

# Analysis of Variance : Chap 5 Review

STAT 701 – Semhar Michael

# Simultaneous Inference and Multiple Comparisons

- ▶ Multiplicity is an intrinsic problem of any simultaneous inference
- ▶ If each of  $k$ , say, null hypotheses is tested at nominal level  $\alpha$  on the same data set, the overall type I error rate can be substantially larger than  $\alpha$ 
  - ▶ *i.e* the probability of at least one erroneous rejection is larger than  $\alpha$  for  $k \geq 2$
- ▶ Simultaneous inference procedures adjust for multiplicity and thus ensure that the overall type I error remains below the pre-specified significance level  $\alpha$

# Multiple comparison

- ▶ The term *multiple comparison* procedure refers to simultaneous inference
  - ▶ *i.e.* simultaneous tests or confidence intervals, where the main interest is in comparing characteristics of different groups represented by a nominal factor

# Revisit Chap 5 - ANOVA

- ▶ Analysis of Variance
  - ▶ the question of interest involves assessing whether certain populations differ in mean value of a single variable
  - ▶ Model  $y_{ijk} = \mu + \gamma_i + \beta_j + (\gamma\beta)_{ij} + \epsilon_{ijk}$

## Revisit Chap 5 - ANOVA - *weightgain* data

The *weightgain* data arise from an experiment to study the gain in weight of rats fed on four different diets, distinguished by - amount of protein (low and high) and - by source of protein (beef and cereal).

Ten rats are randomized to each of the four treatments and the weight gain in grams recorded. The question of interest is **how diet affects weight gain**.

## Revisit Chap 5 - ANOVA - *weightgain* data

```
library(HSAUR3)
```

```
## Loading required package: tools
```

```
data(weightgain)
```

```
head(weightgain)
```

##	source	type	weightgain
## 1	Beef	Low	90
## 2	Beef	Low	76
## 3	Beef	Low	90
## 4	Beef	Low	64
## 5	Beef	Low	86
## 6	Beef	Low	51

## Revisit Chap 5 - ANOVA - *weightgain* data

```
tapply(weightgain$weightgain,  
  list(weightgain$source, weightgain$type), mean)
```

```
##           High  Low  
## Beef      100.0 79.2  
## Cereal    85.9 83.9
```

```
tapply(weightgain$weightgain,  
  list(weightgain$source, weightgain$type), sd)
```

```
##           High      Low  
## Beef      15.13642 13.88684  
## Cereal    15.02184 15.70881
```

# Revisit Chap 5 - ANOVA

- ▶ Analysis of Variance
  - ▶ the question of interest involves assessing whether certain populations differ in mean value of a single variable
  - ▶ Model  $y_{ijk} = \mu + \gamma_i + \beta_j + (\gamma\beta)_{ij} + \epsilon_{ijk}$
- ▶  $y_{ijk}$  represents the  $k$ th measurement made in cell  $(i, j)$  of the factorial design,
- ▶  $\mu$  is the overall mean
- ▶  $\gamma_i$  is the main effect of the first factor
- ▶  $\beta_j$  is the main effect of the second factor
- ▶  $(\gamma\beta)_{ij}$  is the interaction effect of the two factors
- ▶  $\epsilon_{ijk} \sim N(0, \sigma^2)$



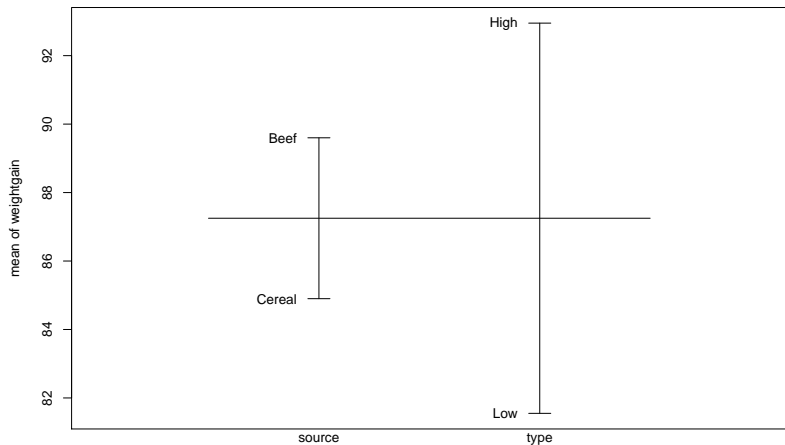
# Revisit Chap 5 - ANOVA

The assumptions made in deriving the F-tests are:

- ▶ The observations are independent of each other,
- ▶ The observations in each cell arise from a population having a normal distribution, and
- ▶ The observations in each cell are from populations having the same variance.

## Revisit Chap 5 - ANOVA - *weightgain* data

```
plot.design(weightgain)
```



Factors

## Revisit Chap 5 - ANOVA - *weightgain* data

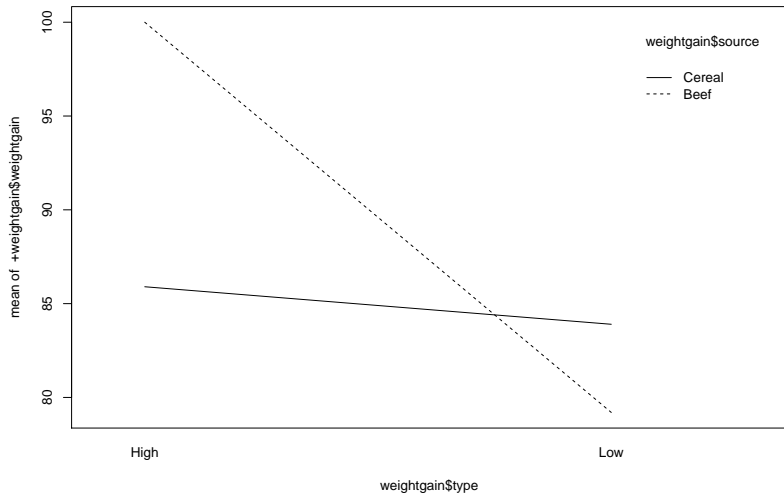
```
wg_aov <- aov(weightgain ~ source * type, data = weightgain)
summary(wg_aov)
```

```
##              Df Sum Sq Mean Sq F value Pr(>F)
## source         1    221   220.9    0.988 0.3269
## type           1   1300  1299.6    5.812 0.0211 *
## source:type     1    884   883.6    3.952 0.0545 .
## Residuals     36   8049   223.6
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

- ▶ Type is significant, source is not and
- ▶ The interaction between the two approaches significance at 0.05 level

## Revisit Chap 5 - ANOVA - *weightgain* data

```
interaction.plot(weightgain$type, weightgain$source,  
+ weightgain$weightgain)
```



## Revisit Chap 5 - ANOVA - *weightgain* data

- ▶ for low-protein diets, the use of cereal as the source of the protein leads to a greater weight gain than using beef. For high-protein diets the reverse is the case with the beef/high diet leading to the highest weight gain.

## Revisit Chap 5 - ANOVA - *weightgain* data

```
coef(wg_aov)
```

```
##           (Intercept)           sourceCereal           t
##              100.0              -14.1
## sourceCereal:typeLow
##              18.8
```

## Revisit Chap 5 - ANOVA - *weightgain* data

The significant type-source interaction found in the two-way analysis of variance of the data along with the associated interaction plot demonstrates that for low-protein diets the use of cereal as the source of protein leads to greater weight gain than using beef; for high protein diets the reverse is the case with the beef-high diet leading to the highest weight gain

## Revisit Chap 5 - ANOVA - *foster* data

- ▶ The *foster* data (Hand et al., 1994) are from a foster feeding experiment with rat mothers and litters of four different genotypes: A, B, I and J .
- ▶ The measurement is the litter weight (in grams) after a trial feeding period.
- ▶ Here the investigator's interest lies in uncovering the effect of genotype of mother and litter on litter weight.



## Revisit Chap 5 - ANOVA - *foster* data

```
data(foster)
head(foster, n = 4)
```

```
##    litgen motgen weight
## 1      A      A   61.5
## 2      A      A   68.2
## 3      A      A   64.0
## 4      A      A   65.0
```

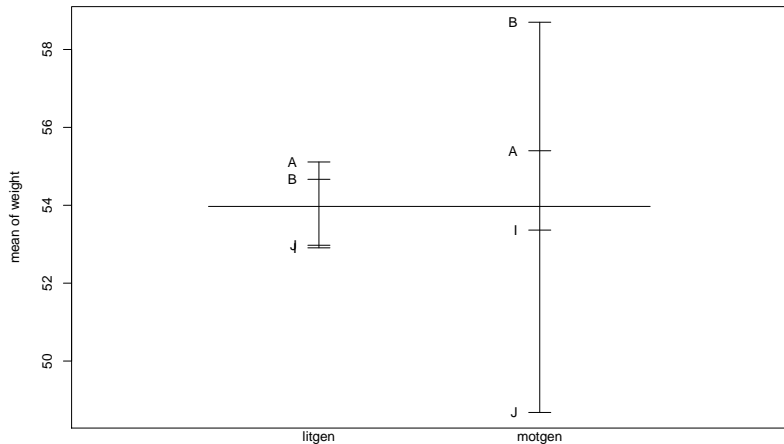
```
table(foster$litgen, foster$motgen)
```

```
##
##      A B I J
## A  5 3 4 5
## B  4 5 4 2
## I  3 3 5 3
## J  4 3 3 5
```

## Revisit Chap 5 - ANOVA - *foster* data

- ▶ differences in litter weight for the four levels of mother's genotype are substantial; the corresponding differences for the genotype of the litter are much smaller.

```
plot.design(foster)
```



## Revisit Chap 5 - ANOVA - *foster* data

```
summary(aov(weight ~ litgen * motgen, data = foster))
```

```
##              Df Sum Sq Mean Sq F value    Pr(>F)
## litgen         3   60.2    20.05    0.370 0.77522
## motgen         3  775.1   258.36    4.763 0.00574 **
## litgen:motgen   9  824.1    91.56    1.688 0.12005
## Residuals     45 2440.8    54.24
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1
```

- indicates that the main effect of mother's genotype is highly significant

## Revisit Chap 5 - ANOVA - *foster* data

Investigate the effect of genotype  $B$  on litter weight in more detail by the use of multiple comparison procedures (see Everitt, 1996, and Chapter 14).

- ▶ Such procedures allow a comparison of all pairs of levels of a factor whilst maintaining the nominal significance level at its specified value and producing adjusted confidence intervals for mean differences. One such procedure is called *Tukey honest significant differences* suggested by Tukey (1953)

## Revisit Chap 5 - ANOVA - *foster* data

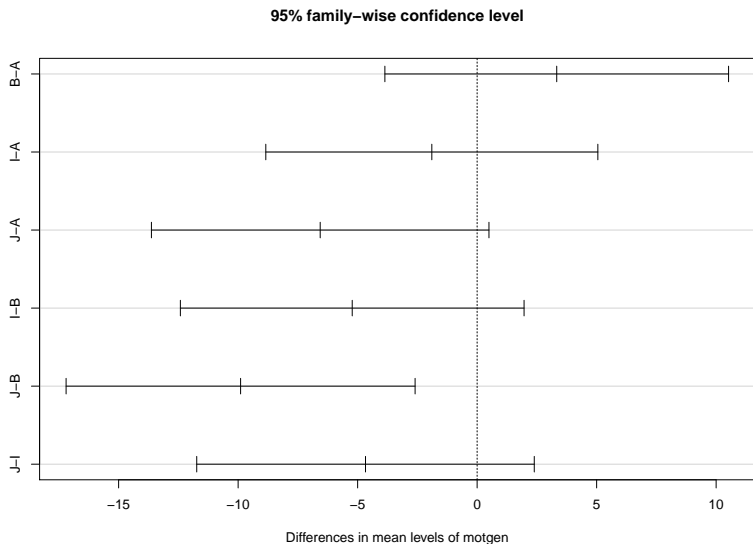
- Here, we are interested in simultaneous confidence intervals for the weight differences between all four genotypes of the mother.

```
foster_aov <- aov(weight ~ litgen * motgen, data = foster)
foster_hsd <- TukeyHSD(foster_aov, "motgen")
foster_hsd
```

```
##      Tukey multiple comparisons of means
##      95% family-wise confidence level
##
## Fit: aov(formula = weight ~ litgen * motgen, data = foster)
##
## $motgen
##           diff          lwr          upr      p adj
## B-A  3.330369  -3.859729  10.5204672  0.6078581
## I-A -1.895574  -8.841869   5.0507207  0.8853702
## J-A -6.566168 -13.627285   0.4949498  0.0767540
## I-B -5.225943 -12.416041   1.9641552  0.2266493
## J-B -9.896537 -17.197624  -2.5954489  0.0040509
## J-I -4.670593 -11.731711   2.3905240  0.3035490
```

# Revisit Chap 5 - ANOVA - *foster* data

```
plot(foster_hsd)
```



## Revisit Chap 5 - ANOVA - *foster* data

- ▶ Analysis of variance indicates that the effect of mother's genotype on weight is highly significant. Detailed investigation of the mother's genotype effect by using Tukey honest significant difference multiple comparison test suggest that the effect is largely produced by the difference between the *J* and *B* genotypes with the population mean of the former being between about 3 and 17 grams lower than the latter.
- ▶ Care needs to be taken when using Tukey's HSD on unbalanced data.

# Back to Chap 15