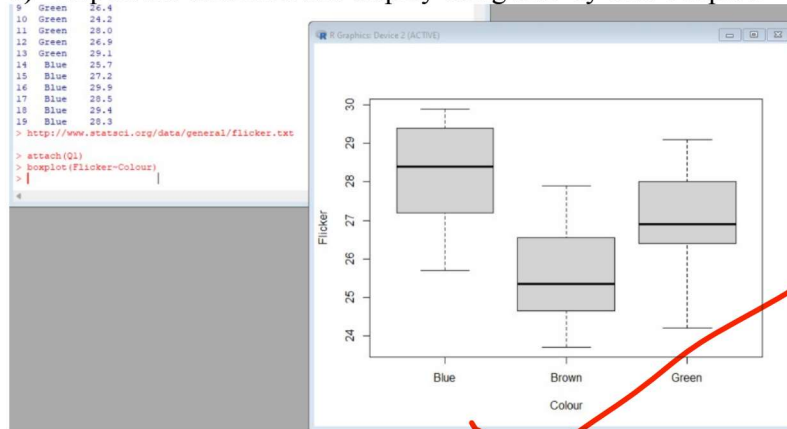




Q.N. 1) The dataset <http://www.statsci.org/data/general/flicker.txt> measures the critical flicker frequency for 19 subjects with different eye colors.

a) Import the data in R and display using side-by-side boxplot.



b) Fit a linear model to estimate the value of the parameters  $\mu, \tau_2, \tau_3$ .

$\mu = 28.167$

$\tau_2 = -2.579$

$\tau_3 = -1.247$

c) Print the *anova()* of the model developed in part (b) # use options (*show.signif.stars=FALSE*)

```
> options (show.signif.stars=FALSE)
> anova(model)
Error in anova(model) : could not find function "anova"
> anova(model)
Analysis of Variance Table

Response: Flicker
      Df Sum Sq Mean Sq F value    Pr(>F)
Colour  2  22.997  11.4986   4.8023 0.02325
Residuals 16  38.310   2.3944
> |
```

d) Fit analysis of variance model fit using aov function

```
> fit=aov(Flicker~Colour)
> fit
Call:
aov(formula = Flicker ~ Colour)

Terms:
              Colour Residuals
Sum of Squares  22.99729  38.31008
Deg. of Freedom      2       16

Residual standard error: 1.547378
Estimated effects may be unbalanced
```

e) Calculate the values of the means using `>model.tables(fit, type= "means")`

```

> model.tables(fit,type="mean")
Tables of means
Grand mean

26.75263

Colour
  Blue Brown Green
28.17 25.59 26.92
rep  6.00  8.00  5.00
> |

```

f) Perform the Tukey HSD test to determine which pair are different.

```

> TukeyHSD(fit)
Tukey multiple comparisons of means
 95% family-wise confidence level

Fit: aov(formula = Flicker ~ Colour)

$Colour
      diff      lwr      upr    p adj
Brown-Blue -2.579167 -4.7354973 -0.422836 0.0183579
Green-Blue  -1.246667 -3.6643959  1.171063 0.3994319
Green-Brown  1.332500 -0.9437168  3.608717 0.3124225

```

Brown and Blue are different

Q. N. 2) The survival times in unites of 10 hours for animals exposed to four different poisons are provided in the link

<https://raw.githubusercontent.com/mariarizzo/RbyExample/master/Rx-data/poison.csv>

a) Import the data in R and fit a two-way ANOVA model

```

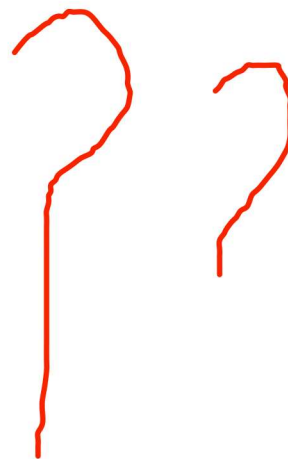
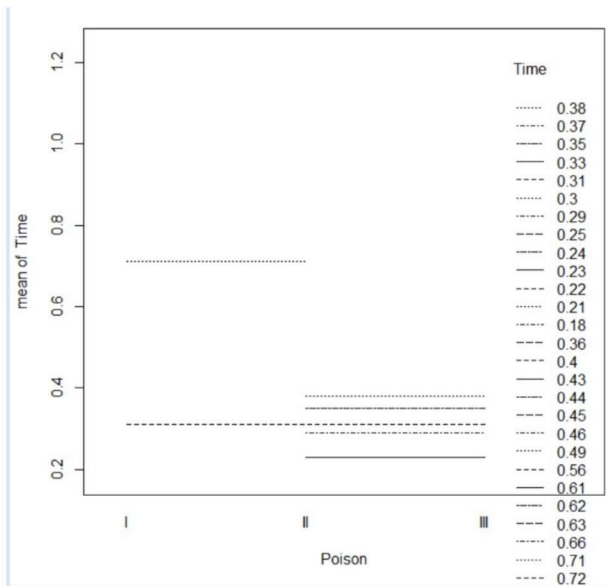
> attach(Q2)
> table(Treatment)
Treatment
 A  B  C  D
12 12 12 12
> table(Treatment)
Treatment
 A  B  C  D
12 12 12 12
> fit=aov(Time~Poison*Treatment)
> fit
Call:
aov(formula = Time ~ Poison * Treatment)

Terms:
              Poison Treatment Poison:Treatment Residuals
Sum of Squares  1.0370792 0.9201167           0.2502708 0.8001000
Deg. of Freedom      2         3              6         36

Residual standard error: 0.1490805
Estimated effects may be unbalanced
> |

```

b) Draw the interaction plots using > interaction.plot(Poison,Treatment, response=Time)



c) Calculate value of the means using `>model.tables (model, type= "means")`

```
> model.tables(fit,type="means")
Tables of means
Grand mean

0.4791667

Poison
Poison
  I    II   III
0.6175 0.5444 0.2756

Treatment
Treatment
  A    B    C    D
0.3142 0.6767 0.3925 0.5333

Poison:Treatment
Treatment
Poison A    B    C    D
  I    0.4125 0.8800 0.5675 0.6100
  II   0.3200 0.8150 0.3750 0.6675
  III  0.2100 0.3350 0.2350 0.3225
> |
```

d) Perform TukeyHSD `> TukeyHSD(model, which=c("Posion","Treatment"))`

```
> TukeyHSD(fit, which=c("Poison", "Treatment"))
Tukey multiple comparisons of means
95% family-wise confidence level

Fit: aov(formula = Time ~ Poison * Treatment)

$Poison
      diff      lwr      upr    p adj
II-I  -0.073125 -0.2019588  0.05570882 0.3580369
III-I  -0.341875 -0.4707088 -0.21304118 0.0000005
III-II -0.268750 -0.3975838 -0.13991618 0.0000325

$Treatment
      diff      lwr      upr    p adj
B-A  0.36250000  0.19858517  0.5264148 0.0000046
C-A  0.07833333 -0.08558150  0.2422482 0.5769172
D-A  0.21916667  0.05525184  0.3830815 0.0050213
C-B -0.28416667 -0.44808150 -0.1202518 0.0002320
D-B -0.14333333 -0.30724816  0.0205815 0.1045211
D-C  0.14083333 -0.02308150  0.3047482 0.1136890
```

e) Perform pairwise.t.test (Time, Poison)

```
> pairwise.t.test(Time, Poison)

Pairwise comparisons using t tests with pooled SD

data: Time and Poison

      I      II
II  0.3282  -
III 9.6e-05 0.0014

P value adjustment method: holm
```

Only 0.0014 is smaller than 0.05, which means there is significant difference between II and III