ANOVA

sn

2024-05-20

1. Null Hypothesis: There is no difference between any of the groups.

2. F = between-group variability/within-group variability

3. Types of ANOVA:

1-way ANOVA: 1 factor (e.g. effect of 3 doses of a drug on heart rate)

2-way ANOVA: 2 factors (e.g. effect of age and sex on salary)

3-way ANOVA: 3 factors (e.g. effect of age, sex and education on salary)

4. Assumptions for ANOVA:

i.Independent random sampling

ii.Normality of residuals (distances from group mean)

model <- aov(grade ~ attendance * previous_grades, data = class)

* is for model with interaction; + is for model without interaction

method1:hist(resid(model), main = "residuals")

method2:plot(model, 2)

method3:Shapiro-Wilk test

iii.Equality of Variances

plot(model, 1)

5. ANOVA test

summary(model)

6. What groups exactly are different?

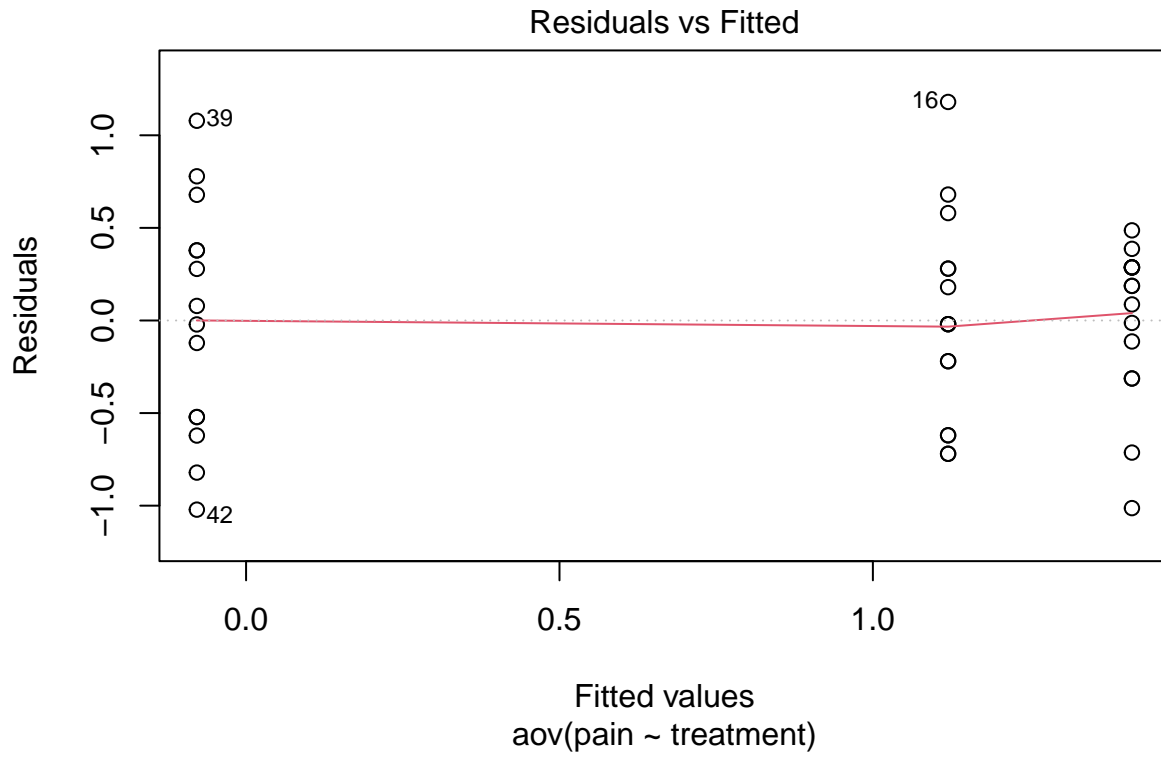TukeyHSD(model)

P1. Drug trial dataset

H0: There is no effect of treatment types on pain.

HA: At least one of those factors (placebo or drugA or drugB) influences pain.

```
# 1.Independent random sampling:yes
# 2.Normality of residuals:yes
drugmodel = aov(pain~treatment, data = trial)
plot(drugmodel, 2)
```


Q–Q Residuals
Theoretical Quantiles
aov(pain ~ treatment)
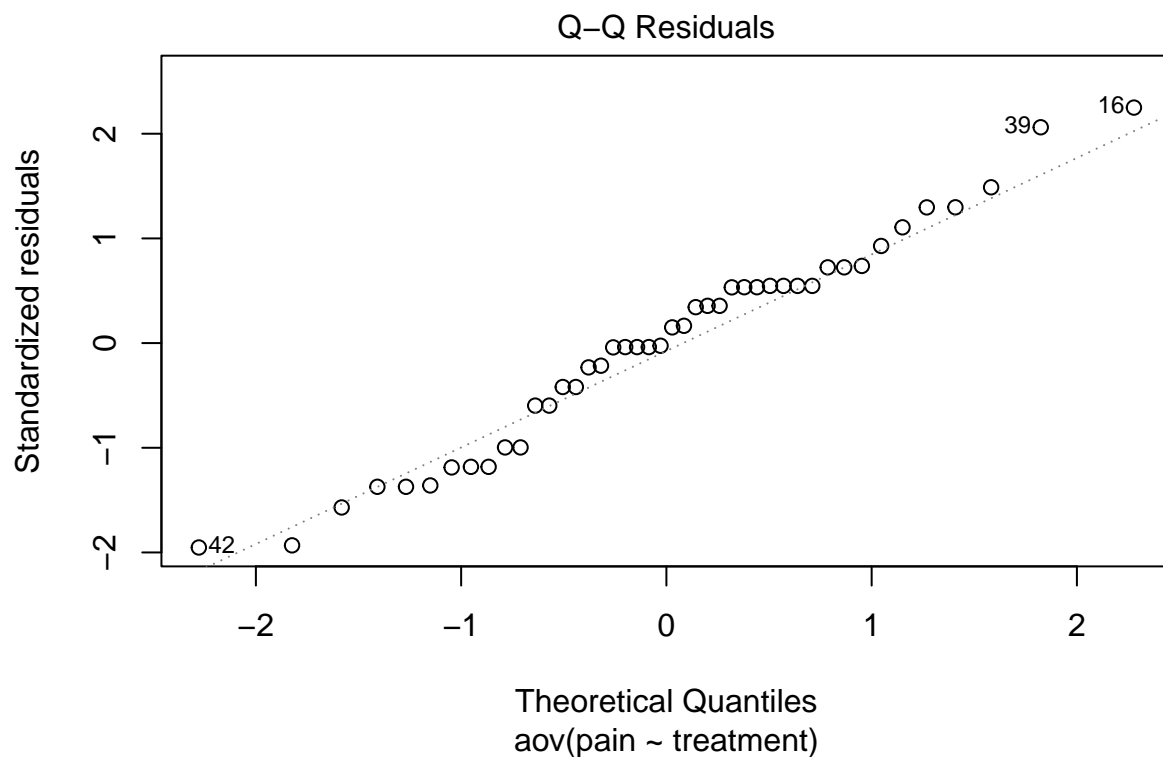
```
# 3.Equality of Variances:yes
plot(drugmodel, 1) #"Residuals vs Fitted" plot, looking for similar heights of "columns"
```

Residuals vs Fitted

Fitted values
aov(pain ~ treatment)

```r
#perform ANOVA
summary(drugmodel)
```

```
##             Df Sum Sq Mean Sq F value   Pr(>F)
## treatment    2  17.92   8.960    30.4 8.01e-09 ***
## Residuals   41  12.09   0.295
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
#Run a post-hoc test
TukeyHSD(drugmodel)
```

```
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = pain ~ treatment, data = trial)
##
## $treatment
##                    diff        lwr        upr     p adj
## drugB-drugA   -1.1985714 -1.6891632 -0.7079797 0.0000016
## placebo-drugA  0.2933333 -0.1887258  0.7753924 0.3110505
## placebo-drugB  1.4919048  1.0013130  1.9824965 0.0000000
```

P2. Weight loss in mice

H0: There is no effect of genotypes on weight_gain.

HA: At least one of those genotypes (AA or AB or BB) influences weight_gain.

```
#visualise
p <- ggplot(data = mouse, aes(x = genotype, y = weight_gain, fill = diet))
p + geom_boxplot()
```
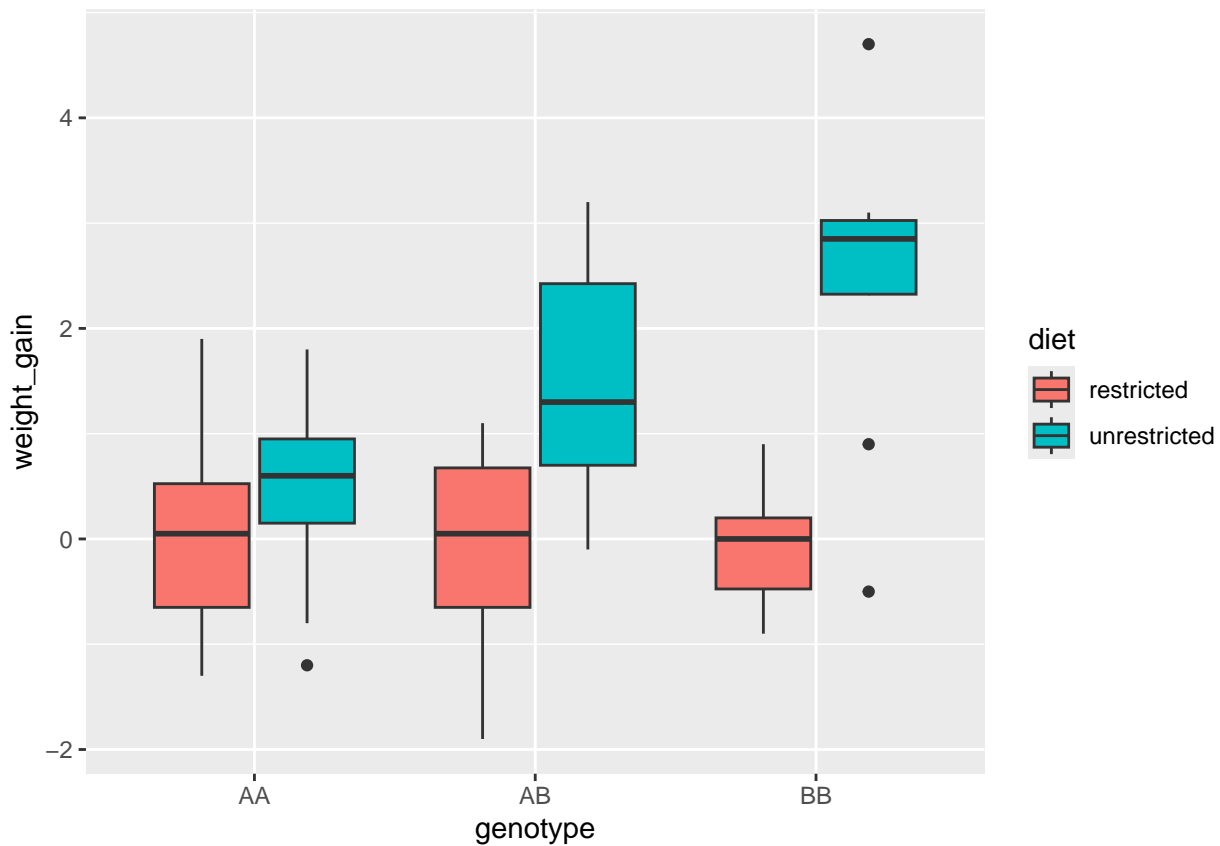


```
# prepare model
mousemodel = aov(weight_gain~genotype * diet, data = mouse)

#check normality of residuals:yes
shapiro.test(resid(mousemodel))
```

```
##
##  Shapiro-Wilk normality test
##
## data:  resid(mousemodel)
## W = 0.98974, p-value = 0.7851
```

```
#check equality of Variances:yes
plot(mousemodel, 1)
```

Residuals vs Fitted

Fitted values
aov(weight_gain ~ genotype * diet)
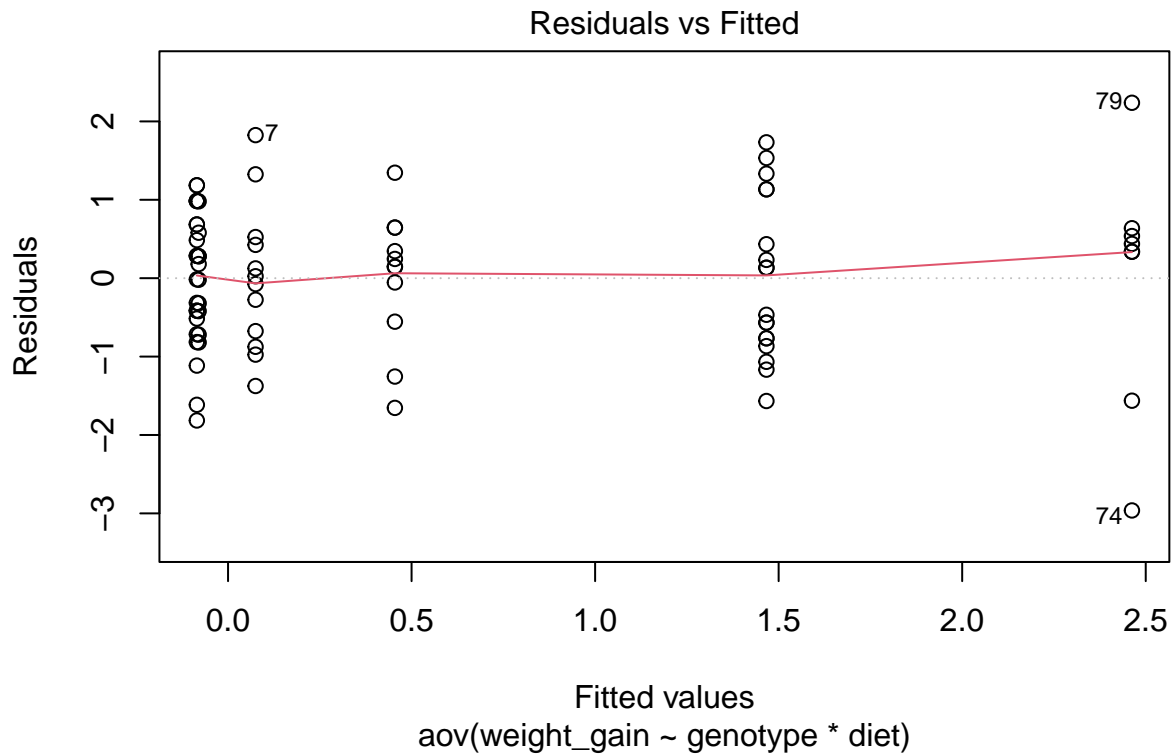
```
#perform ANOVA
summary(mousemodel)
```

```
##               Df Sum Sq Mean Sq F value   Pr(>F)
## genotype       2   6.40    3.20   3.276  0.04342 *
## diet           1  40.39   40.39  41.362 1.16e-08 ***
## genotype:diet  2  11.97    5.99   6.130  0.00346 **
## Residuals     73  71.29    0.98
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#Run a post-hoc test
TukeyHSD(mousemodel)
```

```
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = weight_gain ~ genotype * diet, data = mouse)
##
## $genotype
##            diff       lwr      upr     p adj
```

```
## AB-AA 0.3934783 -0.2311222 1.018079 0.2935392
## BB-AA 0.7934783  0.0494578 1.537499 0.0338875
## BB-AB 0.4000000 -0.2764864 1.076486 0.3387304
##
## $diet
##                          diff       lwr      upr p adj
## unrestricted-restricted 1.432486 0.9884195 1.876552     0
##
## $`genotype:diet`
##                                   diff         lwr        upr     p adj
## AB:restricted-AA:restricted    -0.1600000 -1.21611661 0.8961166 0.9977516
## BB:restricted-AA:restricted    -0.1550000 -1.39340649 1.0834065 0.9991025
## AA:unrestricted-AA:restricted   0.3795455 -0.82776637 1.5868573 0.9401208
## AB:unrestricted-AA:restricted   1.3916667  0.31377217 2.4695612 0.0041690
## BB:unrestricted-AA:restricted   2.3875000  1.06735424 3.7076458 0.0000176
## BB:restricted-AB:restricted     0.0050000 -1.11518082 1.1251808 1.0000000
## AA:unrestricted-AB:restricted   0.5395455 -0.54615997 1.6252509 0.6937938
## AB:unrestricted-AB:restricted   1.5516667  0.61198003 2.4913533 0.0001032
## BB:unrestricted-AB:restricted   2.5475000  1.33756643 3.7574336 0.0000005
## AA:unrestricted-BB:restricted   0.5345455 -0.72918895 1.7982799 0.8167215
## AB:unrestricted-BB:restricted   1.5466667  0.40593036 2.6874030 0.0022395
## BB:unrestricted-BB:restricted   2.5425000  1.17056429 3.9144357 0.0000105
## AB:unrestricted-AA:unrestricted 1.0121212 -0.09478011 2.1190225 0.0925815
## BB:unrestricted-AA:unrestricted 2.0079545  0.66402047 3.3518886 0.0005552
## BB:unrestricted-AB:unrestricted 0.9958333 -0.23315548 2.2248221 0.1800034
```

#A allele is related to weight gain