Sq F value    Pr(>F)
x2      1  3.4410   3.4410  21.1754 0.001752 **
x3      1  0.8653   0.8653   5.3248 0.049879 *
x12     1  0.0462   0.0462   0.2840 0.608558
x13     1  0.0018   0.0018   0.0114 0.917740
x1      1  0.1200   0.1200   0.7385 0.415160
Residuals 8  1.3000   0.1625
```

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

```
> # p-value for Gender main effect test is .415160 from last line (NOTE this is not
equal to .897785 from original anova table)
```

```
> bdreg=lm(GrowthRate~x1+x12+x13+x2+x3) #test for BoneDevelopment main effects (put
x2 and x3 last)
> anova(bdreg)
Analysis of Variance Table
```

```
Response: GrowthRate
      Df Sum Sq Mean Sq F value    Pr(>F)
x1      1  0.0029   0.0029   0.0176 0.897785
x12     1  0.0207   0.0207   0.1275 0.730302
x13     1  0.2610   0.2610   1.6062 0.240678
x2      1  3.6006   3.6006  22.1577 0.001527 **
x3      1  0.5891   0.5891   3.6252 0.093392 .
Residuals 8  1.3000   0.1625
```

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

```
> F=(3.6006+0.5891)/2/.1625
```

```
> F
```

```
[1] 12.89138
```

```
> 1-pf(F,2,8)
```

```
[1] 0.003144698
```

```
> # NOTE: not equal to p-value of .002713 from original anova table
```

```

> # multiple comparisons of bone development levels - use my "multcomp" function
> a=aoov(GrowthRate~Treatment) #run as one-way anova
> anova(a)
Analysis of Variance Table

```

```

Response: GrowthRate
      Df Sum Sq Mean Sq F value Pr(>F)
Treatment  5 4.4743  0.8949  5.5068 0.01722 *
Residuals  8 1.3000  0.1625
---

```

```

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

```

```

> #define appropriate contrasts for all comparisons of the three bd levels
> cm=matrix(c(.5,-.5,0,.5,-.5,0,.5,0,-.5,.5,0,-.5,0,.5,-.5,0,.5,-.5),6,3)
> cm

```

```

      [,1] [,2] [,3]
[1,]  0.5  0.5  0.0
[2,] -0.5  0.0  0.5
[3,]  0.0 -0.5 -0.5
[4,]  0.5  0.5  0.0
[5,] -0.5  0.0  0.5
[6,]  0.0 -0.5 -0.5

```

```

> multcomp(a, cm, "tukey", .9)

```

```

      contrast estimate          lb          ub
1 +(0.5)1-(0.5)2+(0.5)4-(0.5)5      0.2 -0.3251437 0.7251437
2 +(0.5)1-(0.5)3+(0.5)4-(0.5)6      1.3  0.7748563 1.8251437
3 +(0.5)2-(0.5)3+(0.5)5-(0.5)6      1.1  0.6394185 1.5605815

```

```

> multcomp(a, cm, "scheffe", .95)

```

```

      contrast estimate          lb          ub
1 +(0.5)1-(0.5)2+(0.5)4-(0.5)5      0.2 -0.4147778 0.8147778
2 +(0.5)1-(0.5)3+(0.5)4-(0.5)6      1.3  0.6852222 1.9147778
3 +(0.5)2-(0.5)3+(0.5)5-(0.5)6      1.1  0.5608042 1.6391958

```

```

> multcomp(a, cm, "bonf", .95)

```

```

      contrast estimate          lb          ub
1 +(0.5)1-(0.5)2+(0.5)4-(0.5)5      0.2 -0.3152183 0.7152183
2 +(0.5)1-(0.5)3+(0.5)4-(0.5)6      1.3  0.7847817 1.8152183
3 +(0.5)2-(0.5)3+(0.5)5-(0.5)6      1.1  0.6481237 1.5518763

```