ANOVA

Flicker data: Measures of ‘critical flicker frequency’ for 19 subjects with different eye colors. An individual’s “critical flicker frequency is the highest frequency at which the flicker in a flickering light source can be detected. At frequencies above critical frequency, light source appears to be continuous”

(a)

Brown	Green	Blue
26.8	26.4	25.7
27.9	24.2	27.2
23.7	28.0	29.9
25.0	26.9	28.5
26.3	29.1	29.4
24.8		28.3
25.7		
24.5		

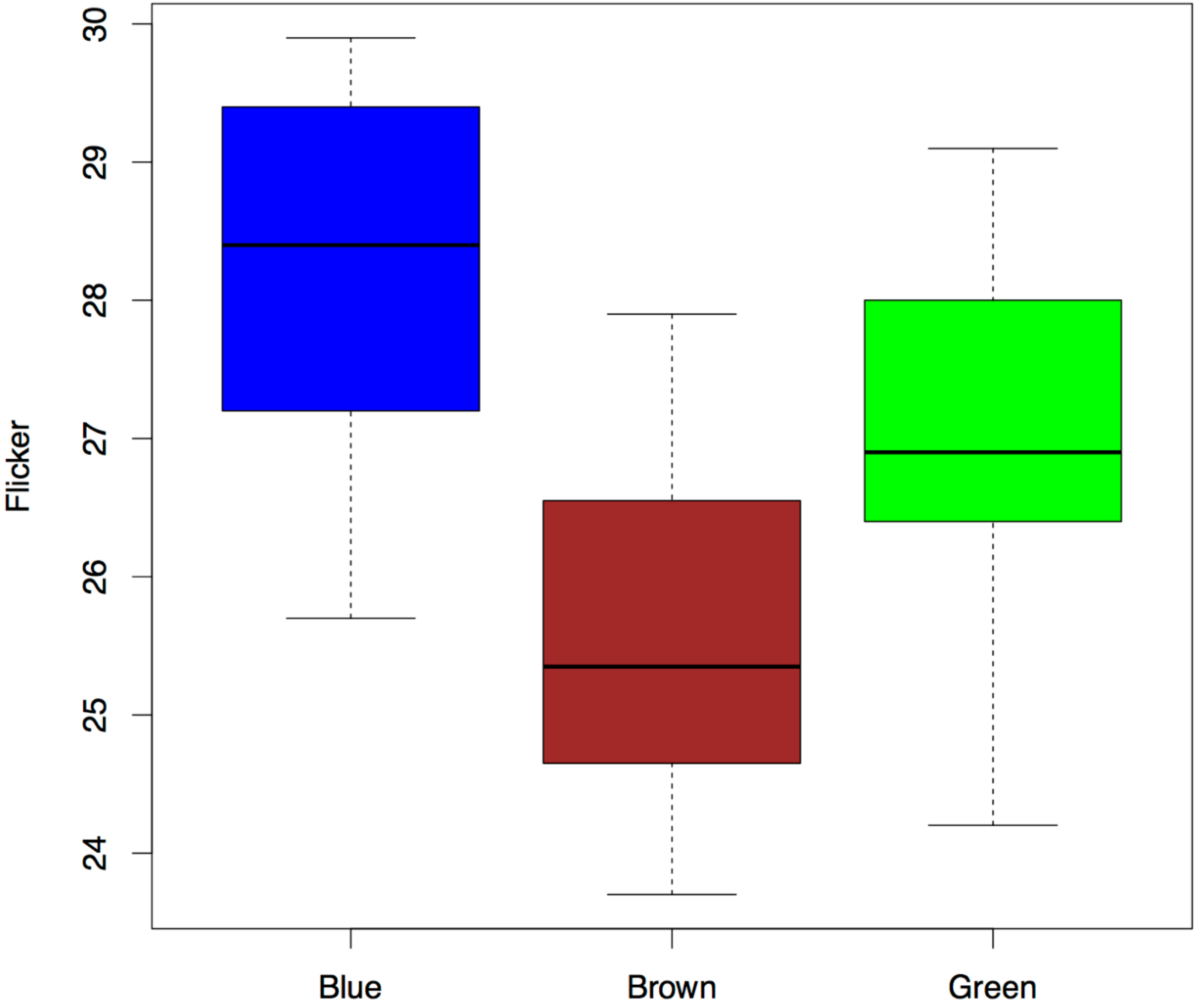
(b)

Colour	Flicker
Brown	26.8
Brown	27.9
Brown	23.7
Brown	25.0
Brown	26.3
Brown	24.8
Brown	25.7
Brown	24.5
Green	26.4
Green	24.2
Green	28.0
Green	26.9
Green	29.1
Blue	25.7
Blue	27.2
Blue	29.9
Blue	28.5
Blue	29.4
Blue	28.3

ANOVA

```
> flicker = read.table(file=
+"http://www.statsci.org/data/general/flicker.txt",
+ header=TRUE,stringsAsFactors=TRUE)
> is.factor(flicker$Colour)
[1] TRUE
> levels(flicker$Colour)
[1] "Blue"  "Brown" "Green"
> unclass(flicker$Colour)
 [1] 2 2 2 2 2 2 2 2 3 3 3 3 3 1 1 1 1 1 1
attr(,"levels")
[1] "Blue"  "Brown" "Green"

> attach(flicker)
> colors_flicker=c('Blue','Brown','Green')
> boxplot(Flicker ~ Colour, ylab=“Flicker”,
col=colors_flicker)
```

ANOVA



ANOVA

```
> meansd = function(x) c(mean=mean(x), sd=sd(x))
> by(Flicker, Colour, FUN=meansd)
Colour: Blue
     mean        sd
28.166667  1.527962
----------------------------------------------------------------
Colour: Brown
     mean        sd
25.587500  1.365323
----------------------------------------------------------------
Colour: Green
     mean        sd
26.920000  1.843095

> oneway.test(Flicker ~ Colour)

   One-way analysis of means (not assuming equal variances)

data:  Flicker and Colour
F = 5.0505, num df = 2.0000, denom df = 8.9259, p-value = 0.03412
```

we can also use `var.equal=TRUE`
in such case p-value=.02325

ANOVA

```
> L = lm(Flicker ~ Colour)
> summary(L)

Call:
lm(formula = Flicker ~ Colour)

Residuals:
    Min      1Q  Median      3Q     Max
-2.7200 -0.8771  0.1125  1.1462  2.3125
```

ColourBlue

```
Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  28.1667     0.6317  44.588  < 2e-16
ColourBrown  -2.5792     0.8357  -3.086  0.00708
ColourGreen  -1.2467     0.9370  -1.331  0.20200

Residual standard error: 1.547 on 16 degrees of freedom
Multiple R-squared:  0.3751, Adjusted R-squared:  0.297
F-statistic: 4.802 on 2 and 16 DF,  p-value: 0.02325
```

ANOVA

```
> model.matrix(L)
   (Intercept) ColourBrown ColourGreen
1            1           1           0
2            1           1           0
3            1           1           0
4            1           1           0
5            1           1           0
6            1           1           0
7            1           1           0
8            1           1           0
9            1           0           1
10           1           0           1
11           1           0           1
12           1           0           1
13           1           0           1
14           1           0           0
15           1           0           0
16           1           0           0
17           1           0           0
18           1           0           0
19           1           0           0
```

ANOVA

```
> M = aov(Flicker ~ Colour)
> model.tables(M, type="means")
Tables of means
Grand mean

26.75263

 Colour
     Blue Brown Green
    28.17 25.59 26.92
rep  6.00  8.00  5.00
> model.tables(M)
Tables of effects

 Colour
     Blue  Brown   Green
    1.414 -1.165 0.1674
rep 6.000  8.000 5.0000
```

ANOVA

```
> anova(L)
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
```

- Residual mean square error is equal to the square residual standard error of the linear model, i.e., (1.547)^2 = 2.39

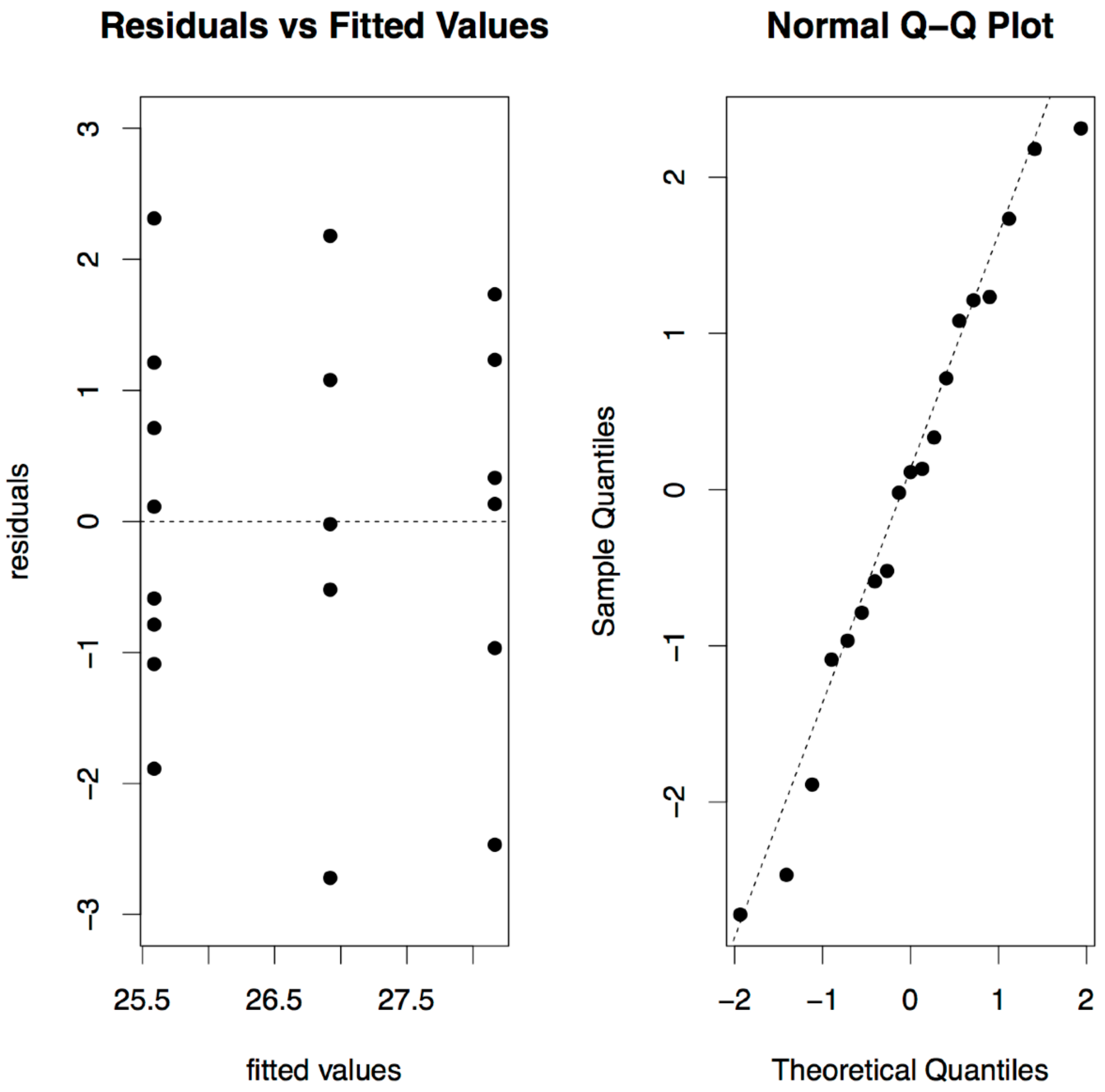
ANOVA

```
> L1=lm(Flicker ~ Colour - 1)
> summary(L1)

Call:
lm(formula = Flicker ~ Colour - 1)

Residuals:
    Min      1Q  Median      3Q     Max 
-2.7200 -0.8771  0.1125  1.1462  2.3125 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
ColourBlue   28.1667     0.6317   44.59   <2e-16
ColourBrown  25.5875     0.5471   46.77   <2e-16
ColourGreen  26.9200     0.6920   38.90   <2e-16

Residual standard error: 1.547 on 16 degrees of freedom
Multiple R-squared:  0.9972,Adjusted R-squared:  0.9967 
F-statistic:  1896 on 3 and 16 DF,  p-value: < 2.2e-16
```

Careful with the interpretation of the F test and R^2 in this case!

ANOVA

```
> plot(L$fit, L$res,pch=19,xlab="fitted values",ylab="residuals",
+       main="Residuals vs Fitted Values",ylim=c(-3,3))
> abline(h=0,lty=2)
> qqnorm(L$res,pch=19)
> qqline(L$res,lty=2)
```



ANOVA

Comparison of treatment means

- Fisher’s least significant difference:

$$H_0 : \mu_i = \mu_j \quad vs \quad H_1 : \mu_i \neq \mu_j , \quad 1 \leq i < j \leq a$$

$$T = \frac{\bar{y}_i - \bar{y}_j}{\sqrt{MSE \left(\frac{1}{n_i} + \frac{1}{n_j} \right)}}$$

Under the null hypothesis this is distributed according to a Student-t distribution with $N - a$ with $N = \sum_{i=1}^{a} n_i$

Then, the least significant difference is defined as:

$$LSD = t_{N-a}^{\alpha/2} \sqrt{MSE \left(\frac{1}{n_i} + \frac{1}{n_j} \right)}$$

ANOVA

Then, the pair of means for groups i and j are significantly different if $|\bar{y}_i - \bar{y}_j| > LSD$

```
> MSE = 2.3944
> t97.5 = qt(.975, df=16) #97.5th percentile of t
> n = table(Colour) #sample sizes
> means = by(Flicker, Colour, mean) #treatment means
> outer(means, means, "-")
       Colour
Colour       Blue    Brown     Green
  Blue   0.000000 2.579167  1.246667
  Brown -2.579167 0.000000 -1.332500
  Green -1.246667 1.332500  0.000000
```

```
> n
Colour
 Blue Brown Green
    6     8     5
```

ANOVA

```
> t97.5 * sqrt(MSE * outer(1/n, 1/n, "+"))
       Colour
Colour      Blue    Brown    Green
  Blue  1.893888 1.771570 1.986326
  Brown 1.771570 1.640155 1.870064
  Green 1.986326 1.870064 2.074650
```

Then,

Pair	diff	LSD
Blue-Brown	2.5792	1.7716
Blue-Green	1.2467	1.9863
Brown-Green	-1.3325	1.8701

Problem: Multiple testing. You may reject the null when it is true. Use this only after F-test

ANOVA

- The function `pairwise.t.test` summarizes pairwise t-test with p-values adjusted to control for the type 1 error rate:

```
> pairwise.t.test(Flicker, Colour)

  Pairwise comparisons using t tests with pooled SD

data:  Flicker and Colour

      Blue  Brown
Brown 0.021 -
Green 0.301 0.301

P value adjustment method: holm
```

- You can customize the p-value adjustment method using p.adjust, available options: `holm`, `hochberg`, `hommel`, `bonferroni`, `BH`, `BY`, `fdr`, or `none`

ANOVA

```
> pairwise.t.test(Flicker, Colour, p.adjust="none")

  Pairwise comparisons using t tests with pooled SD

data:  Flicker and Colour

      Blue   Brown
Brown 0.0071 -
Green 0.2020 0.1504

P value adjustment method: none
> pairwise.t.test(Flicker, Colour, p.adjust="bonferroni")

  Pairwise comparisons using t tests with pooled SD

data:  Flicker and Colour

      Blue  Brown
Brown 0.021 -
Green 0.606 0.451

P value adjustment method: bonferroni
```

ANOVA

- Tuckey's multiple comparisons method: based on the range. The studentized range statistic is given by:

$$q = \frac{\bar{y}_{max} - \bar{y}_{min}}{\sqrt{\frac{MSE}{n}}}$$

We need to compute

Quantile of the studentized-range distribution

$$w = q_{\alpha}(a, df)\sqrt{\frac{MSE}{n}}$$

with a the number of treatments, n the group sample size and df the degrees of freedom for the error. Then,

$$\left|\bar{y}_i - \bar{y}_j\right| > w$$

For unequal group sizes use the Tukey-Kramer method with

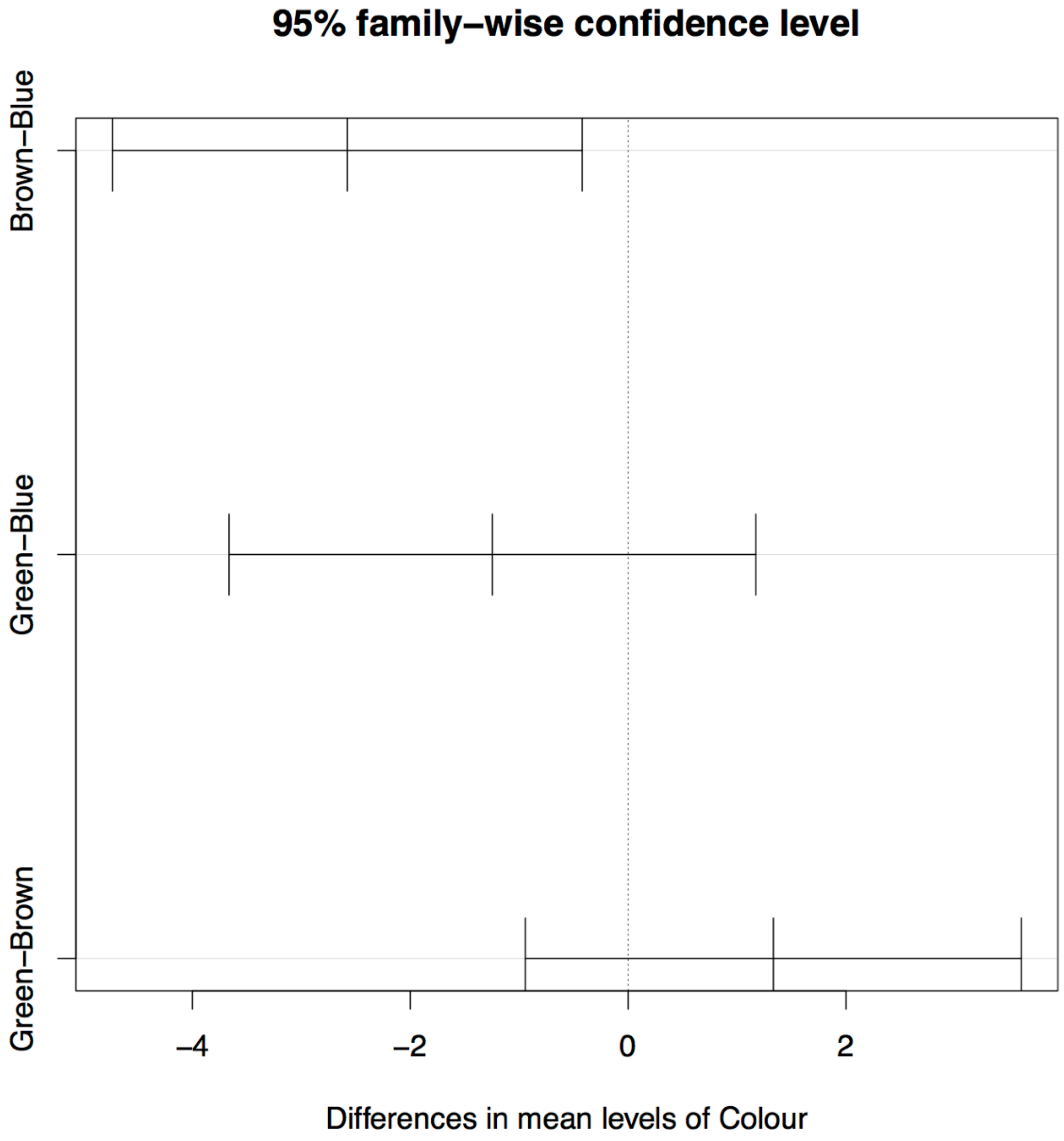
ANOVA

$$w = q_\alpha(a, df)\sqrt{\frac{MSE}{2}\left(\frac{1}{n_i} + \frac{1}{n_j}\right)}$$

Tukey’s multiple comparison procedure is sometimes called “Tukey’s Honest Significant Difference” (`TukeyHSD`)

```
> qtukey(.95, nmeans=3, df=16)
[1] 3.649139
> M=aov(L)
> TukeyHSD(M)
  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
```

ANOVA


95% family–wise confidence level
Brown–Blue
Green–Blue
Green–Brown
−4
−2
0
2
Differences in mean levels of Colour

Randomized block model

Randomized block designs: We want to model the effect of a treatment or factor when the samples are not independent.

Example, Exam Scores: Exam scores in five subjects for 88 students. A one-way ANOVA is not appropriate: exam scores for each subject are not independent given that the same 88 students took each exam. We want to incorporate the effect of the student in the model in order to appropriately study the factor (exam topics).

```
> library(bootstrap)
> head(scor)
  mec vec alg ana sta
1  77  82  67  67  81
2  63  78  80  70  81
3  75  73  71  66  81
4  55  72  63  70  68
5  63  63  65  70  63
6  53  61  72  64  73
```

Mechanics: Closed book

Vectors: Closed book

Algebra: Open book

Analysis: Open book

Statistics: Open book

Randomized block model

```
> sapply(scor, mean, data=scor)
     mec      vec      alg      ana      sta 
38.95455 50.59091 50.60227 46.68182 42.30682 
> scor.long = stack(scor)
> block = factor(rep(1:88, times=5))
> scor.long = data.frame(scor.long, block)
> head(scor.long) #top
  values ind block
1     77 mec     1
2     63 mec     2
3     75 mec     3
4     55 mec     4
5     63 mec     5
6     53 mec     6
> tail(scor.long) #bottom
    values ind block
435     18 sta    83
436     17 sta    84
437     18 sta    85
438     21 sta    86
439     20 sta    87
440     14 sta    88
```

Randomized block model

```
> names(scor.long) = c("score", "exam", "student")
> str(scor.long)
'data.frame':440 obs. of  3 variables:
 $ score  : num  77 63 75 55 63 53 51 59 62 64 ...
 $ exam   : Factor w/ 5 levels "alg","ana","mec",..: 3 3 3 3 3 3 3
3 3 3 ...
 $ student: Factor w/ 88 levels "1","2","3","4",..: 1 2 3 4 5 6 7
8 9 10 ...
```

Model:

type of exam

$$y_{i,j} = \mu + \overset{\downarrow}{\alpha_i} + \underset{\uparrow}{\beta_j} + \epsilon_{i,j}$$

student effect

Randomized block model

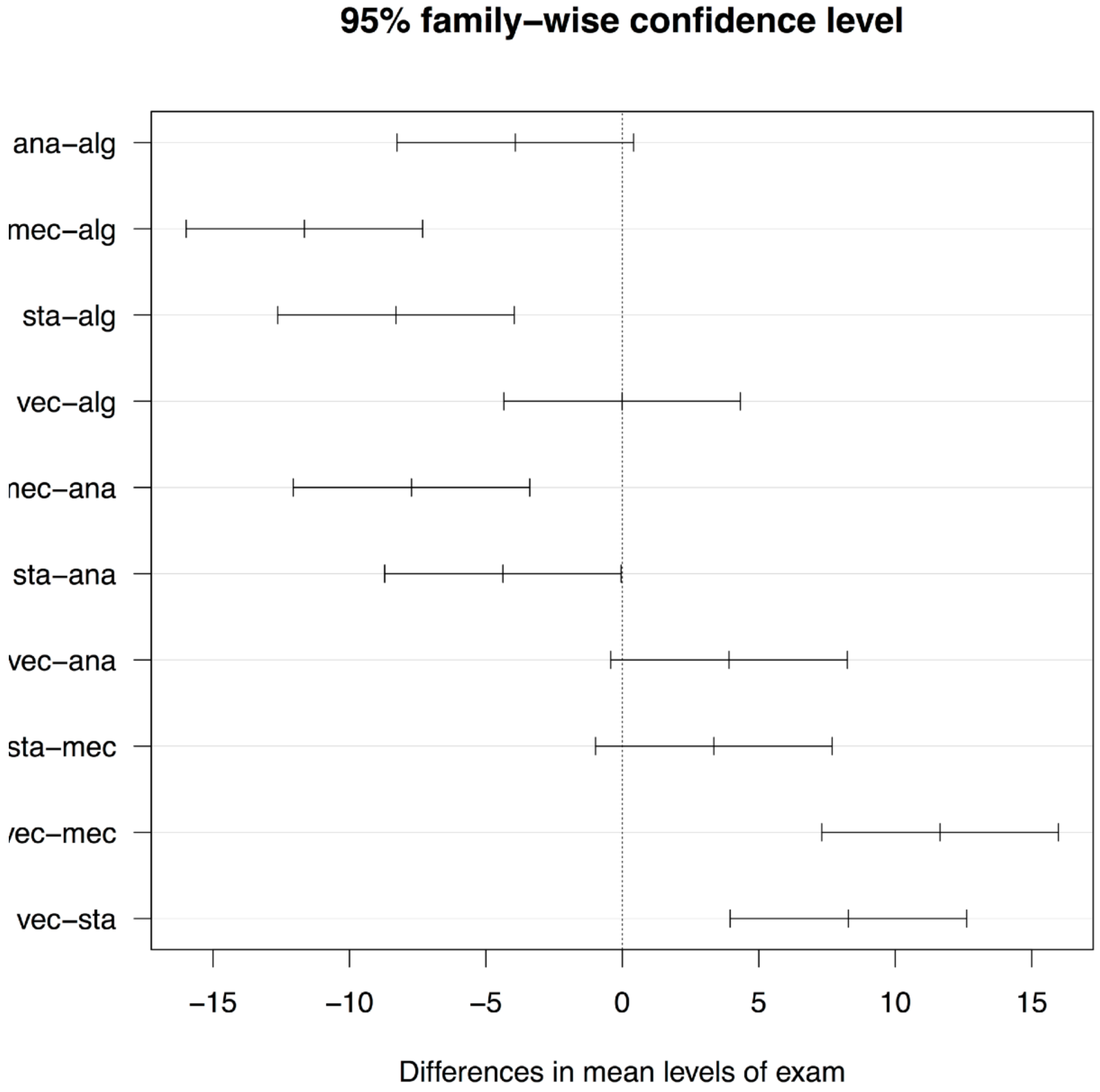
```
> L = aov(score ~ exam + student, data=scor.long)
> summary(L)
             Df Sum Sq Mean Sq F value   Pr(>F)    
exam          4   9315  2328.7  21.201 1.16e-15 ***
student      87  58313   670.3   6.102  < 2e-16 ***
Residuals   348  38225   109.8                     
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

```
> model.tables(L, cterms="exam")
Tables of effects
 exam 
exam
   alg    ana    mec    sta    vec 
 4.775  0.855 -6.873 -3.520  4.764 
```

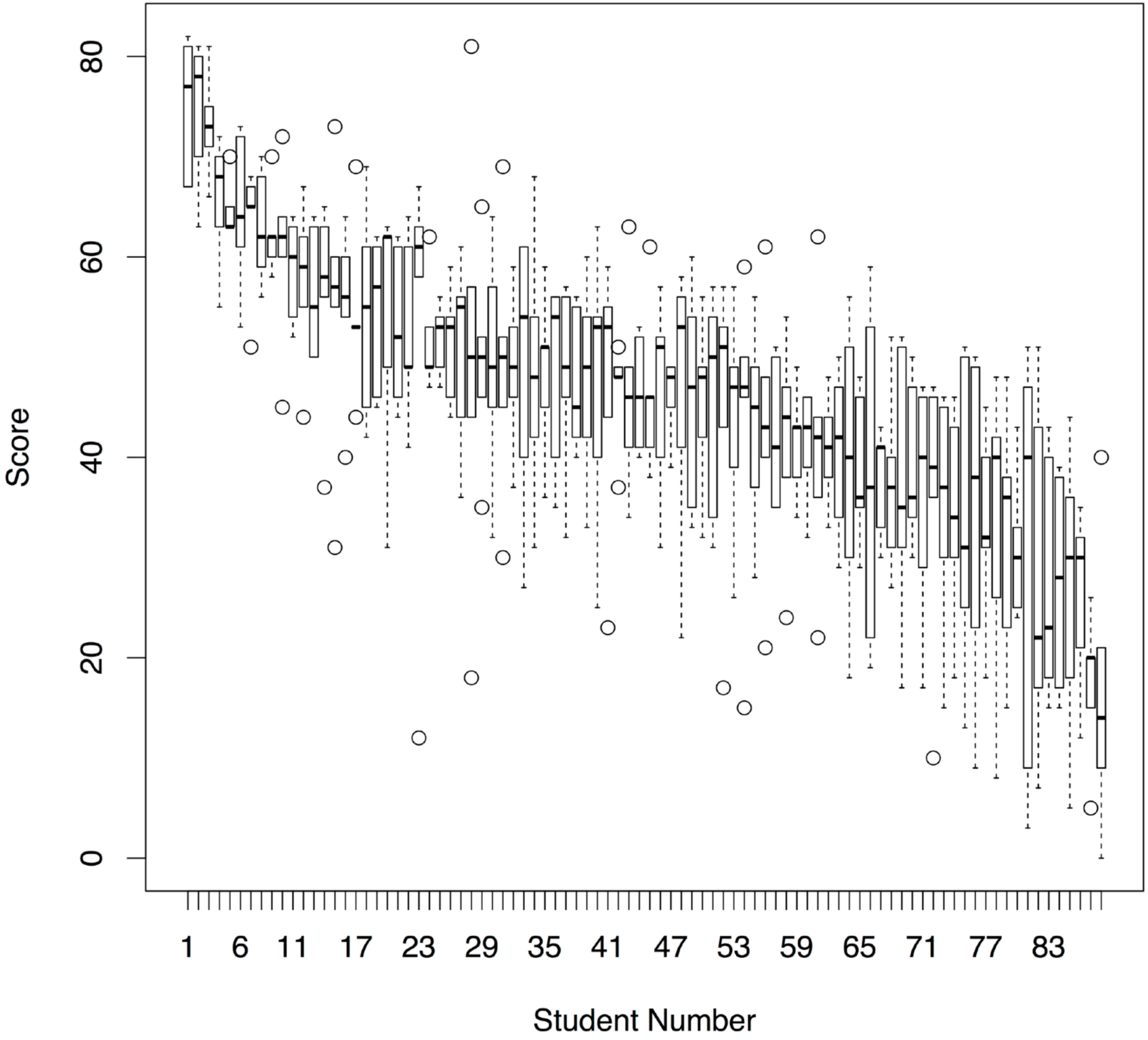
```
> model.tables(L, cterms="exam", type="mean")
Tables of means
Grand mean
45.82727 
 exam 
exam
  alg   ana   mec   sta   vec 
50.60 46.68 38.95 42.31 50.59 
```

Randomized block model

```
> CIs = TukeyHSD(L, which=1)
> plot(CIs, las=1)
```



Randomized block model



Two-way ANOVA

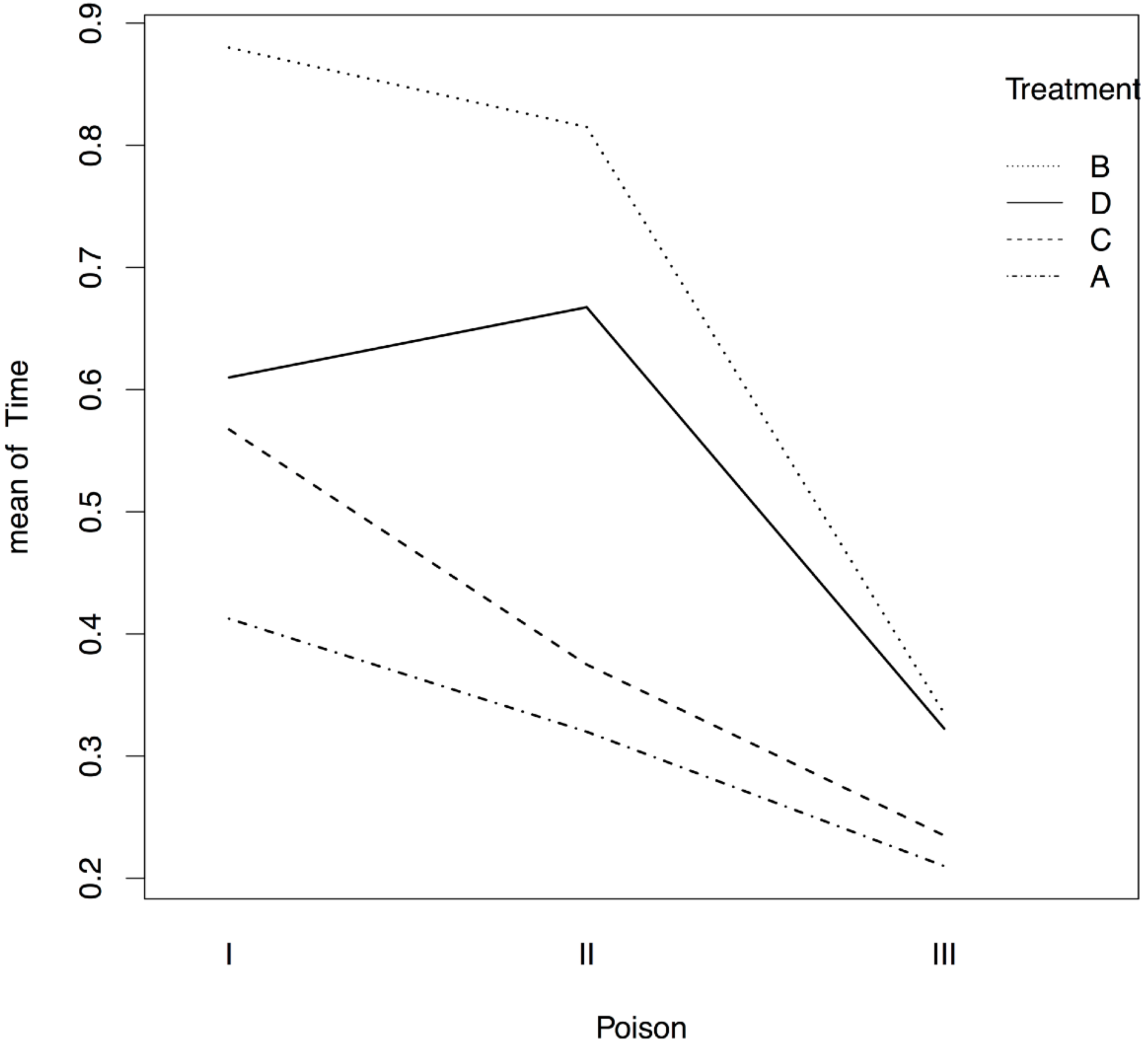
Example: Survival times in units of 10 hours for animals exposed to 3 types of poison and 4 types of antidotes

	treatment			
poison	A	B	C	D
I	0.31	0.82	0.43	0.45
	0.45	1.10	0.45	0.71
	0.46	0.88	0.63	0.66
	0.43	0.72	0.76	0.62
II	0.36	0.92	0.44	0.56
	0.20	0.61	0.35	1.02
	0.40	0.49	0.31	0.71
	0.23	1.24	0.40	0.38
III	0.22	0.30	0.23	0.30
	0.21	0.37	0.25	0.36
	0.18	0.38	0.24	0.31
	0.23	0.29	0.22	0.33

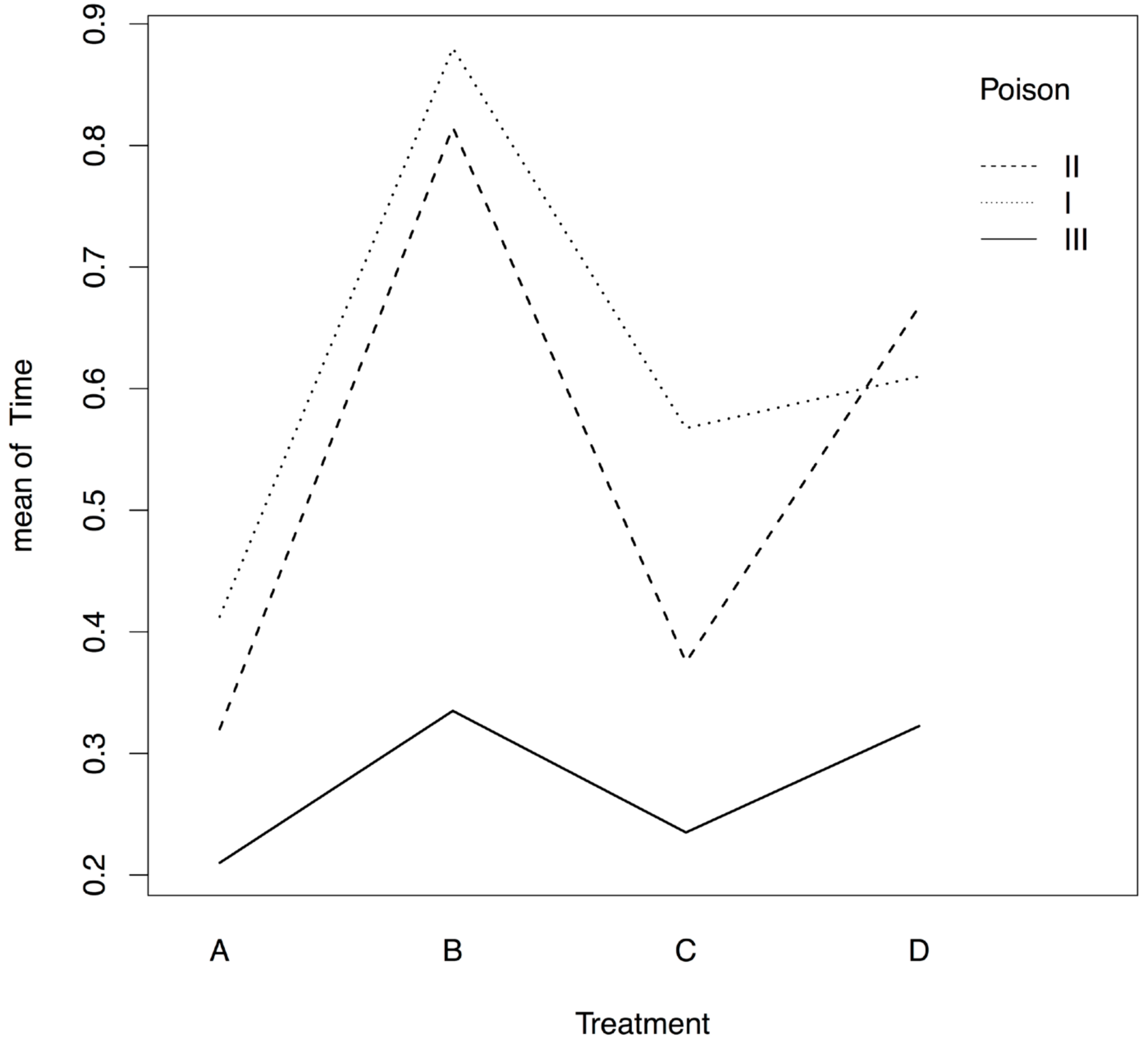
Two-way ANOVA

Interaction plots

```
> with(data=poison, expr={
+   interaction.plot(Poison, Treatment, response=Time,lwd=2)
+   interaction.plot(Treatment, Poison, response=Time,lwd=2),
+  })
```



Two-way ANOVA



Two-way ANOVA

```
> L = aov(Time ~ Poison * Treatment, data = poison)
> anova(L)
Analysis of Variance Table

Response: Time
                 Df  Sum Sq Mean Sq F value    Pr(>F)
Poison            2 1.03708 0.51854 23.3314 3.176e-07
Treatment         3 0.92012 0.30671 13.8000 3.792e-06
Poison:Treatment  6 0.25027 0.04171  1.8768    0.1118
Residuals        36 0.80010 0.02222
```

- We see that the interaction effect is not significant

Two-way ANOVA

```
> L1 = aov(Time ~ Poison + Treatment, data = poison)
> anova(L1)
Analysis of Variance Table

Response: Time
          Df  Sum Sq Mean Sq F value    Pr(>F)
Poison     2 1.03708 0.51854  20.734 5.448e-07
Treatment  3 0.92012 0.30671  12.264 6.743e-06
Residuals 42 1.05037 0.02501
```

- The Poison and Treatment effects are significant

Two-way ANOVA

```
> model.tables(L, 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
```

Two-way ANOVA

```
> model_L=lm(Time~Poison*Treatment, data=poison)
> summary(model_L)
Call:
lm(formula = Time ~ Poison * Treatment, data = poison)

Residuals:
     Min       1Q   Median       3Q      Max
-0.32500 -0.04875  0.00625  0.04312  0.42500

Coefficients:
                     Estimate Std. Error t value Pr(>|t|)
(Intercept)           0.41250    0.07454   5.534 2.92e-06
PoisonII             -0.09250    0.10542  -0.877   0.3860
PoisonIII            -0.20250    0.10542  -1.921   0.0627
TreatmentB            0.46750    0.10542   4.435 8.32e-05
TreatmentC            0.15500    0.10542   1.470   0.1501
TreatmentD            0.19750    0.10542   1.874   0.0691
PoisonII:TreatmentB   0.02750    0.14908   0.184   0.8547
PoisonIII:TreatmentB -0.34250    0.14908  -2.297   0.0275
PoisonII:TreatmentC  -0.10000    0.14908  -0.671   0.5066
PoisonIII:TreatmentC -0.13000    0.14908  -0.872   0.3890
PoisonII:TreatmentD   0.15000    0.14908   1.006   0.3211
PoisonIII:TreatmentD -0.08500    0.14908  -0.570   0.5721
```

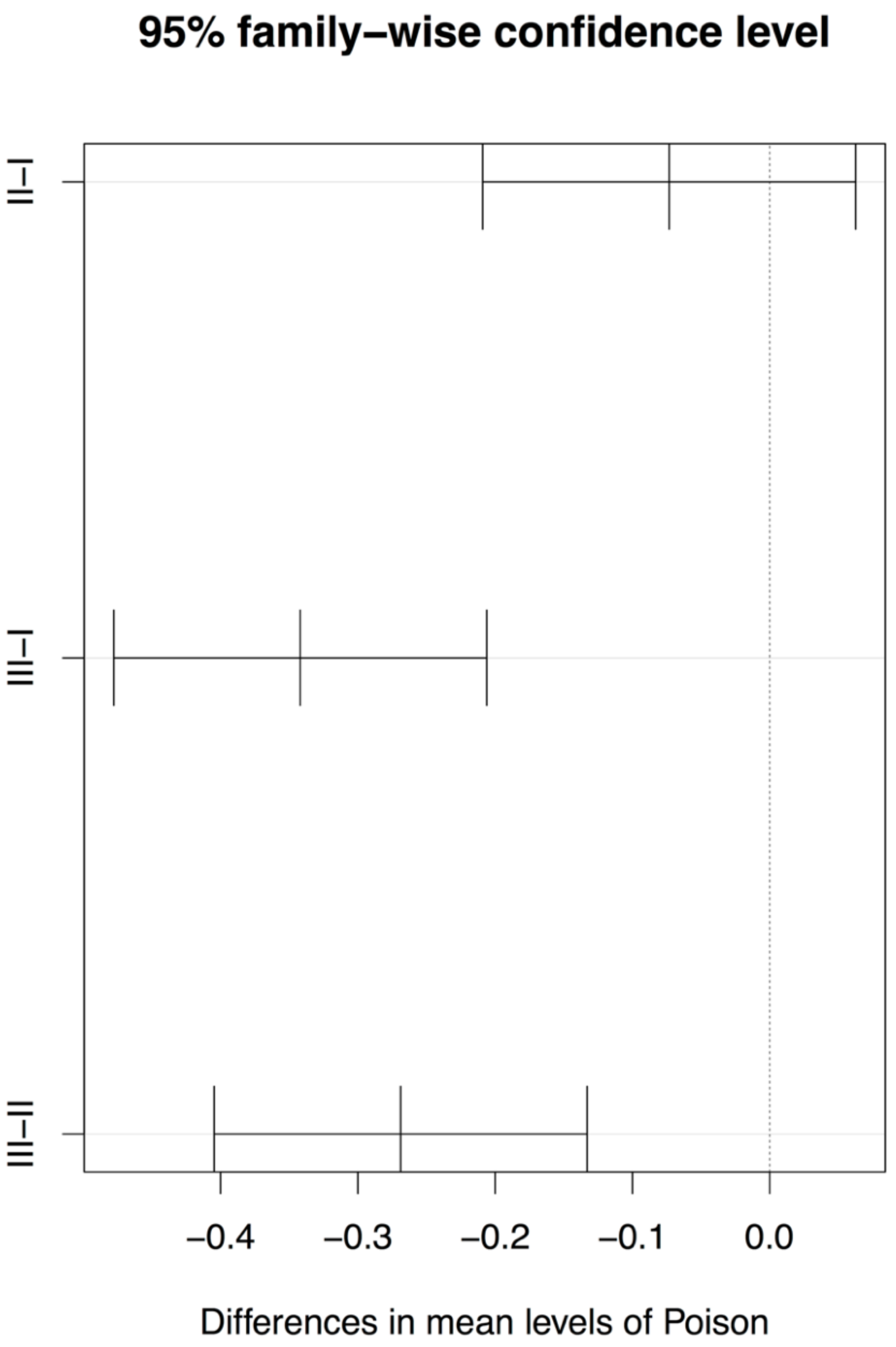
Two-way ANOVA

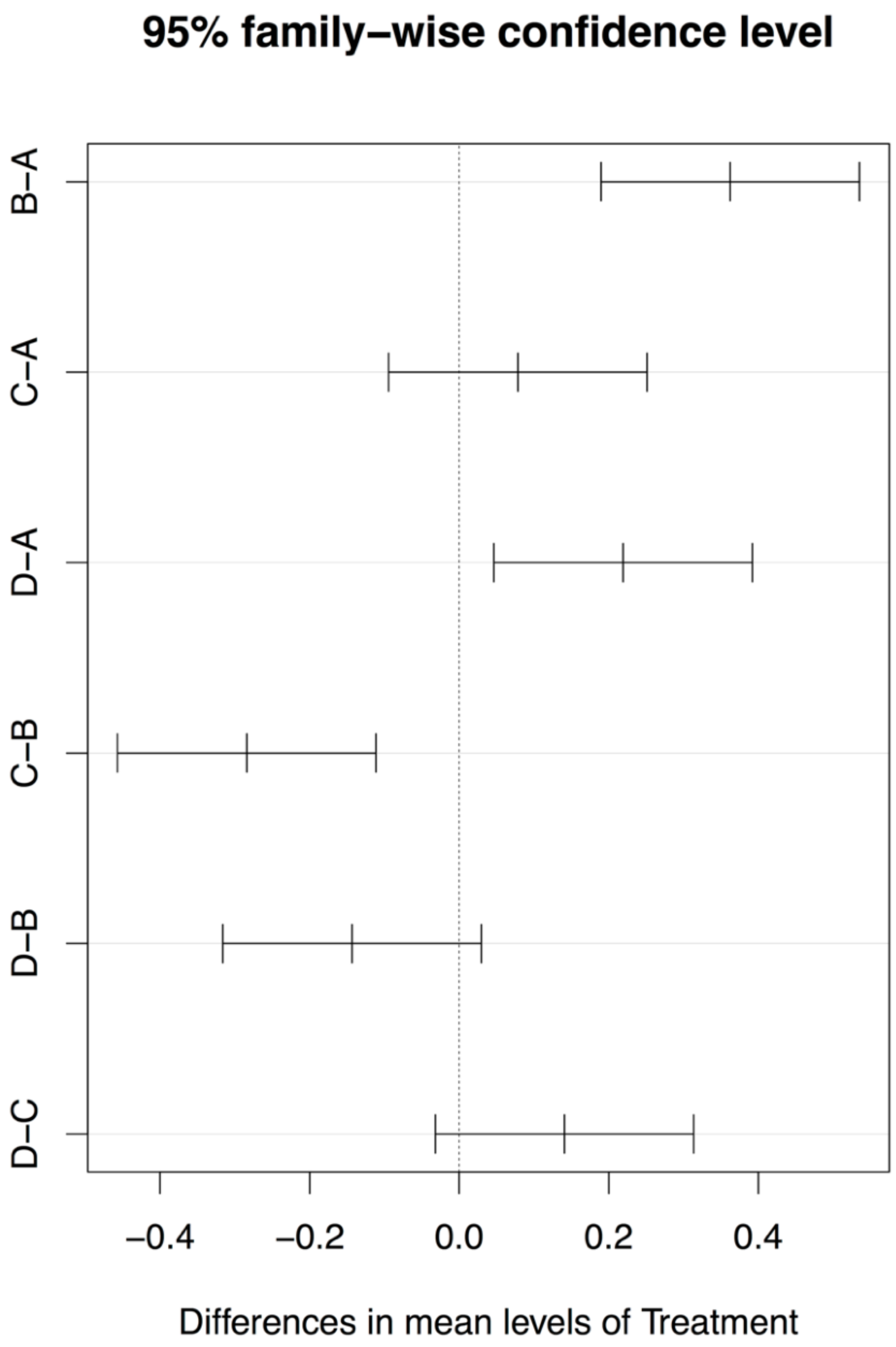
```
> model_L1=lm(Time~Poison+Treatment, data=poison)
> summary(model_L1)
Call:
lm(formula = Time ~ Poison + Treatment, data = poison)
Residuals:
     Min       1Q   Median       3Q      Max 
-0.25188 -0.09646 -0.01469  0.06203  0.49812 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)    
(Intercept)  0.45250    0.05591   8.093 4.15e-10 
PoisonII    -0.07312    0.05591  -1.308  0.19803    
PoisonIII   -0.34187    0.05591  -6.115 2.72e-07 
TreatmentB   0.36250    0.06456   5.615 1.42e-06 
TreatmentC   0.07833    0.06456   1.213  0.23179    
TreatmentD   0.21917    0.06456   3.395  0.00151 

Residual standard error: 0.1581 on 42 degrees of freedom
Multiple R-squared:  0.6508,	Adjusted R-squared:  0.6092 
F-statistic: 15.65 on 5 and 42 DF,  p-value: 1.094e-08
```

Two-way ANOVA

```
> TukeyHSD(L1, which=c("Poison", "Treatment"))
  Tukey multiple comparisons of means
    95% family-wise confidence level

Fit: aov(formula = Time ~ Poison + Treatment, data = poison)

$Poison
            diff        lwr         upr     p adj
II-I   -0.073125 -0.2089618  0.06271181 0.3987984
III-I  -0.341875 -0.4777118 -0.20603819 0.0000008
III-II -0.268750 -0.4045868 -0.13291319 0.0000582

$Treatment
           diff         lwr        upr     p adj
B-A  0.36250000  0.18980177  0.5351982 0.0000083
C-A  0.07833333 -0.09436490  0.2510316 0.6219967
D-A  0.21916667  0.04646843  0.3918649 0.0079262
C-B -0.28416667 -0.45686490 -0.1114684 0.0004077
D-B -0.14333333 -0.31603157  0.0293649 0.1344032
D-C  0.14083333 -0.03186490  0.3135316 0.1451135
```

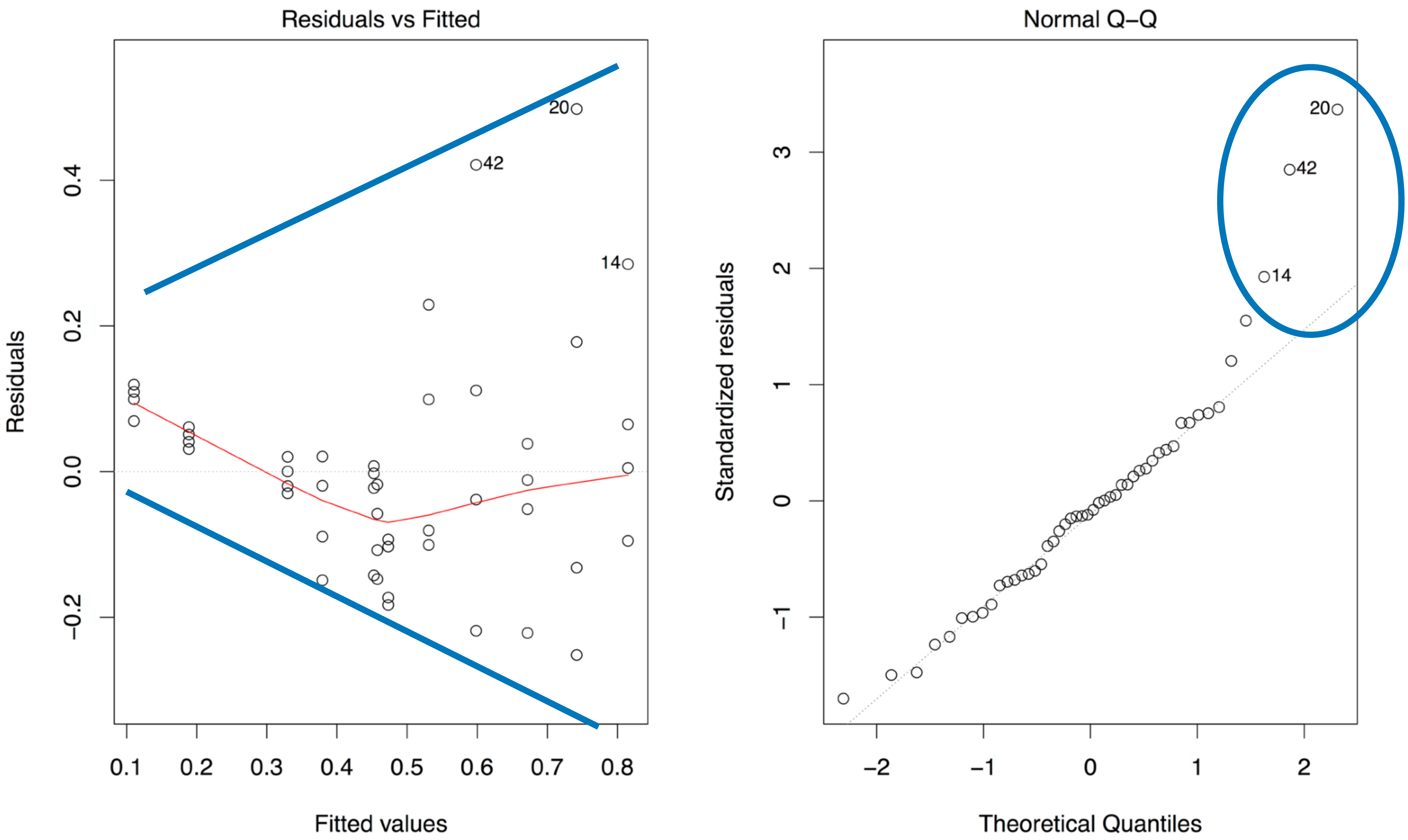
Two-way ANOVA





Two-way ANOVA

Residual analysis, model Time ~ Poison + Treatment



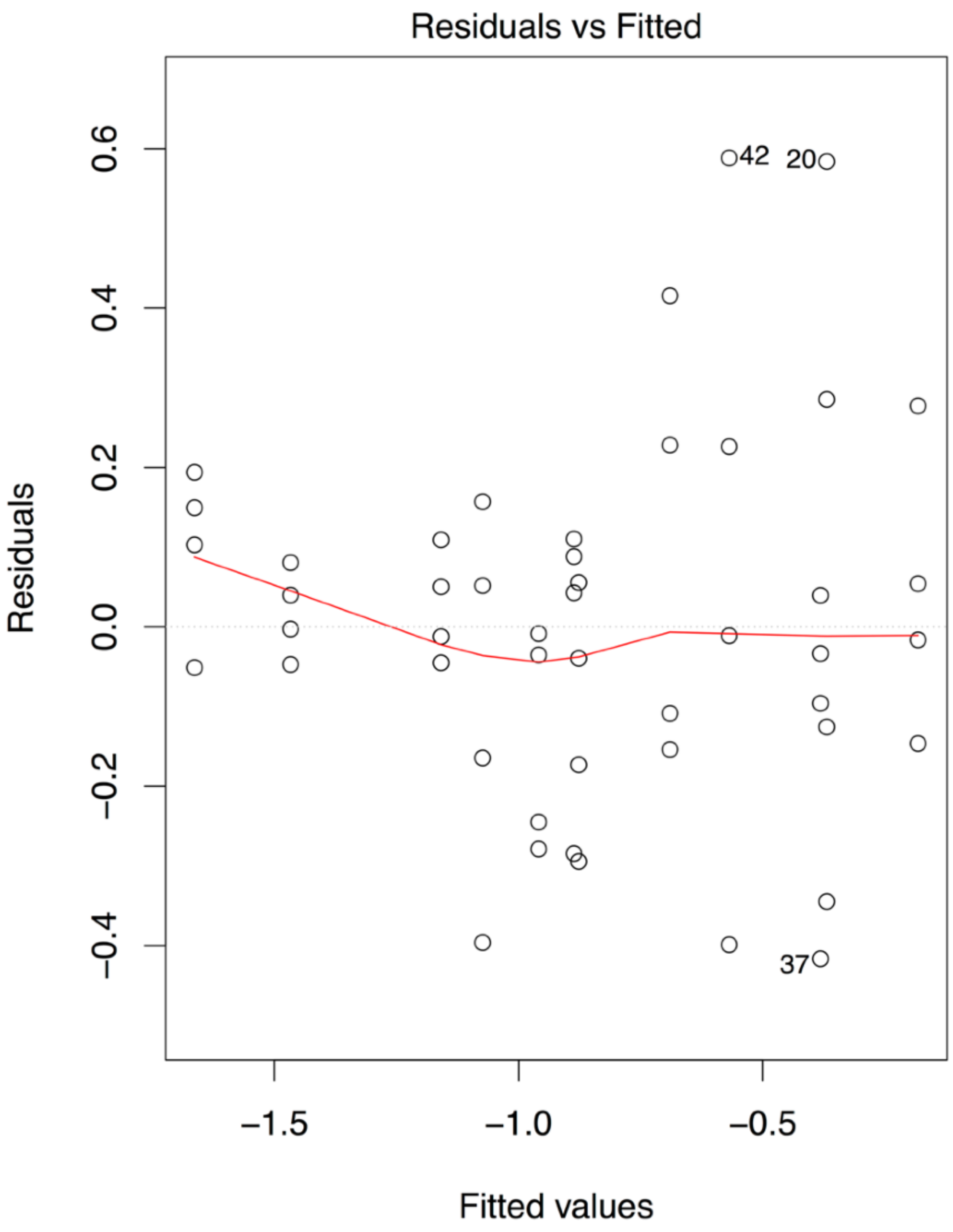
Two-way ANOVA

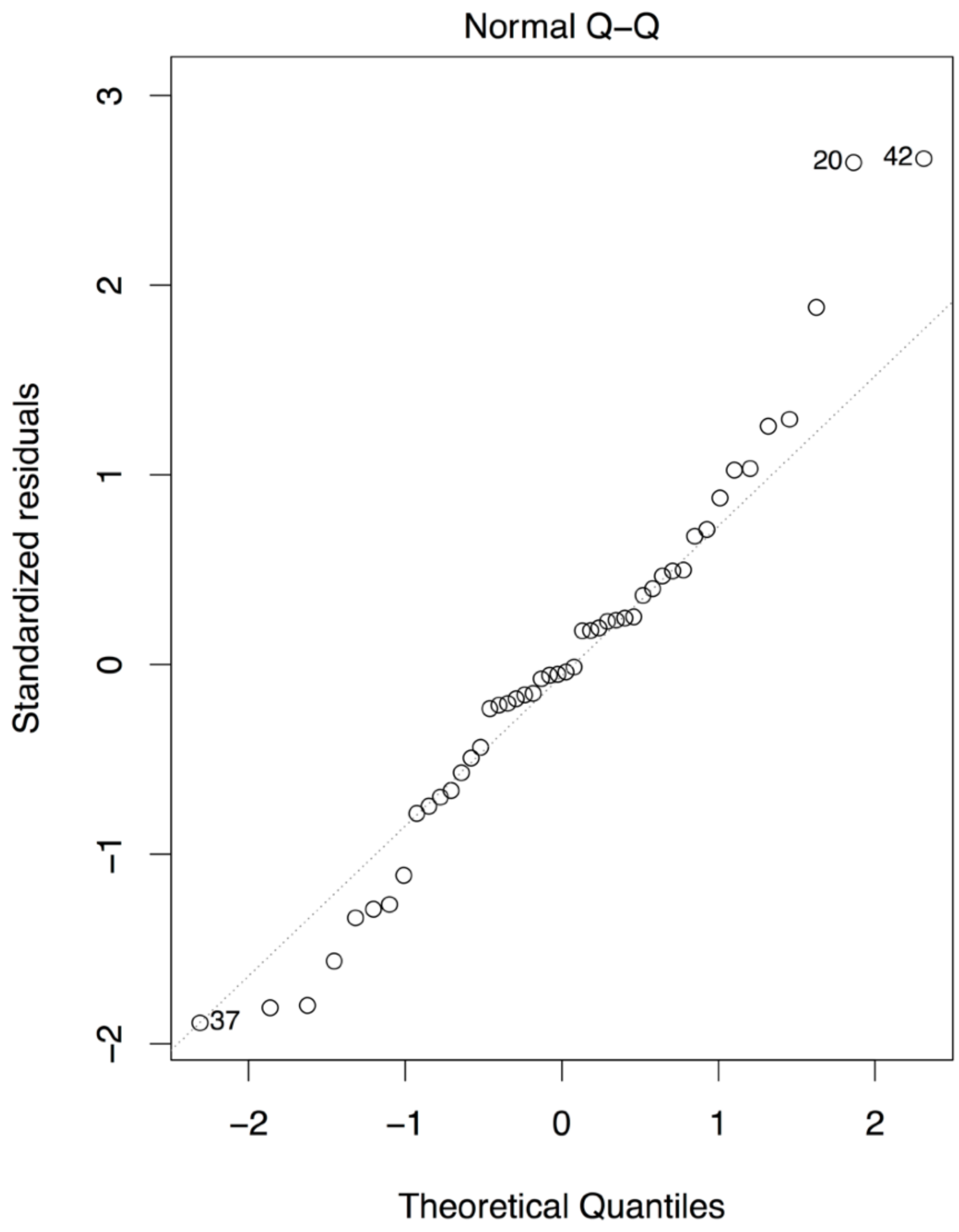
Transformations

```
> model_log=lm(log(Time) ~ Poison + Treatment, data=poison)
> anova(aov(model_log))
Analysis of Variance Table

Response: log(Time)
          Df Sum Sq Mean Sq F value    Pr(>F)
Poison     2 5.2631 2.63156  47.326 1.739e-11
Treatment  3 3.5485 1.18283  21.272 1.550e-08
Residuals 42 2.3354 0.05561
```

Two-way ANOVA

Transformations





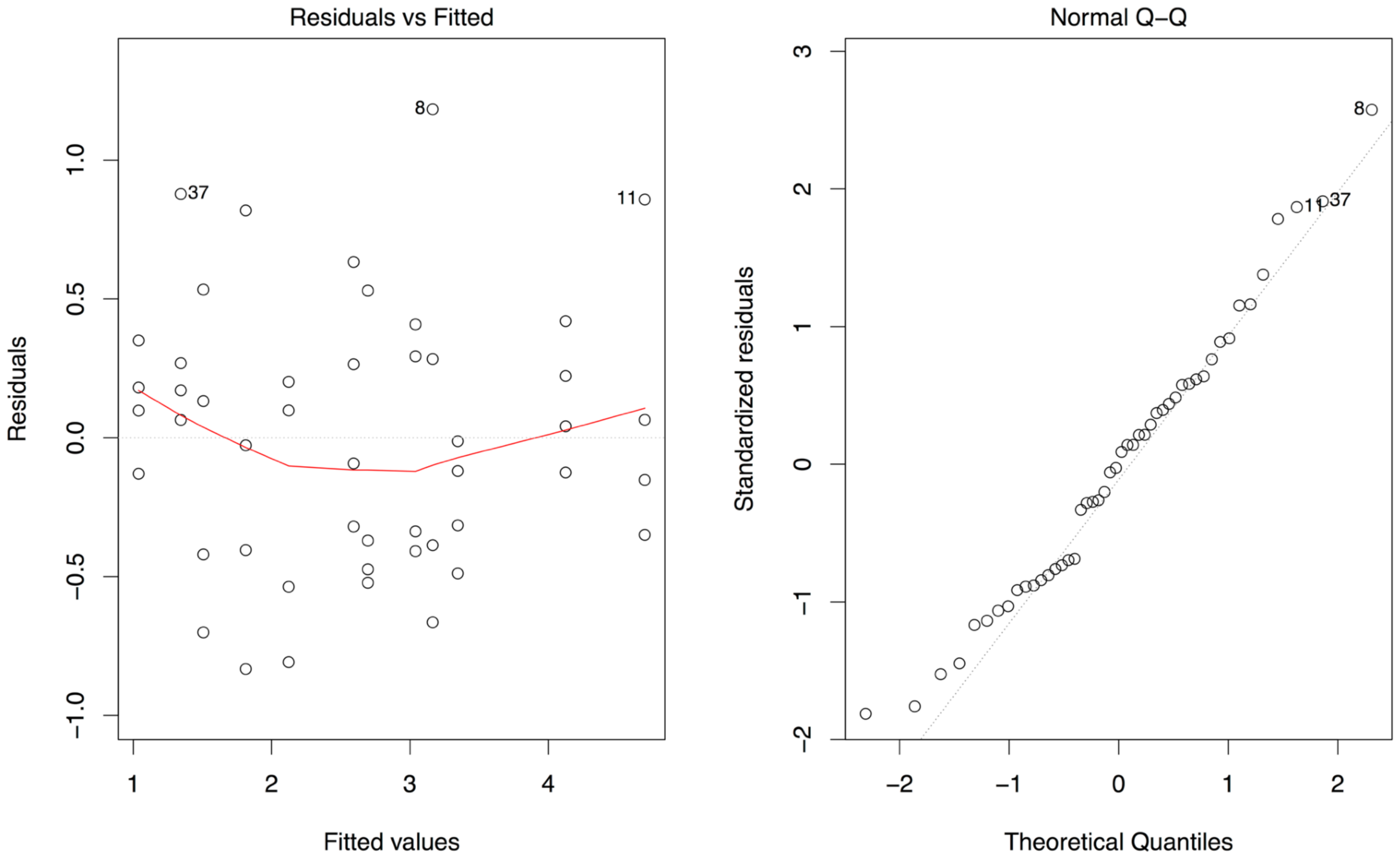
Two-way ANOVA

Transformations

```
> model_reciprocal=lm(1/Time ~ Poison + Treatment,
data=poison)
> anova(aov(model_reciprocal))
Analysis of Variance Table

Response: 1/Time
          Df Sum Sq Mean Sq F value    Pr(>F)
Poison     2 35.064 17.5319  72.683 2.300e-14
Treatment  3 20.341  6.7805  28.110 3.934e-10
Residuals 42 10.131  0.2412
> pdf(file='plot.pdf',pointsize = 18,height=10,width=15)
> par(mfrow=c(1,2))
> plot(model_reciprocal,which=1:2)
> dev.off()
```

Two-way ANOVA

Transformations


Residuals vs Fitted
Residuals
Fitted values
Normal Q−Q
Standardized residuals
Theoretical Quantiles