General Linear Model - Specific Designs

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Contents

1 Introduction

In this section we will illustrate how specific designs, e.g.

- two-way anova designs
- block designs

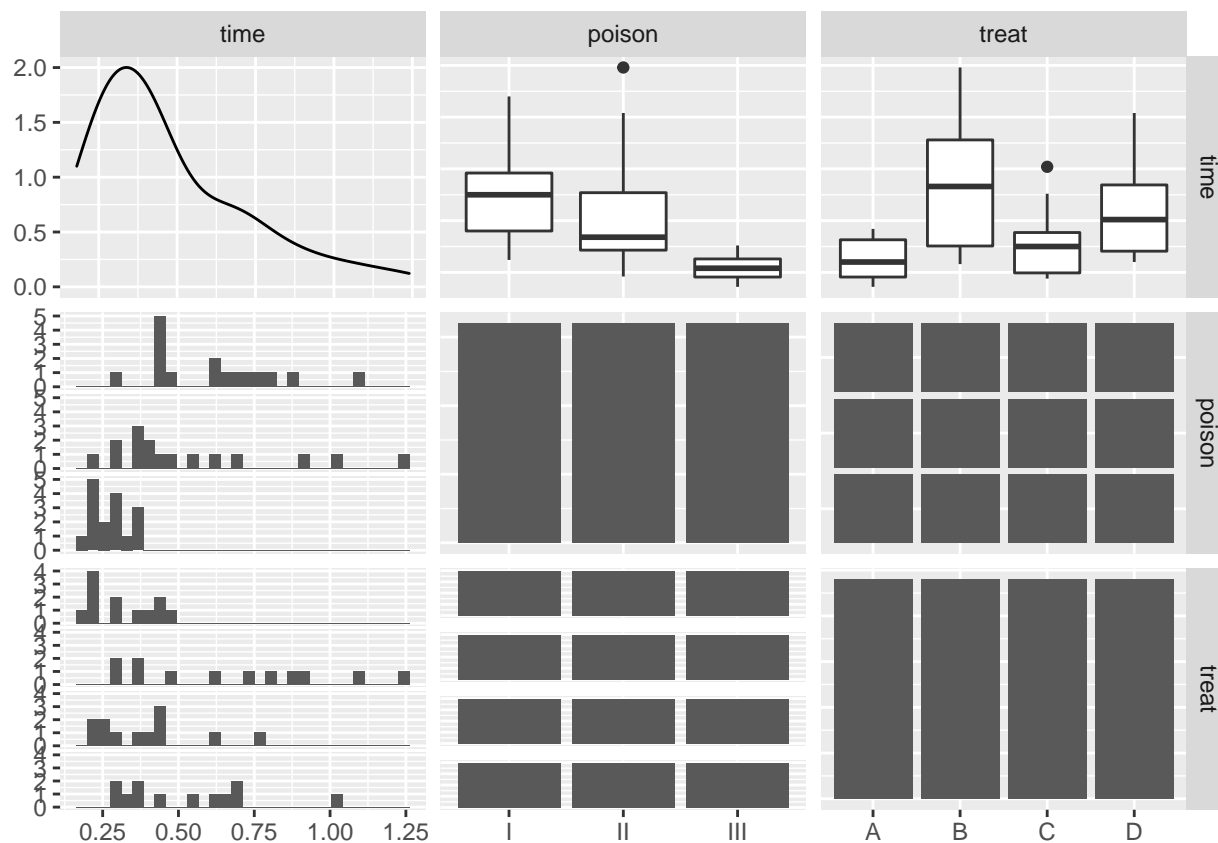can be analysed using the general linear model.

2 Two-way anova

2.1 Data

48 rats were allocated to

- 3 poisons (I,II,III) and
- 4 treatments (A,B,C,D).

```
library(faraway)
data(rats)

library(GGally)
rats %>%
  ggpairs()
```
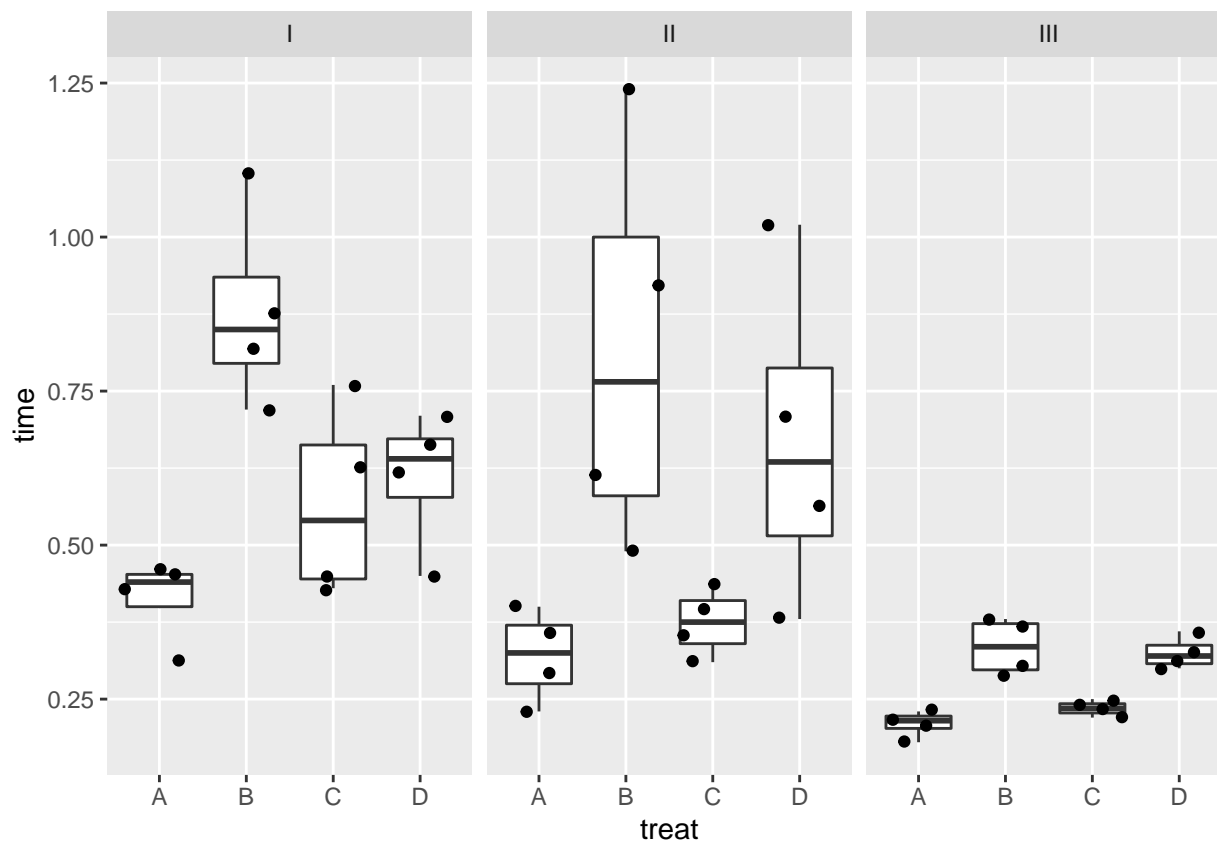
We have a design with a continuous response time (survival) and two factors:

- Poison: I, II, III
- Treatment: A, B, C, D

The data exploration indicates that there seems to be an effect of both treatment and poison.

```
rats %>%
  ggplot(aes(x=treat,y=time)) +
  geom_boxplot(outlier.shape=NA) +
  geom_jitter() +
  facet_wrap(~poison)
```

- There might be an interaction, i.e. the effect of the treatment might be different according to the poison that has been adopted.
- The boxplots also indicate that the data are heteroscedastic.

2.2 Model

We will model the data with a main effect for poison and treatment and an interaction.

$$y_i = \beta_0 + \beta_{II}x_{iII} + +\beta_{III}x_{iIII} + \beta_B x_{iB} + \beta_C x_{iC} + \beta_D x_{iD} + \epsilon_i$$

with $i = 1, \ldots, n$, $n = 48$, x_{iII}, x_{iIII}, x_{iB}, x_{iC} and x_{iD} dummy variables for poison II, poison II, treatment B, treatment C and treatment D, respectively.

```
rats1 <- lm(time~poison*treat, rats)
summary(rats1)


Call:
lm(formula = time ~ poison * treat, data = rats)

Residuals:
     Min       1Q   Median       3Q      Max
-0.32500 -0.04875  0.00500  0.04312  0.42500

Coefficients:
```
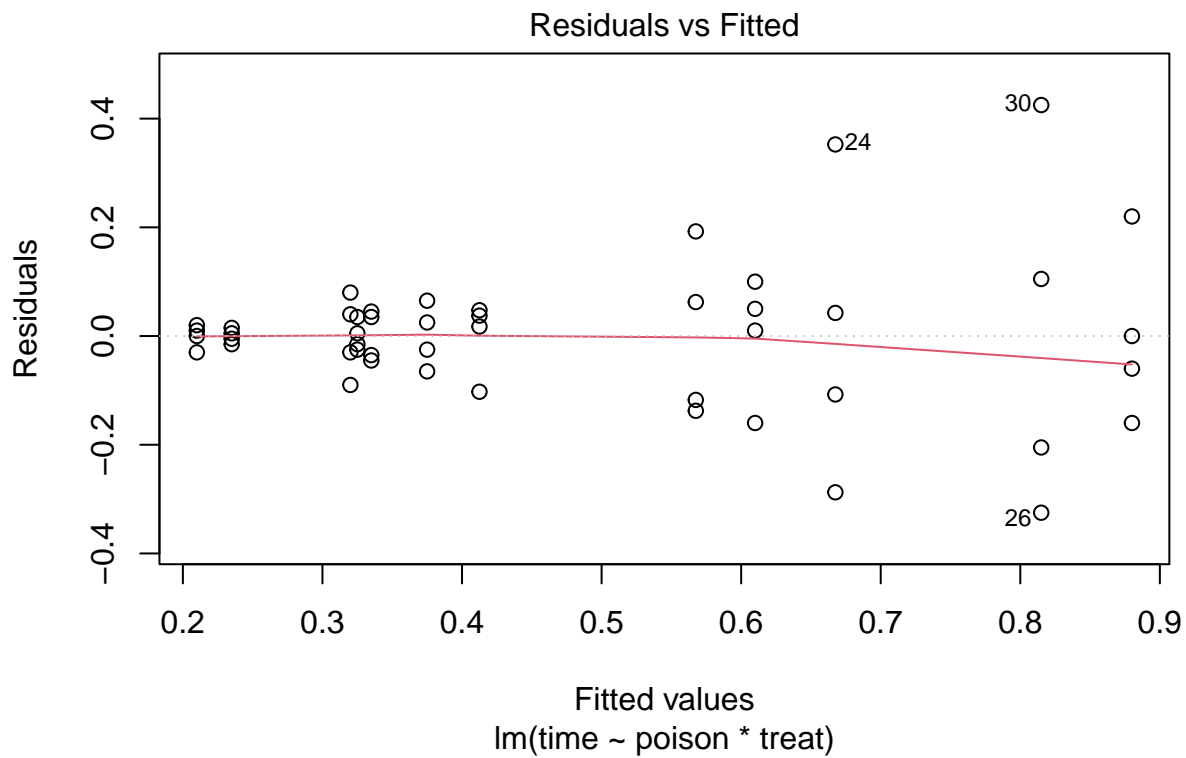
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```
                Estimate Std. Error t value Pr(>|t|)
(Intercept)      0.41250    0.07457   5.532 2.94e-06 ***
poisonII        -0.09250    0.10546  -0.877   0.3862
poisonIII       -0.20250    0.10546  -1.920   0.0628 .
treatB           0.46750    0.10546   4.433 8.37e-05 ***
treatC           0.15500    0.10546   1.470   0.1503
treatD           0.19750    0.10546   1.873   0.0692 .
poisonII:treatB  0.02750    0.14914   0.184   0.8547
poisonIII:treatB -0.34250   0.14914  -2.297   0.0276 *
poisonII:treatC  -0.10000   0.14914  -0.671   0.5068
poisonIII:treatC -0.13000   0.14914  -0.872   0.3892
poisonII:treatD  0.15000    0.14914   1.006   0.3212
poisonIII:treatD -0.08250   0.14914  -0.553   0.5836
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.1491 on 36 degrees of freedom
Multiple R-squared:  0.7335,    Adjusted R-squared:  0.6521
F-statistic:  9.01 on 11 and 36 DF,  p-value: 1.986e-07
```

```
plot(rats1)
```


Residuals vs Fitted

lm(time ~ poison * treat)

Normal Q–Q

lm(time ~ poison * treat)

Scale−Location

√|Standardized residuals|

Fitted values
lm(time ~ poison * treat)

Constant Leverage:
Residuals vs Factor Levels
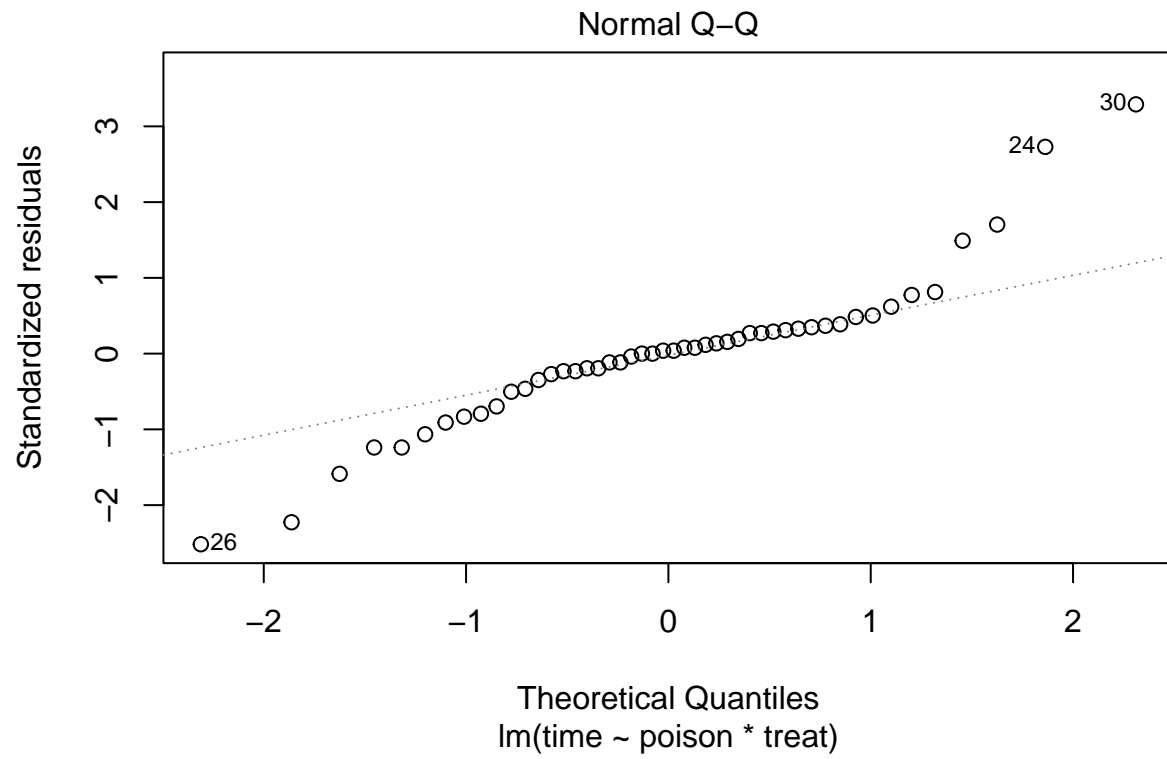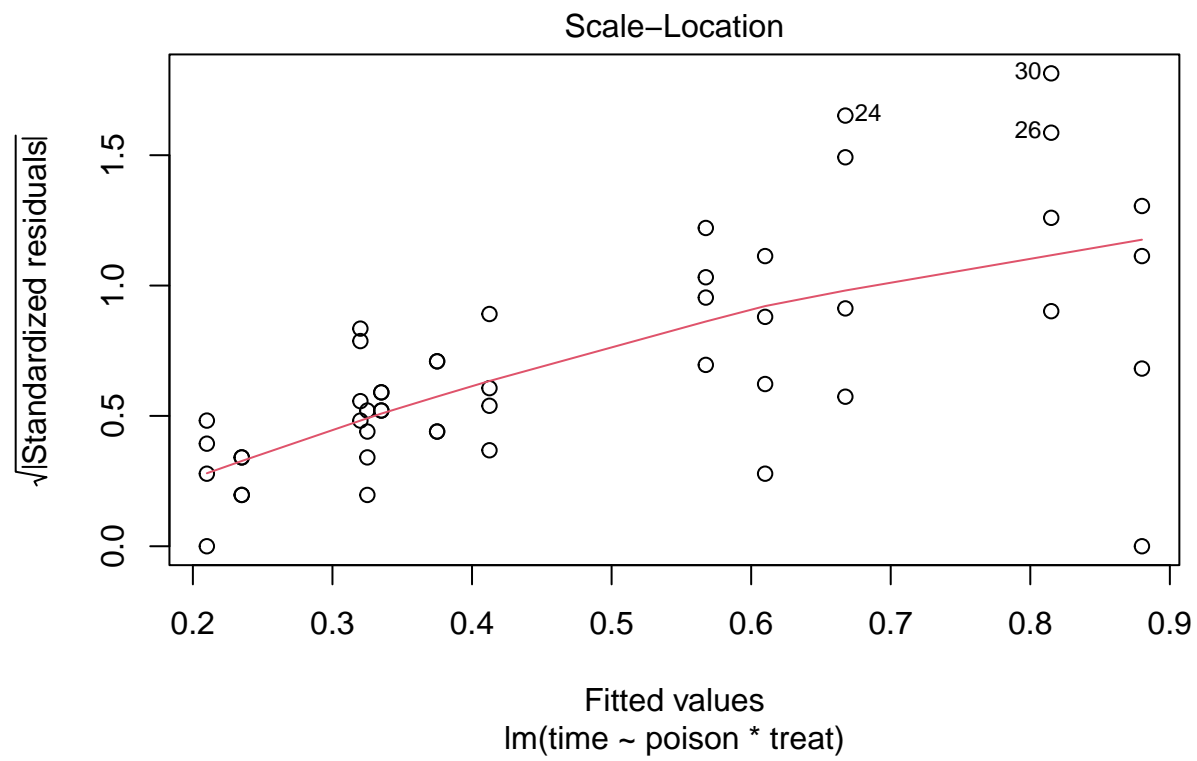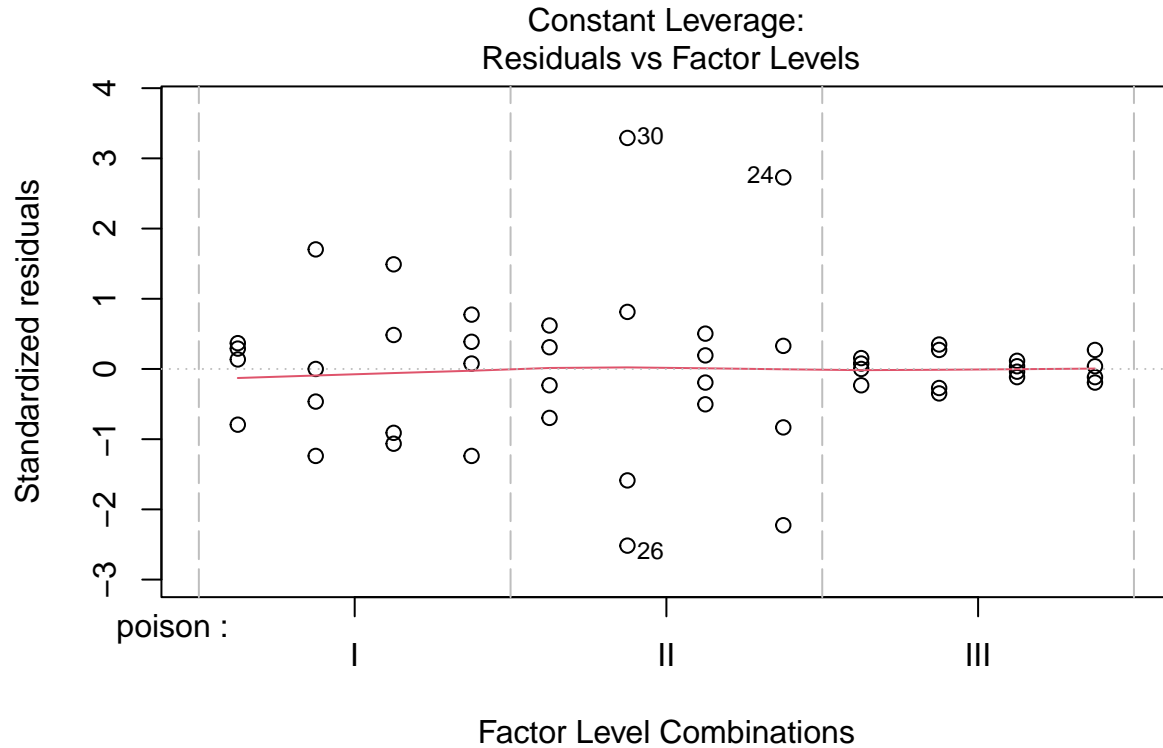
The errors, however, seem to be heteroscedastic and there seems to be a mean - variance relationship and they are also appear to be distributed with broader tails than the normal distribution.

2.2.1 Transformations

```
rats %>%
  ggplot(aes(x=treat,y=log2(time))) +
  geom_boxplot(outlier.shape=NA) +
  geom_jitter() +
  facet_wrap(~poison)
```
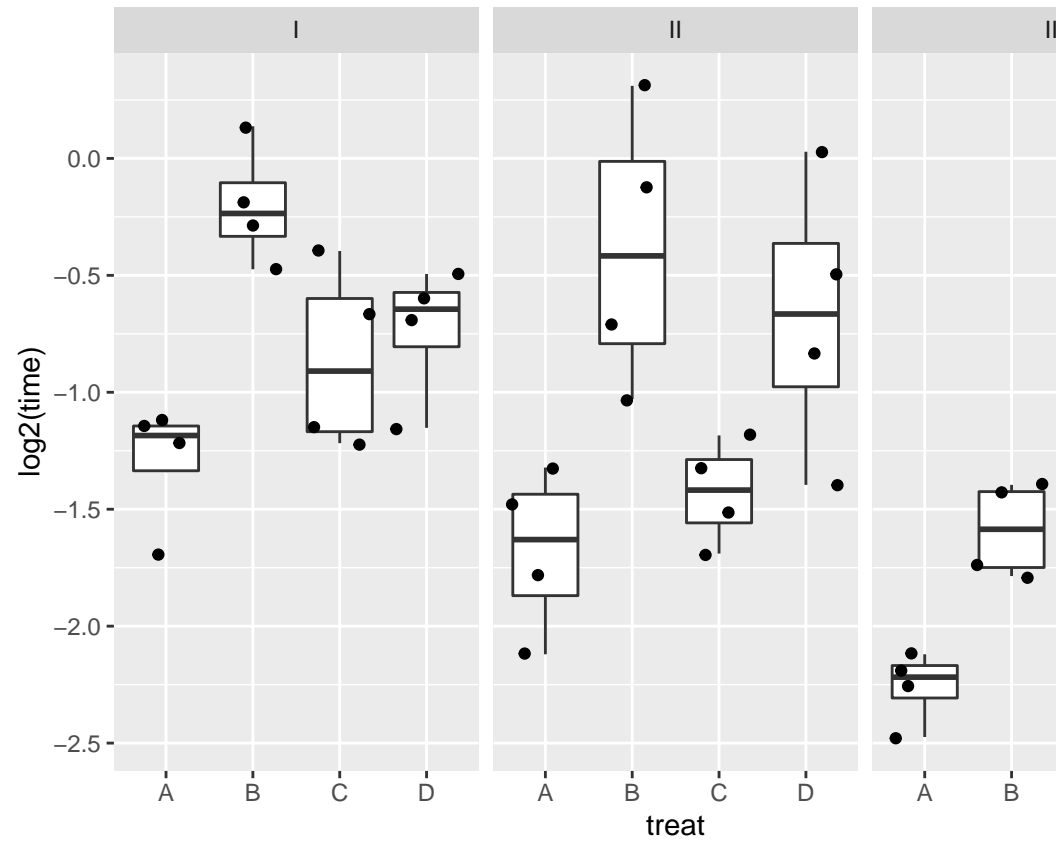
2.2.1.1 log transformation

```
rats2 <- lm(time %>% log2~poison*treat, rats)
plot(rats2)
```

Residuals vs Fitted

Fitted values
lm(time %>% log2 ~ poison * treat)

Normal Q–Q

Standardized residuals

Theoretical Quantiles
lm(time %>% log2 ~ poison * treat)

Scale–Location

√|Standardized residuals|

Fitted values
lm(time %>% log2 ~ poison * treat)

Constant Leverage:
Residuals vs Factor Levels

Factor Level Combinations
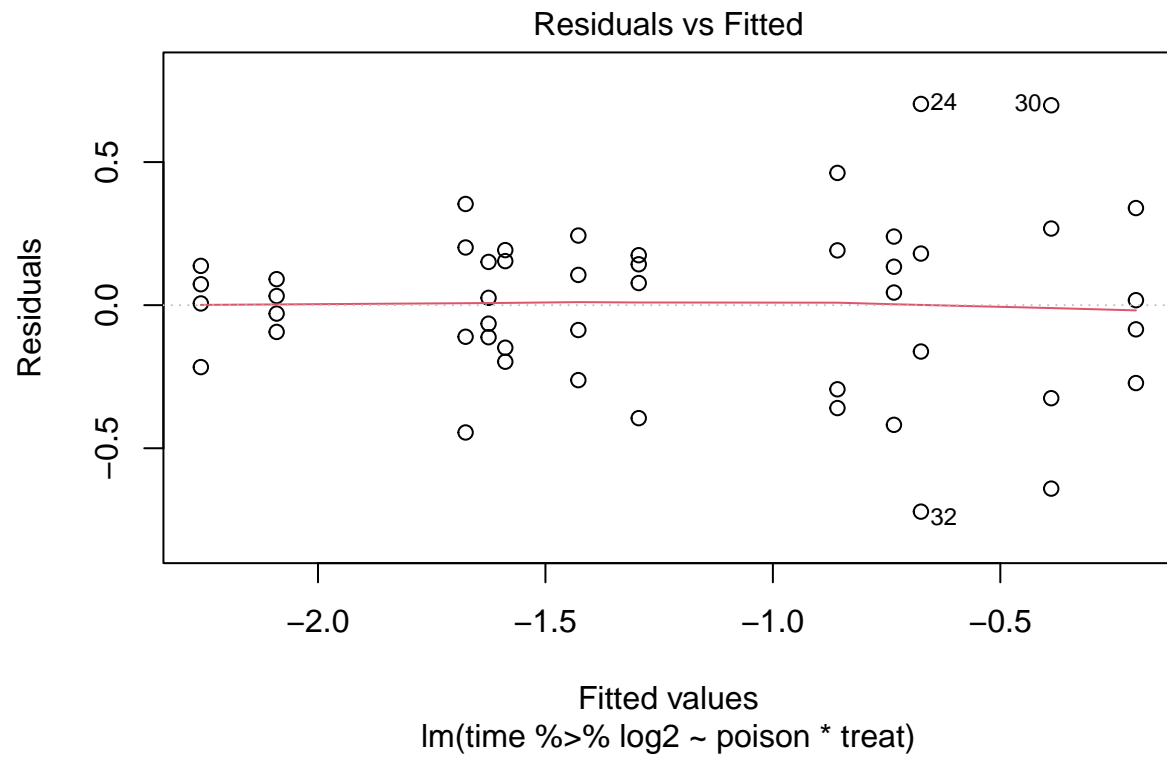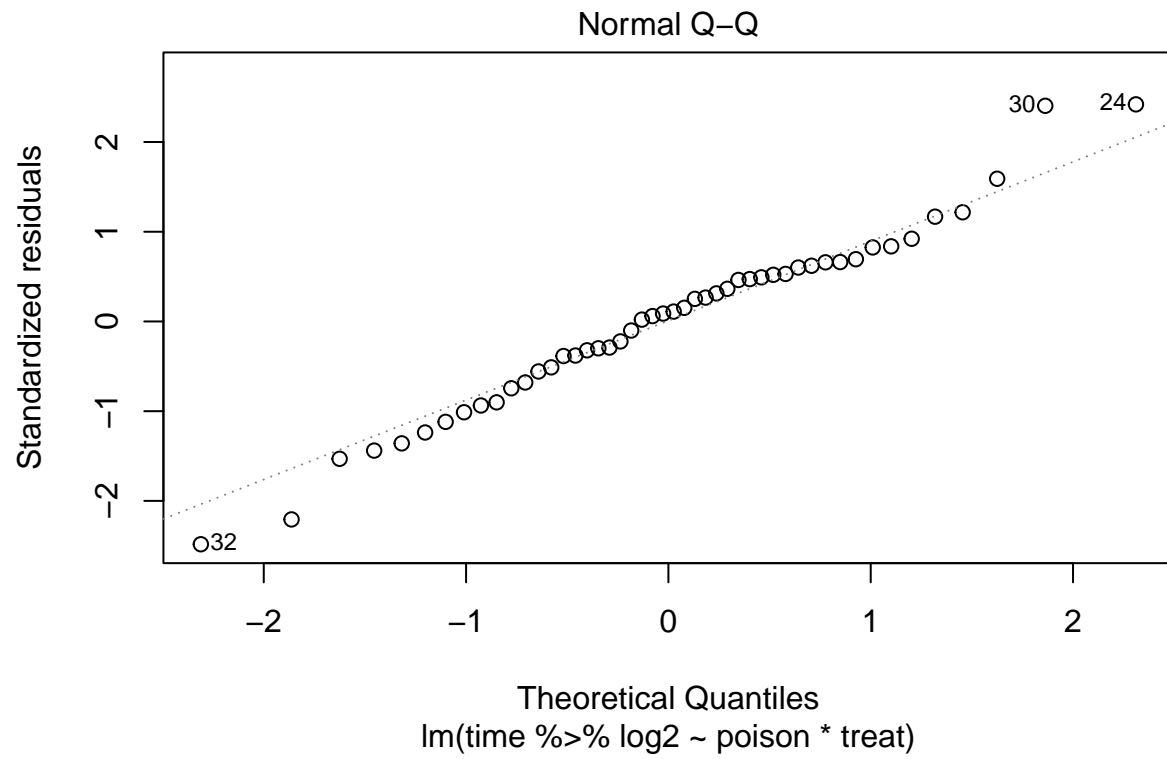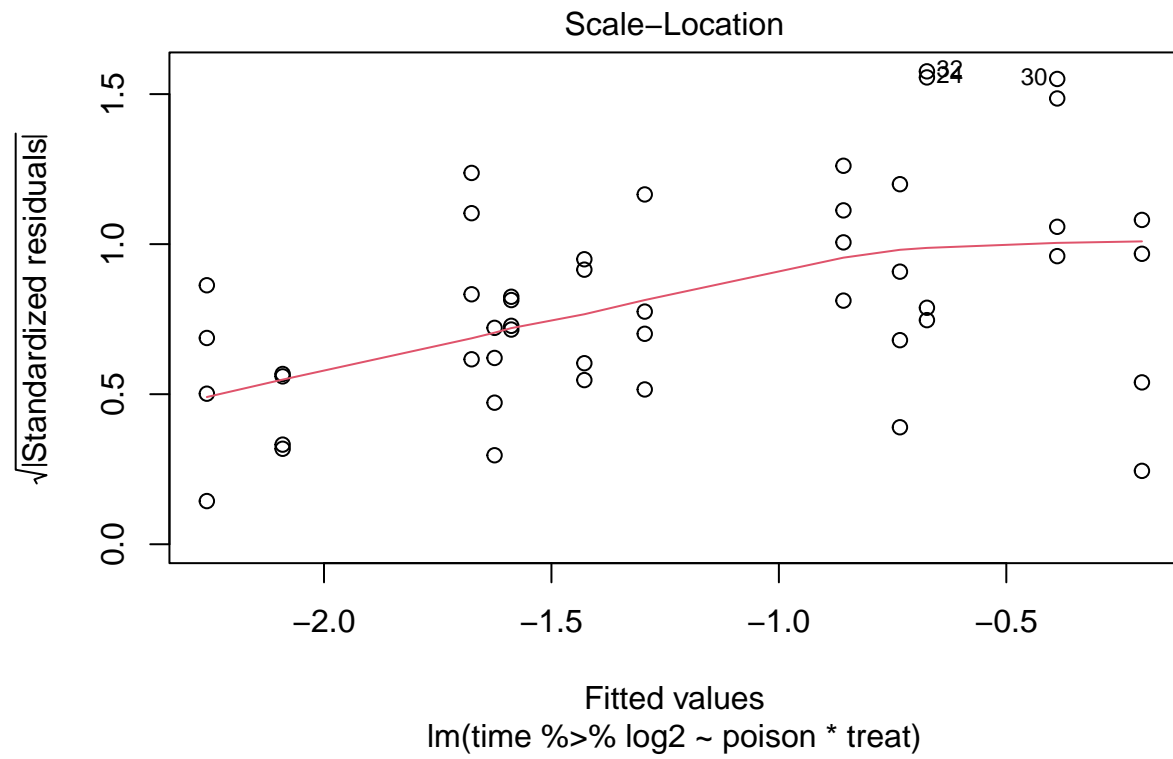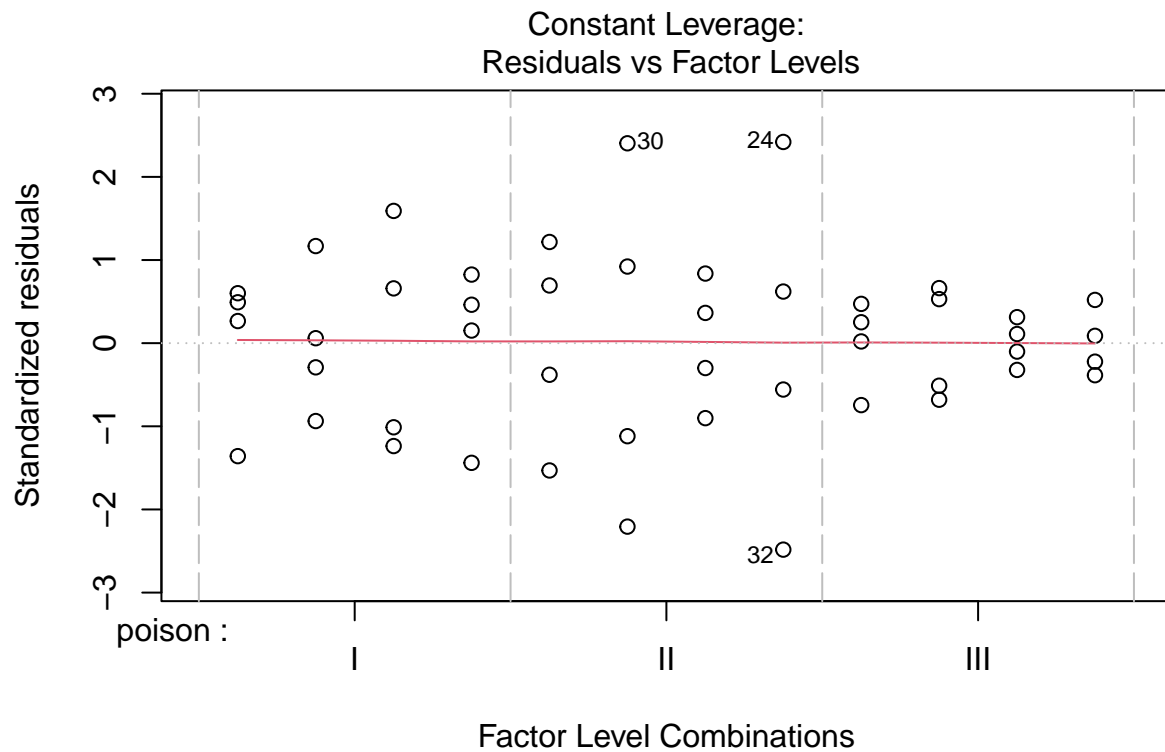
Log transformation does not remove the heteroscedasticity completely.

```
rats %>%
  ggplot(aes(x=treat,y=1/time)) +
  geom_boxplot(outlier.shape=NA) +
  geom_jitter() +
  facet_wrap(~poison)
```
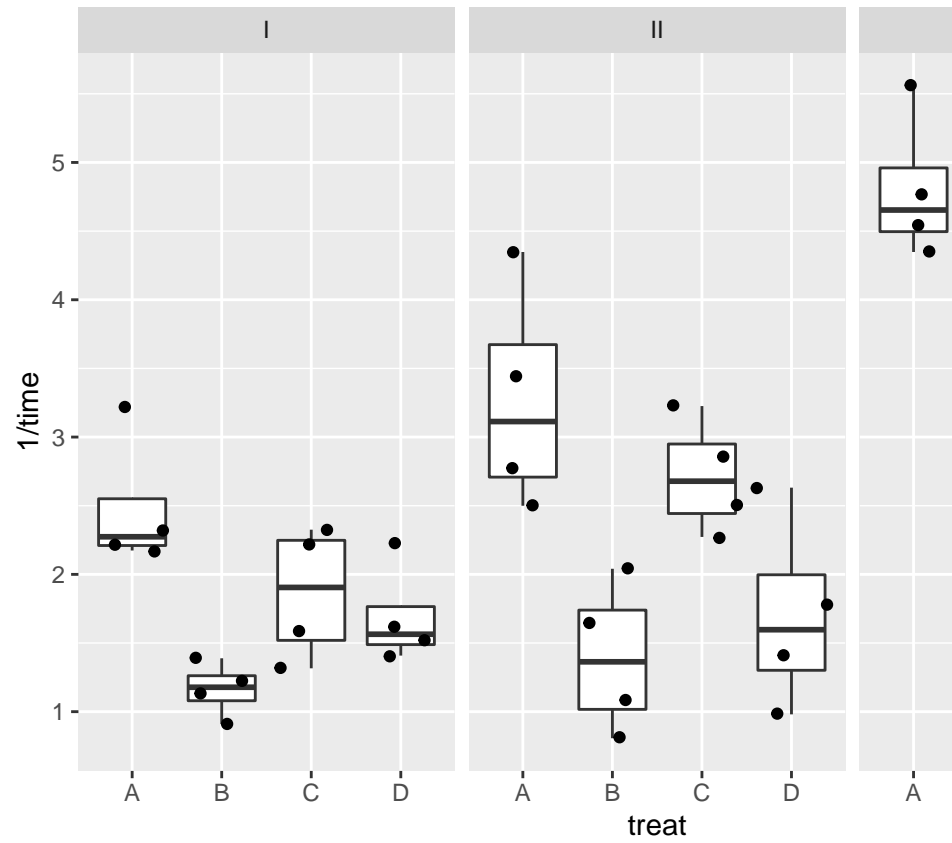
2.2.1.2 Reciprocal transformation

```
rats3 <- lm(1/time~poison*treat, rats)
plot(rats3)
```

Residuals vs Fitted

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Residuals

Fitted values
lm(1/time ~ poison * treat)

Normal Q–Q

Standardized residuals

Theoretical Quantiles
lm(1/time ~ poison * treat)

Scale−Location

√|Standardized residuals|

Fitted values
lm(1/time ~ poison * treat)

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Constant Leverage:
Residuals vs Factor Levels
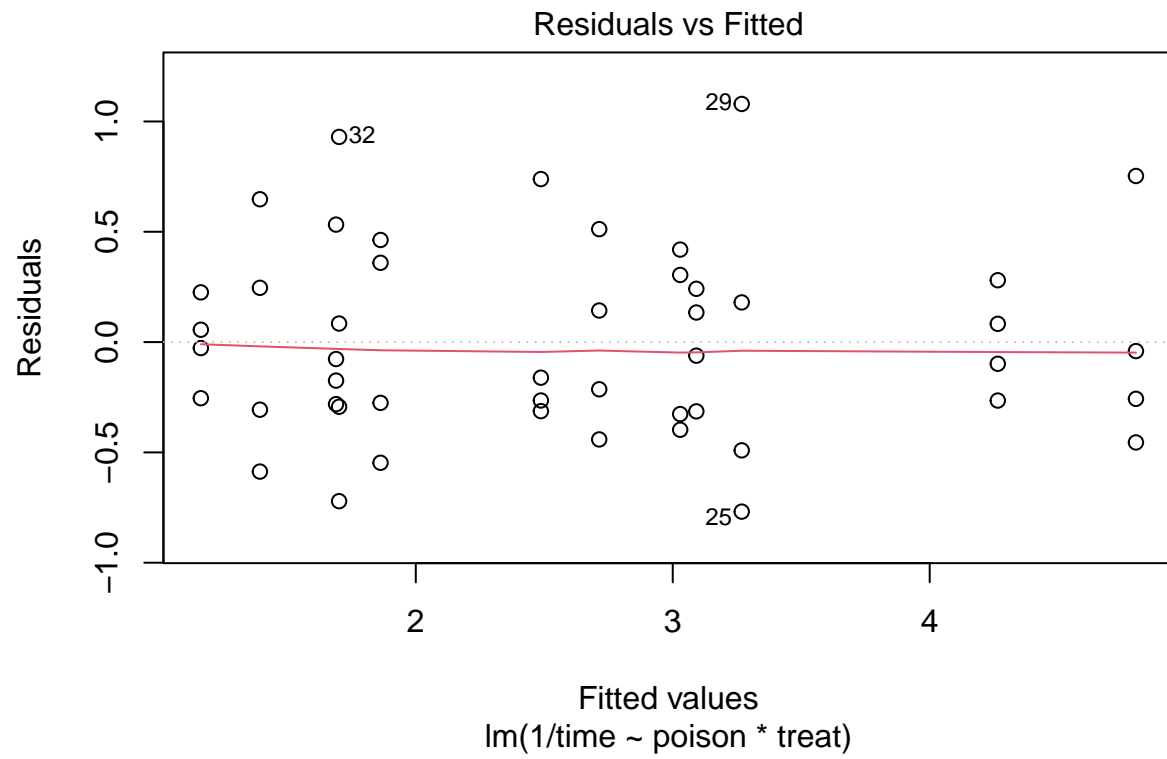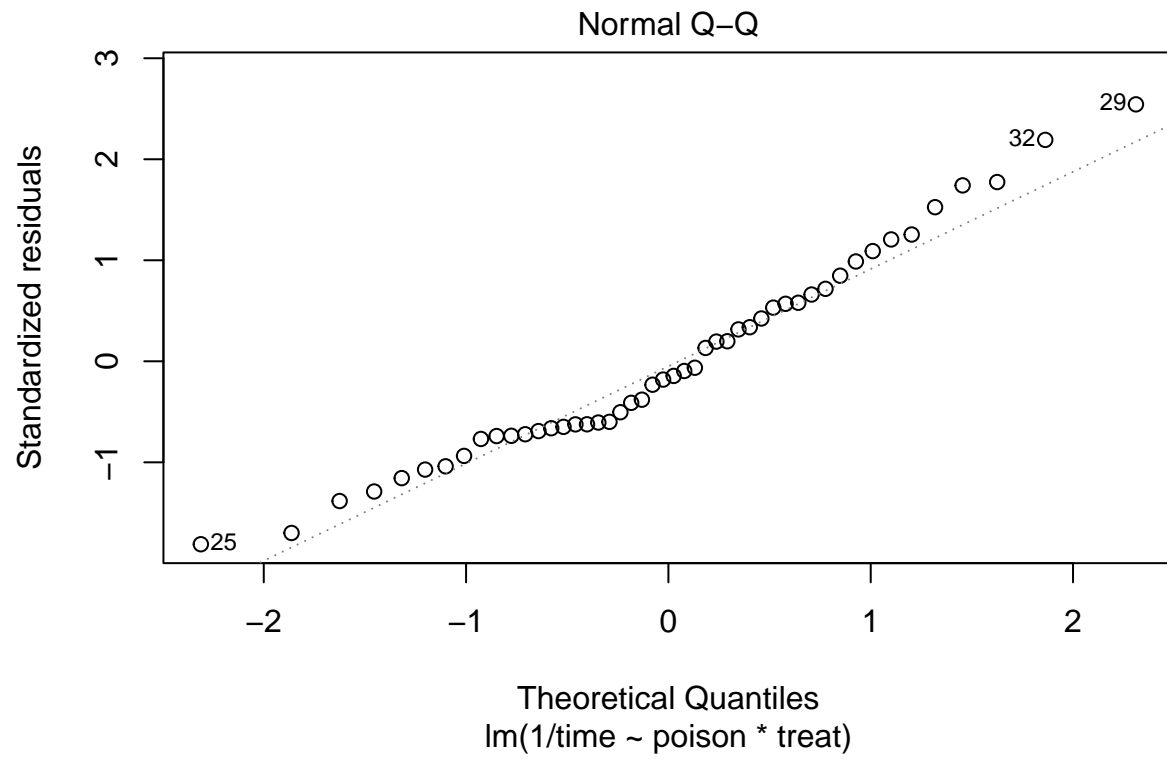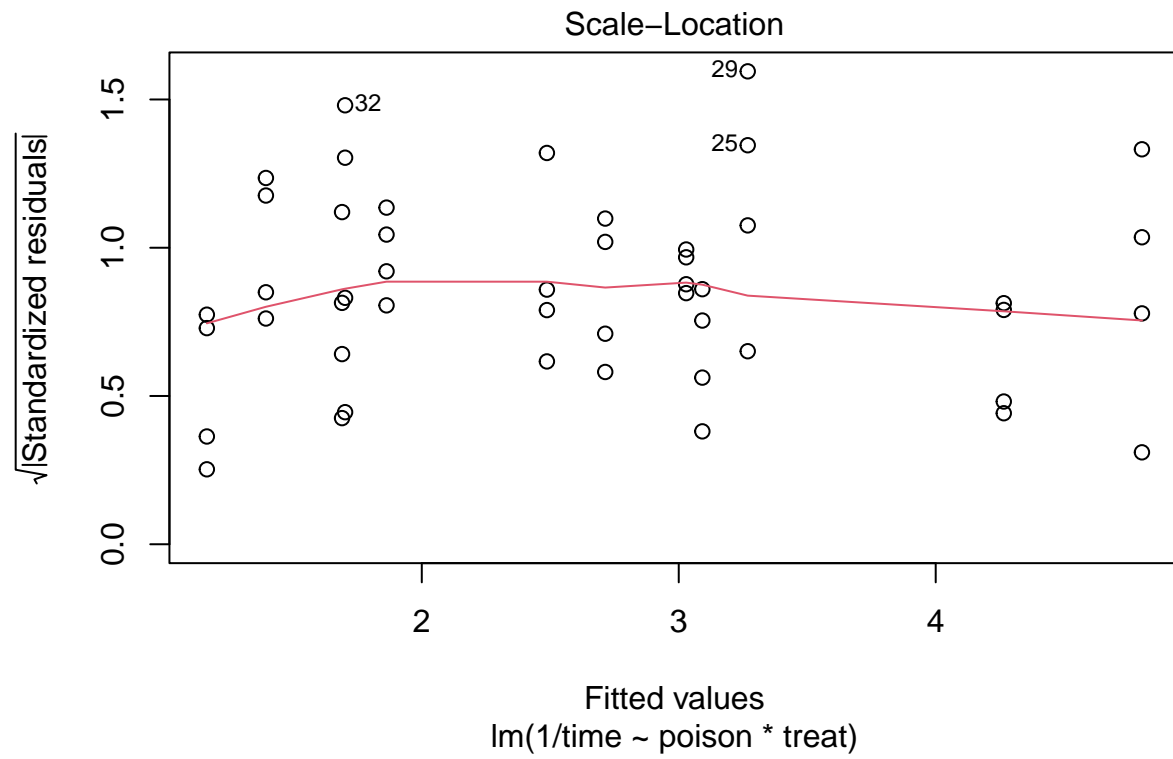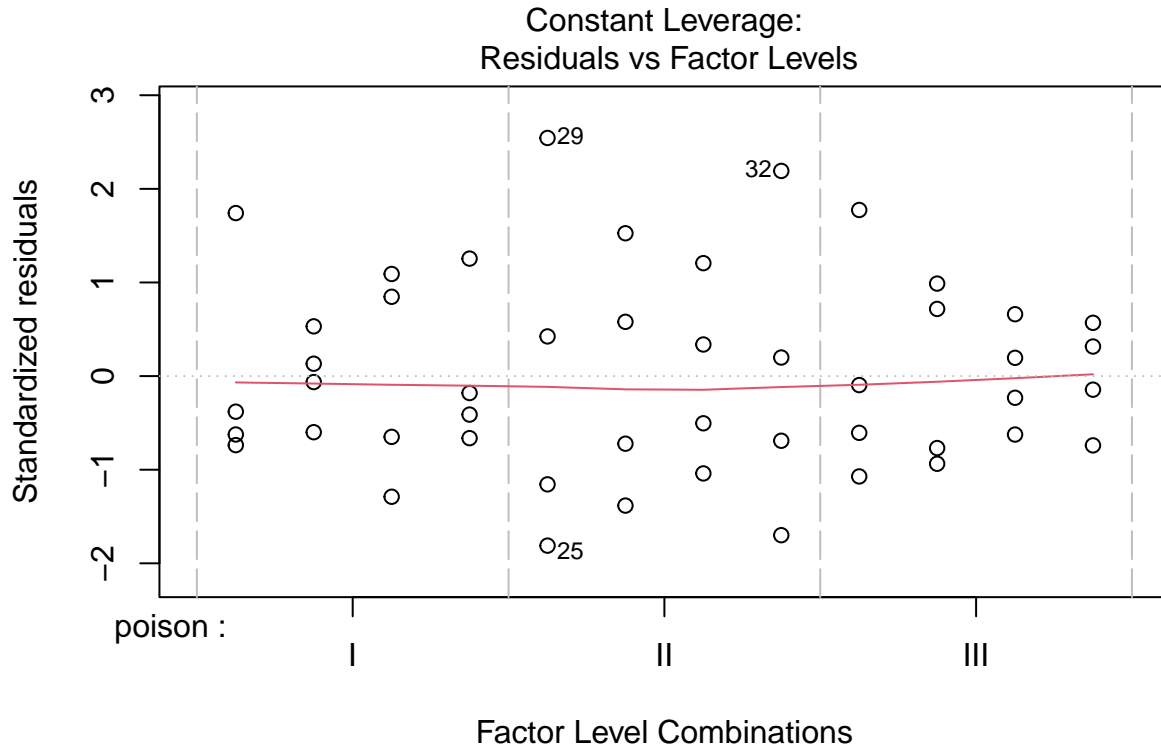
The reciprocal transformation seems to do perform better and can be interpreted as the rate of dying.

2.2.2 Inference

There are multiple interaction terms involved in the factorial design. We will first assess them together, which can be done using the anova table.

```
library(car)
Anova(rats3, type="III")
```

```
Anova Table (Type III tests)

Response: 1/time
             Sum Sq Df  F value      Pr(>F)
(Intercept)  24.7383  1 103.0395 4.158e-12 ***
poison       11.1035  2  23.1241 3.477e-07 ***
treat         3.5723  3   4.9598  0.005535 **
poison:treat  1.5708  6   1.0904  0.386733
Residuals     8.6431 36
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

2.2.2.1 Removing the non-significant interaction term The interaction appears to be not significant at the 5% level.

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A common practice is to remove the interaction from the analysis. We then obtain an additive model and the effects of the two treatments can be assessed separately.

```
rats4 <- lm(1/time~poison + treat, rats)
plot(rats4)
```


Residuals vs Fitted

Fitted values
lm(1/time ~ poison + treat)

Normal Q–Q

Standardized residuals

Theoretical Quantiles
lm(1/time ~ poison + treat)

Scale−Location

√|Standardized residuals|

Fitted values
lm(1/time ~ poison + treat)

Constant Leverage:
Residuals vs Factor Levels
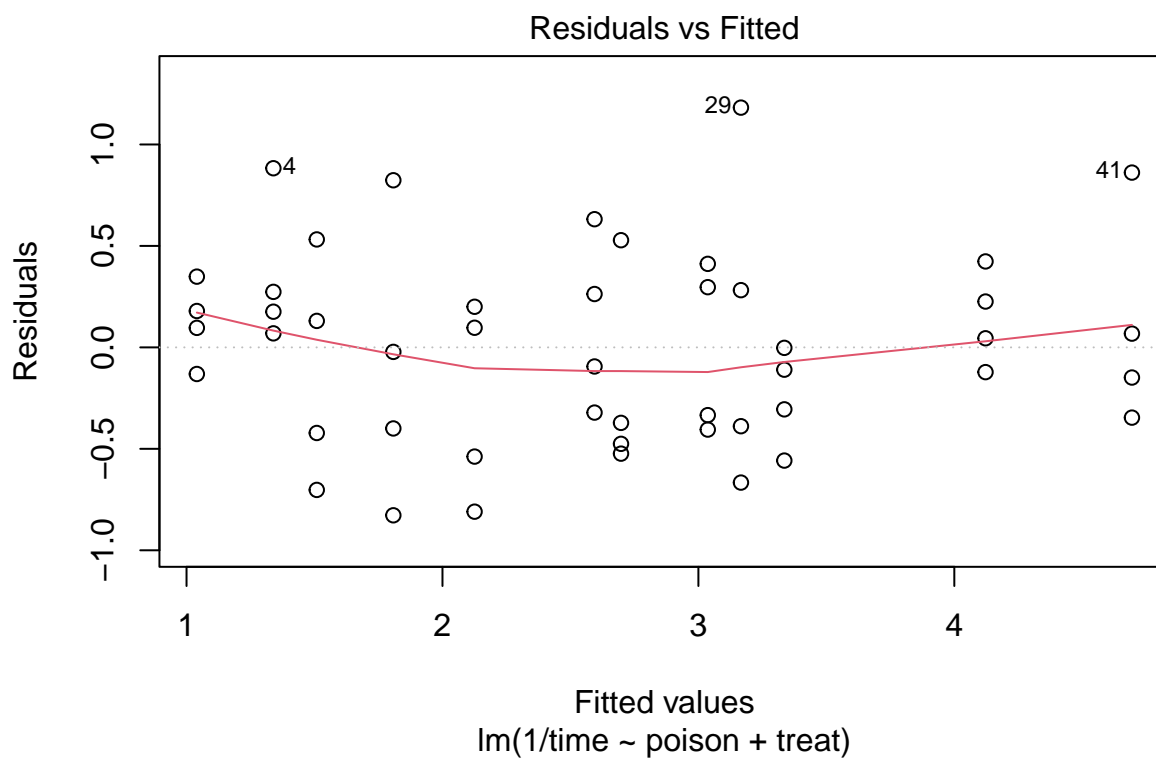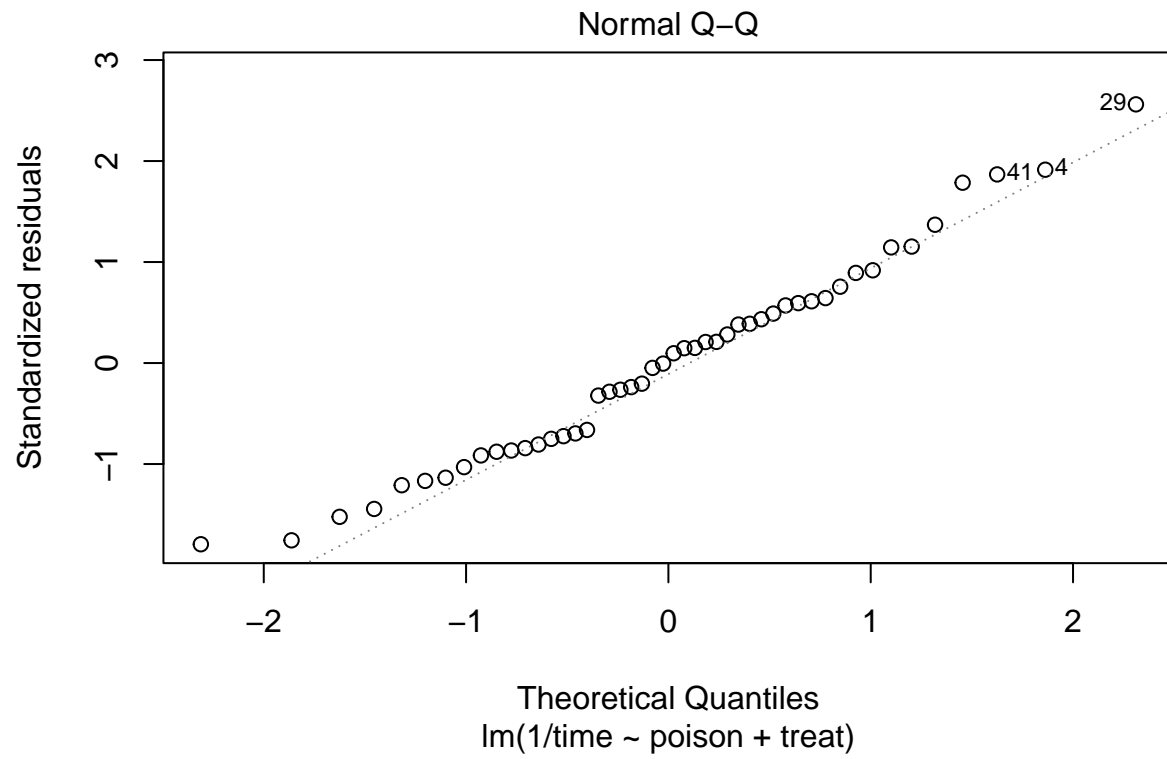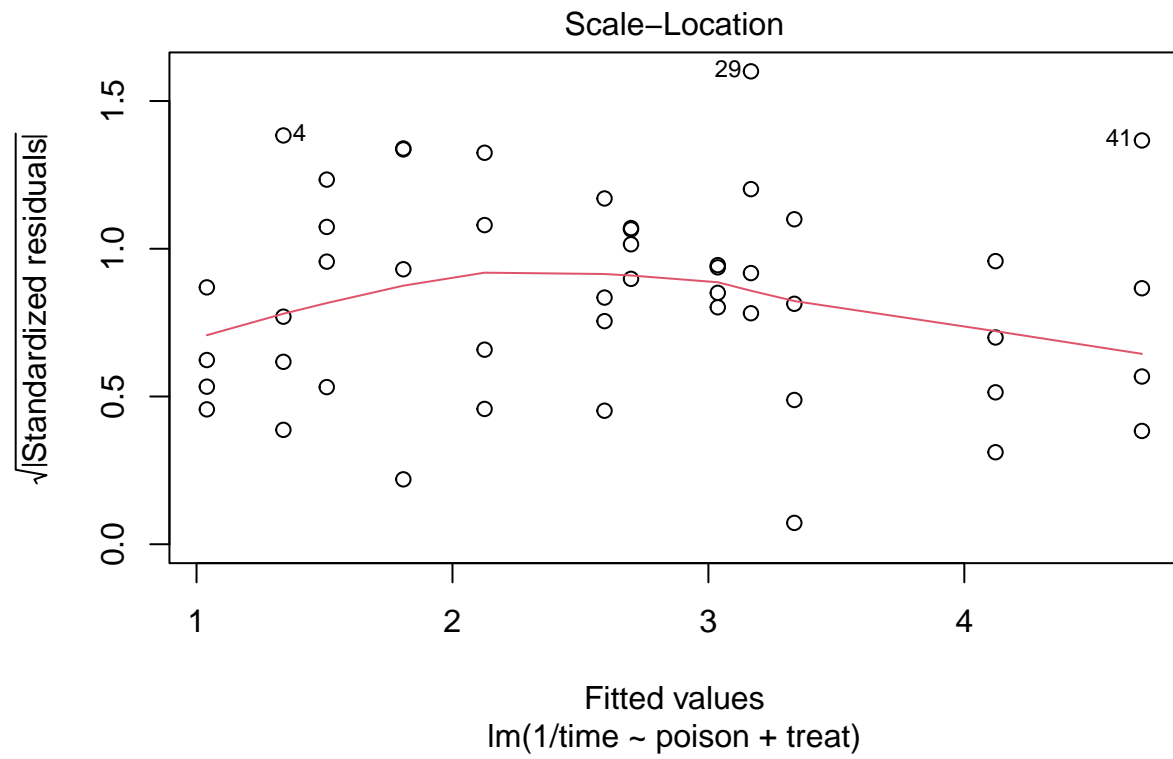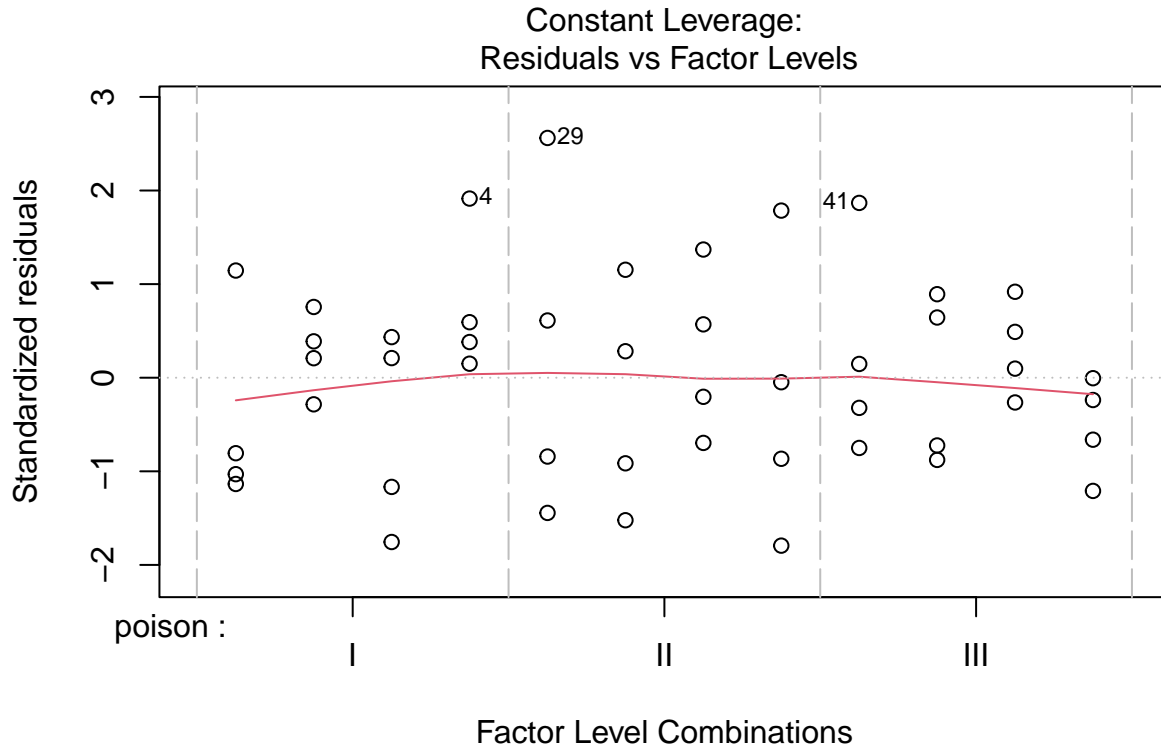
```
Anova(rats4, type="III")
```

```
Anova Table (Type III tests)

Response: 1/time
            Sum Sq Df F value      Pr(>F)
(Intercept) 58.219  1 239.399 < 2.2e-16 ***
poison      34.877  2  71.708 2.865e-14 ***
treat       20.414  3  27.982 4.192e-10 ***
Residuals   10.214 42
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The anova table shows that the effect of the poison and the treatment are both extremely significant ($p \ll 0.001$).

In the additive model we can assess the effect of the poison type and the treatments, separately in a post-hoc analysis.

```
library(multcomp)
comparisons <- glht(rats4, linfct = mcp(poison = "Tukey", treat="Tukey"))
summary(comparisons)
```

```
        Simultaneous Tests for General Linear Hypotheses
```

```
Multiple Comparisons of Means: Tukey Contrasts


Fit: lm(formula = 1/time ~ poison + treat, data = rats)

Linear Hypotheses:
                   Estimate Std. Error t value Pr(>|t|)
poison: II - I == 0     0.4686     0.1744    2.688   0.07347 .
poison: III - I == 0    1.9964     0.1744   11.451   < 0.001 ***
poison: III - II == 0   1.5278     0.1744    8.763   < 0.001 ***
treat: B - A == 0      -1.6574     0.2013   -8.233   < 0.001 ***
treat: C - A == 0      -0.5721     0.2013   -2.842   0.05087 .
treat: D - A == 0      -1.3583     0.2013   -6.747   < 0.001 ***
treat: C - B == 0       1.0853     0.2013    5.391   < 0.001 ***
treat: D - B == 0       0.2991     0.2013    1.485   0.61546
treat: D - C == 0      -0.7862     0.2013   -3.905   0.00276 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
(Adjusted p values reported -- single-step method)
```

`confint(comparisons)`

```
      Simultaneous Confidence Intervals

Multiple Comparisons of Means: Tukey Contrasts


Fit: lm(formula = 1/time ~ poison + treat, data = rats)

Quantile = 2.8491
95% family-wise confidence level


Linear Hypotheses:
                   Estimate  lwr        upr
poison: II - I == 0     0.468641 -0.028098  0.965380
poison: III - I == 0    1.996425  1.499686  2.493164
poison: III - II == 0   1.527784  1.031045  2.024523
treat: B - A == 0      -1.657402 -2.230987 -1.083818
treat: C - A == 0      -0.572135 -1.145720  0.001449
treat: D - A == 0      -1.358338 -1.931923 -0.784753
treat: C - B == 0       1.085267  0.511682  1.658852
treat: D - B == 0       0.299064 -0.274521  0.872649
treat: D - C == 0      -0.786203 -1.359788 -0.212618
```

`plot(comparisons)`

95% family–wise confidence level
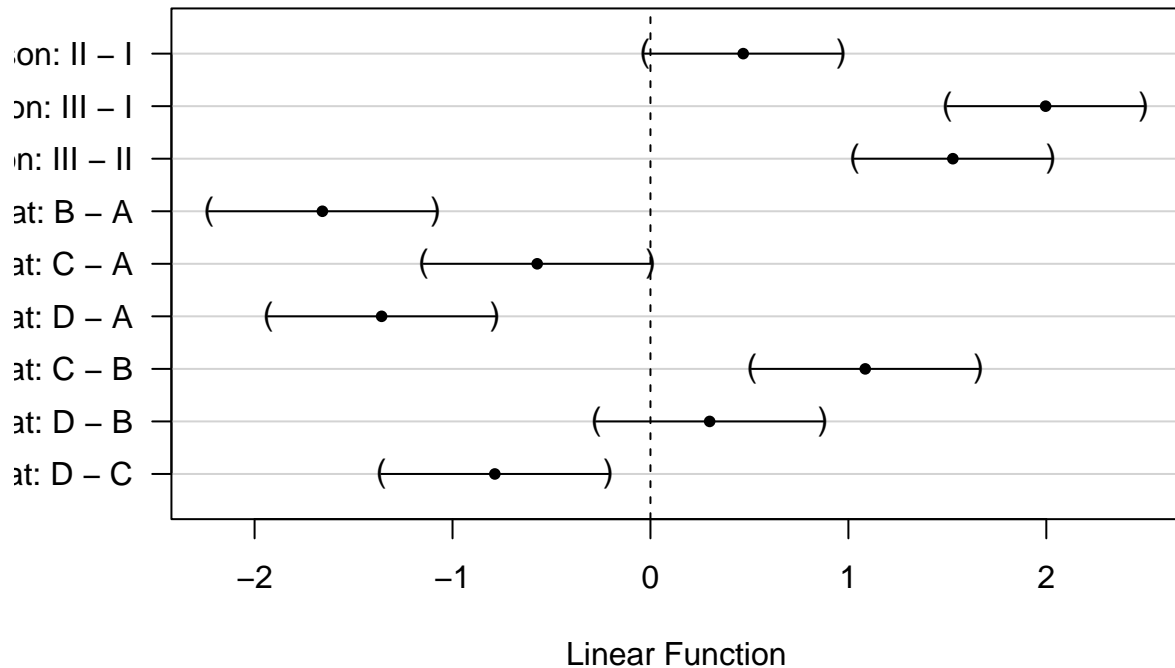
2.2.2.2 Keeping the non-significant interaction term We know that accepting the null hypothesis that there is no interaction is a weak conclusion. It is possible that the experiment was simply underpowered to pick up the interaction. We can choose to keep the interaction in the model.

If the interaction were to be significant, this would mean that the effect of the poison depends on the treatment and vice versa. Then, we cannot study the interactions separately.

```
ExploreModelMatrix::VisualizeDesign(rats,~poison*treat)$plot
```

```
[[1]]
```

poison \ treat	A	B	C	D
III	(Intercept) + poisonIII	(Intercept) + poisonIII + treatB + poisonIII:treatB	(Intercept) + poisonIII + treatC + poisonIII:treatC	(Intercept) + poisonIII + treatD + poisonIII:treatD
II	(Intercept) + poisonII	(Intercept) + poisonII + treatB + poisonII:treatB	(Intercept) + poisonII + treatC + poisonII:treatC	(Intercept) + poisonII + treatD + poisonII:treatD
I	(Intercept)	(Intercept) + treatB	(Intercept) + treatC	(Intercept) + treatD

In case of an interaction we could study the effect of the poison for each treatment separately:

1. For treatment A we would have to assess the following comparisons:

- II-I: $H_0 : \beta_{II} = 0$
- III-I: $H_0 : \beta_{III} = 0$
- III-II: $H_0 : \beta_{III} - \beta_{II} = 0$

2. For treatment B we would have to assess the following comparisons:

- II-I: $H_0 : \beta_{II} + \beta_{II:B} = 0$
- III-I: $H_0 : \beta_{III} + \beta_{III:B} = 0$
- III-II: $H_0 : \beta_{III} + \beta_{III:B} - \beta_{II} - \beta_{II:B} = 0$

3. For treatment C we would have to assess the following comparisons:

- II-I: $H_0 : \beta_{II} + \beta_{II:C} = 0$
- III-I: $H_0 : \beta_{III} + \beta_{III:C} = 0$
- III-II: $H_0 : \beta_{III} + \beta_{III:C} - \beta_{II} - \beta_{II:C} = 0$

4. For treatment C we would have to assess the following comparisons:

- II-I: $H_0 : \beta_{II} + \beta_{II:D} = 0$
- III-I: $H_0 : \beta_{III} + \beta_{III:D} = 0$
- III-II: $H_0 : \beta_{III} + \beta_{III:D} - \beta_{II} - \beta_{II:D} = 0$

The same holds for assessing the effect of the treatment:

For treatment C we would have to assess the following comparisons:

1. Poison I

- B-A: $H_0 : \beta_B = 0$
- C-A: $H_0 : \beta_C = 0$
- D-A: $H_0 : \beta_D = 0$
- C-B: $H_0 : \beta_C - \beta_B = 0$
- D-B: $H_0 : \beta_D - \beta_B = 0$
- D-C: $H_0 : \beta_D - \beta_C = 0$

2. Poison II

- B-A: $H_0 : \beta_B + \beta_{II:B} = 0$
- C-A: $H_0 : \beta_C + \beta_{II:C} = 0$
- D-A: $H_0 : \beta_D + \beta_{II:D} = 0$
- C-B: $H_0 : \beta_C + \beta_{II:C} - \beta_B - \beta_{II:B} = 0$
- D-B: $H_0 : \beta_D + \beta_{II:D} - \beta_B - \beta_{II:B} = 0$
- D-C: $H_0 : \beta_D + \beta_{II:D} - \beta_C - \beta_{II:C} = 0$

3. Poison III

- B-A: $H_0 : \beta_B + \beta_{III:B} = 0$
- C-A: $H_0 : \beta_C + \beta_{III:C} = 0$
- D-A: $H_0 : \beta_D + \beta_{II:D} = 0$
- C-B: $H_0 : \beta_C + \beta_{III:C} - \beta_B - \beta_{III:B} = 0$
- D-B: $H_0 : \beta_D + \beta_{III:D} - \beta_B - \beta_{III:B} = 0$
- D-C: $H_0 : \beta_D + \beta_{III:D} - \beta_C - \beta_{III:C} = 0$

```
comparisonsInt <- glht(rats3, linfct = c(
  "poisonII = 0",
  "poisonIII = 0",
  "poisonIII - poisonII = 0",
  "poisonII + poisonII:treatB = 0",
  "poisonIII + poisonIII:treatB = 0",
  "poisonIII + poisonIII:treatB - poisonII- poisonII:treatB = 0",
  "poisonII + poisonII:treatC = 0",
  "poisonIII + poisonIII:treatC = 0",
  "poisonIII + poisonIII:treatC - poisonII- poisonII:treatC = 0",
  "poisonII + poisonII:treatD = 0",
  "poisonIII + poisonIII:treatD = 0",
  "poisonIII + poisonIII:treatD - poisonII- poisonII:treatD = 0",
  "treatB = 0",
  "treatC = 0",
  "treatD = 0",
  "treatC - treatB = 0",
  "treatD - treatB = 0",
  "treatD - treatC = 0",
  "treatB + poisonII:treatB = 0",
  "treatC + poisonII:treatC = 0",
```

```
  "treatD + poisonII:treatD = 0",
  "treatC + poisonII:treatC - treatB - poisonII:treatB = 0",
  "treatD + poisonII:treatD - treatB - poisonII:treatB = 0",
  "treatD + poisonII:treatD - treatC - poisonII:treatC = 0",
  "treatB + poisonIII:treatB = 0",
  "treatC + poisonIII:treatC = 0",
  "treatD + poisonIII:treatD = 0",
  "treatC + poisonIII:treatC - treatB - poisonIII:treatB = 0",
  "treatD + poisonIII:treatD - treatB - poisonIII:treatB = 0",
  "treatD + poisonIII:treatD - treatC - poisonIII:treatC = 0")
)
summary(comparisonsInt)
```

Simultaneous Tests for General Linear Hypotheses

Fit: lm(formula = 1/time ~ poison * treat, data = rats)

Linear Hypotheses:

	Estimate
poisonII == 0	0.78159
poisonIII == 0	2.31580
poisonIII - poisonII == 0	1.53422
poisonII + poisonII:treatB == 0	0.22993
poisonIII + poisonIII:treatB == 0	1.86551
poisonIII + poisonIII:treatB - poisonII - poisonII:treatB == 0	1.63558
poisonII + poisonII:treatC == 0	0.85120
poisonIII + poisonIII:treatC == 0	2.40226
poisonIII + poisonIII:treatC - poisonII - poisonII:treatC == 0	1.55107
poisonII + poisonII:treatD == 0	0.01185
poisonIII + poisonIII:treatD == 0	1.40212
poisonIII + poisonIII:treatD - poisonII - poisonII:treatD == 0	1.39027
treatB == 0	-1.32342
treatC == 0	-0.62416
treatD == 0	-0.79720
treatC - treatB == 0	0.69926
treatD - treatB == 0	0.52622
treatD - treatC == 0	-0.17304
treatB + poisonII:treatB == 0	-1.87508
treatC + poisonII:treatC == 0	-0.55455
treatD + poisonII:treatD == 0	-1.56694
treatC + poisonII:treatC - treatB - poisonII:treatB == 0	1.32053
treatD + poisonII:treatD - treatB - poisonII:treatB == 0	0.30814
treatD + poisonII:treatD - treatC - poisonII:treatC == 0	-1.01239
treatB + poisonIII:treatB == 0	-1.77371
treatC + poisonIII:treatC == 0	-0.53770
treatD + poisonIII:treatD == 0	-1.71088
treatC + poisonIII:treatC - treatB - poisonIII:treatB == 0	1.23601
treatD + poisonIII:treatD - treatB - poisonIII:treatB == 0	0.06283
treatD + poisonIII:treatD - treatC - poisonIII:treatC == 0	-1.17318
	Std. Error
poisonII == 0	0.34647
poisonIII == 0	0.34647
poisonIII - poisonII == 0	0.34647

```
poisonII + poisonII:treatB == 0                                              0.34647
poisonIII + poisonIII:treatB == 0                                            0.34647
poisonIII + poisonIII:treatB - poisonII - poisonII:treatB == 0    0.34647
poisonII + poisonII:treatC == 0                                              0.34647
poisonIII + poisonIII:treatC == 0                                            0.34647
poisonIII + poisonIII:treatC - poisonII - poisonII:treatC == 0    0.34647
poisonII + poisonII:treatD == 0                                              0.34647
poisonIII + poisonIII:treatD == 0                                            0.34647
poisonIII + poisonIII:treatD - poisonII - poisonII:treatD == 0    0.34647
treatB == 0                                                                  0.34647
treatC == 0                                                                  0.34647
treatD == 0                                                                  0.34647
treatC - treatB == 0                                                         0.34647
treatD - treatB == 0                                                         0.34647
treatD - treatC == 0                                                         0.34647
treatB + poisonII:treatB == 0                                                0.34647
treatC + poisonII:treatC == 0                                                0.34647
treatD + poisonII:treatD == 0                                                0.34647
treatC + poisonII:treatC - treatB - poisonII:treatB == 0          0.34647
treatD + poisonII:treatD - treatB - poisonII:treatB == 0          0.34647
treatD + poisonII:treatD - treatC - poisonII:treatC == 0          0.34647
treatB + poisonIII:treatB == 0                                               0.34647
treatC + poisonIII:treatC == 0                                               0.34647
treatD + poisonIII:treatD == 0                                               0.34647
treatC + poisonIII:treatC - treatB - poisonIII:treatB == 0        0.34647
treatD + poisonIII:treatD - treatB - poisonIII:treatB == 0        0.34647
treatD + poisonIII:treatD - treatC - poisonIII:treatC == 0        0.34647
                                                                    t value Pr(>|t|)
poisonII == 0                                                          2.256   0.4100
poisonIII == 0                                                        6.684   <0.01
poisonIII - poisonII == 0                                             4.428   <0.01
poisonII + poisonII:treatB == 0                                      0.664   0.9998
poisonIII + poisonIII:treatB == 0                                    5.384   <0.01
poisonIII + poisonIII:treatB - poisonII - poisonII:treatB == 0   4.721   <0.01
poisonII + poisonII:treatC == 0                                      2.457   0.2939
poisonIII + poisonIII:treatC == 0                                    6.933   <0.01
poisonIII + poisonIII:treatC - poisonII - poisonII:treatC == 0   4.477   <0.01
poisonII + poisonII:treatD == 0                                      0.034   1.0000
poisonIII + poisonIII:treatD == 0                                    4.047   <0.01
poisonIII + poisonIII:treatD - poisonII - poisonII:treatD == 0   4.013   <0.01
treatB == 0                                                          -3.820   0.0124
treatC == 0                                                          -1.801   0.7163
treatD == 0                                                          -2.301   0.3816
treatC - treatB == 0                                                 2.018   0.5678
treatD - treatB == 0                                                 1.519   0.8749
treatD - treatC == 0                                                 -0.499   1.0000
treatB + poisonII:treatB == 0                                        -5.412   <0.01
treatC + poisonII:treatC == 0                                        -1.601   0.8355
treatD + poisonII:treatD == 0                                        -4.523   <0.01
treatC + poisonII:treatC - treatB - poisonII:treatB == 0          3.811   0.0127
treatD + poisonII:treatD - treatB - poisonII:treatB == 0          0.889   0.9973
treatD + poisonII:treatD - treatC - poisonII:treatC == 0          -2.922   0.1159
treatB + poisonIII:treatB == 0                                       -5.119   <0.01
treatC + poisonIII:treatC == 0                                       -1.552   0.8599
```

```
treatD + poisonIII:treatD == 0                                          -4.938   <0.01
treatC + poisonIII:treatC - treatB - poisonIII:treatB == 0               3.567   0.0244
treatD + poisonIII:treatD - treatB - poisonIII:treatB == 0               0.181   1.0000
treatD + poisonIII:treatD - treatC - poisonIII:treatC == 0              -3.386   0.0388


poisonII == 0
poisonIII == 0                                                     ***
poisonIII - poisonII == 0                                         **
poisonII + poisonII:treatB == 0
poisonIII + poisonIII:treatB == 0                                 ***
poisonIII + poisonIII:treatB - poisonII - poisonII:treatB == 0 ***
poisonII + poisonII:treatC == 0
poisonIII + poisonIII:treatC == 0                                 ***
poisonIII + poisonIII:treatC - poisonII - poisonII:treatC == 0 **
poisonII + poisonII:treatD == 0
poisonIII + poisonIII:treatD == 0                                 **
poisonIII + poisonIII:treatD - poisonII - poisonII:treatD == 0 **
treatB == 0                                                       *
treatC == 0
treatD == 0
treatC - treatB == 0
treatD - treatB == 0
treatD - treatC == 0
treatB + poisonII:treatB == 0                                     ***
treatC + poisonII:treatC == 0
treatD + poisonII:treatD == 0                                     **
treatC + poisonII:treatC - treatB - poisonII:treatB == 0         *
treatD + poisonII:treatD - treatB - poisonII:treatB == 0
treatD + poisonII:treatD - treatC - poisonII:treatC == 0
treatB + poisonIII:treatB == 0                                    ***
treatC + poisonIII:treatC == 0
treatD + poisonIII:treatD == 0                                    ***
treatC + poisonIII:treatC - treatB - poisonIII:treatB == 0       *
treatD + poisonIII:treatD - treatB - poisonIII:treatB == 0
treatD + poisonIII:treatD - treatC - poisonIII:treatC == 0       *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
(Adjusted p values reported -- single-step method)
```

`confint(comparisonsInt)`

```
     Simultaneous Confidence Intervals

Fit: lm(formula = 1/time ~ poison * treat, data = rats)

Quantile = 3.2847
95% family-wise confidence level


Linear Hypotheses:
                                                    Estimate
poisonII == 0                                        0.78159
poisonIII == 0                                       2.31580
poisonIII - poisonII == 0                            1.53422
```

```
poisonII + poisonII:treatB == 0                                              0.22993
poisonIII + poisonIII:treatB == 0                                            1.86551
poisonIII + poisonIII:treatB - poisonII - poisonII:treatB == 0   1.63558
poisonII + poisonII:treatC == 0                                              0.85120
poisonIII + poisonIII:treatC == 0                                            2.40226
poisonIII + poisonIII:treatC - poisonII - poisonII:treatC == 0   1.55107
poisonII + poisonII:treatD == 0                                              0.01185
poisonIII + poisonIII:treatD == 0                                            1.40212
poisonIII + poisonIII:treatD - poisonII - poisonII:treatD == 0   1.39027
treatB == 0                                                                 -1.32342
treatC == 0                                                                 -0.62416
treatD == 0                                                                 -0.79720
treatC - treatB == 0                                                         0.69926
treatD - treatB == 0                                                         0.52622
treatD - treatC == 0                                                        -0.17304
treatB + poisonII:treatB == 0                                               -1.87508
treatC + poisonII:treatC == 0                                               -0.55455
treatD + poisonII:treatD == 0                                               -1.56694
treatC + poisonII:treatC - treatB - poisonII:treatB == 0         1.32053
treatD + poisonII:treatD - treatB - poisonII:treatB == 0         0.30814
treatD + poisonII:treatD - treatC - poisonII:treatC == 0        -1.01239
treatB + poisonIII:treatB == 0                                              -1.77371
treatC + poisonIII:treatC == 0                                              -0.53770
treatD + poisonIII:treatD == 0                                              -1.71088
treatC + poisonIII:treatC - treatB - poisonIII:treatB == 0       1.23601
treatD + poisonIII:treatD - treatB - poisonIII:treatB == 0       0.06283
treatD + poisonIII:treatD - treatC - poisonIII:treatC == 0      -1.17318
                                                                             lwr
poisonII == 0                                                               -0.35647
poisonIII == 0                                                               1.17774
poisonIII - poisonII == 0                                                    0.39616
poisonII + poisonII:treatB == 0                                             -0.90813
poisonIII + poisonIII:treatB == 0                                            0.72745
poisonIII + poisonIII:treatB - poisonII - poisonII:treatB == 0   0.49752
poisonII + poisonII:treatC == 0                                             -0.28686
poisonIII + poisonIII:treatC == 0                                            1.26420
poisonIII + poisonIII:treatC - poisonII - poisonII:treatC == 0   0.41301
poisonII + poisonII:treatD == 0                                             -1.12621
poisonIII + poisonIII:treatD == 0                                            0.26406
poisonIII + poisonIII:treatD - poisonII - poisonII:treatD == 0   0.25221
treatB == 0                                                                 -2.46148
treatC == 0                                                                 -1.76222
treatD == 0                                                                 -1.93526
treatC - treatB == 0                                                        -0.43880
treatD - treatB == 0                                                        -0.61184
treatD - treatC == 0                                                        -1.31110
treatB + poisonII:treatB == 0                                               -3.01314
treatC + poisonII:treatC == 0                                               -1.69261
treatD + poisonII:treatD == 0                                               -2.70500
treatC + poisonII:treatC - treatB - poisonII:treatB == 0         0.18247
treatD + poisonII:treatD - treatB - poisonII:treatB == 0        -0.82992
treatD + poisonII:treatD - treatC - poisonII:treatC == 0        -2.15045
treatB + poisonIII:treatB == 0                                              -2.91177
treatC + poisonIII:treatC == 0                                              -1.67576
```

```
treatD + poisonIII:treatD == 0                                      -2.84894
treatC + poisonIII:treatC - treatB - poisonIII:treatB == 0           0.09795
treatD + poisonIII:treatD - treatB - poisonIII:treatB == 0          -1.07523
treatD + poisonIII:treatD - treatC - poisonIII:treatC == 0          -2.31124
                                                                    upr
poisonII == 0                                                        1.91965
poisonIII == 0                                                       3.45386
poisonIII - poisonII == 0                                            2.67228
poisonII + poisonII:treatB == 0                                      1.36799
poisonIII + poisonIII:treatB == 0                                    3.00357
poisonIII + poisonIII:treatB - poisonII - poisonII:treatB == 0  2.77364
poisonII + poisonII:treatC == 0                                      1.98926
poisonIII + poisonIII:treatC == 0                                    3.54032
poisonIII + poisonIII:treatC - poisonII - poisonII:treatC == 0  2.68913
poisonII + poisonII:treatD == 0                                      1.14991
poisonIII + poisonIII:treatD == 0                                    2.54018
poisonIII + poisonIII:treatD - poisonII - poisonII:treatD == 0  2.52833
treatB == 0                                                         -0.18536
treatC == 0                                                          0.51390
treatD == 0                                                          0.34086
treatC - treatB == 0                                                 1.83732
treatD - treatB == 0                                                 1.66428
treatD - treatC == 0                                                 0.96502
treatB + poisonII:treatB == 0                                       -0.73702
treatC + poisonII:treatC == 0                                        0.58351
treatD + poisonII:treatD == 0                                       -0.42888
treatC + poisonII:treatC - treatB - poisonII:treatB == 0             2.45859
treatD + poisonII:treatD - treatB - poisonII:treatB == 0             1.44620
treatD + poisonII:treatD - treatC - poisonII:treatC == 0             0.12567
treatB + poisonIII:treatB == 0                                      -0.63565
treatC + poisonIII:treatC == 0                                       0.60036
treatD + poisonIII:treatD == 0                                      -0.57282
treatC + poisonIII:treatC - treatB - poisonIII:treatB == 0           2.37407
treatD + poisonIII:treatD - treatB - poisonIII:treatB == 0           1.20089
treatD + poisonIII:treatD - treatC - poisonIII:treatC == 0          -0.03512
```

```
plot(comparisonsInt)
```

95% family–wise confidence level
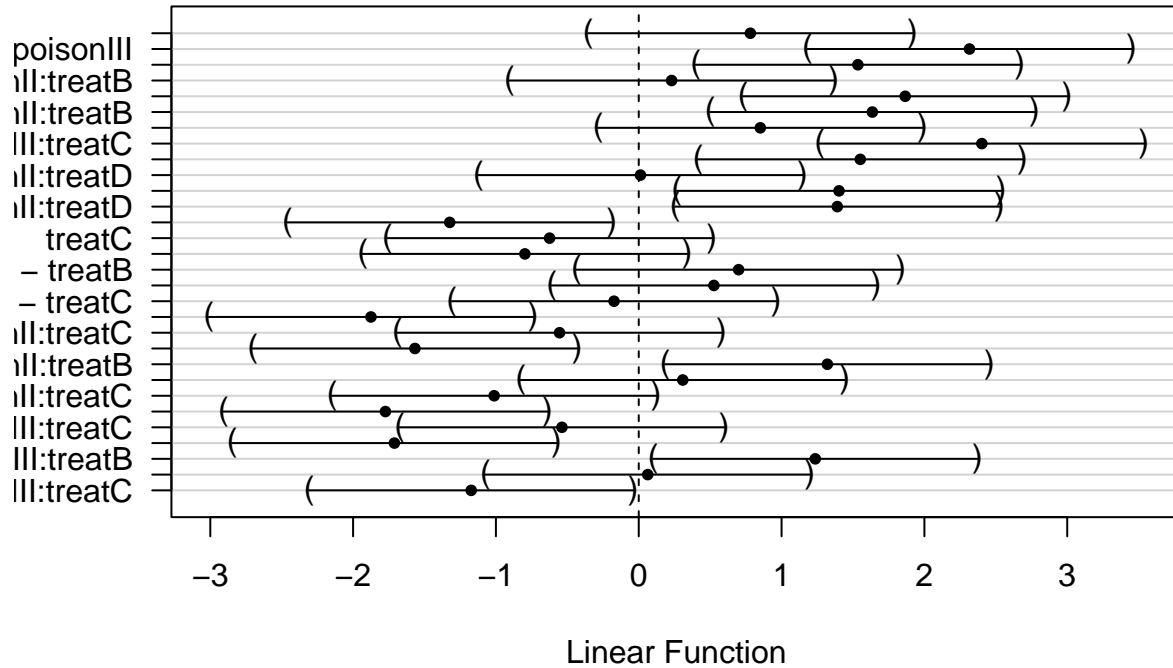
Since the interaction was not significant we also could have used model three to assess the average effect of the poison over all different treatments and the average effect of the treatment over all different poisons. This should give us similar results as removing the interaction from the model.

e.g. poison III vs poison II that would result in

- III-II:

$$H_0 : \frac{(\beta_{III} - \beta_{II}) + (\beta_{III} + \beta_{III:B} - \beta_{II} - \beta_{II:B}) + (\beta_{III} + \beta_{III:C} - \beta_{II} - \beta_{II:C} + +(\beta_{III} + \beta_{III:D} - \beta_{II} - \beta_{II:D}))}{4} = 0$$

$$H_0 : \beta_{III} + \frac{1}{4} \times \beta_{III:B} + \frac{1}{4} \times \beta_{III:C} + \frac{1}{4} \times \beta_{III:D} - \beta_{II} - \frac{1}{4} \times \beta_{II:B} - \frac{1}{4} \times \beta_{II:C} - \frac{1}{4} \times \beta_{II:D} = 0$$

```
contrasts <- c(
  "poisonII + 1/4*poisonII:treatB + 1/4*poisonII:treatC + 1/4*poisonII:treatD = 0",
  "poisonIII + 1/4*poisonIII:treatB + 1/4*poisonIII:treatC + 1/4*poisonIII:treatD= 0",
  "poisonIII + 1/4*poisonIII:treatB + 1/4*poisonIII:treatC + 1/4*poisonIII:treatD - poisonII - 1/4*pois
  "treatB + 1/3*poisonII:treatB + 1/3*poisonIII:treatB = 0",
  "treatC + 1/3*poisonII:treatC + 1/3*poisonIII:treatC = 0",
  "treatD + 1/3*poisonII:treatD + 1/3*poisonIII:treatD = 0",
  "treatC + 1/3*poisonII:treatC + 1/3*poisonIII:treatC - treatB - 1/3*poisonII:treatB - 1/3*poisonIII:t
  "treatD + 1/3*poisonII:treatD + 1/3*poisonIII:treatD  - treatB - 1/3*poisonII:treatB - 1/3*poisonIII:
  "treatD + 1/3*poisonII:treatD + 1/3*poisonIII:treatD  - treatC - 1/3*poisonII:treatC - 1/3*poisonIII:

names(contrasts) <- c("II-I","III-I","III-II","B-A","C-A","D-A","C-B","D-B","D-C")
comparisonsInt <- glht(rats3, linfct = contrasts
)
summary(comparisonsInt)
```

```
        Simultaneous Tests for General Linear Hypotheses

Fit: lm(formula = 1/time ~ poison * treat, data = rats)

Linear Hypotheses:

poisonII + 1/4 * poisonII:treatB + 1/4 * poisonII:treatC + 1/4 * poisonII:treatD == 0
poisonIII + 1/4 * poisonIII:treatB + 1/4 * poisonIII:treatC + 1/4 * poisonIII:treatD == 0
poisonIII + 1/4 * poisonIII:treatB + 1/4 * poisonIII:treatC + 1/4 * poisonIII:treatD - poisonII - 1/4 *
treatB + 1/3 * poisonII:treatB + 1/3 * poisonIII:treatB == 0
treatC + 1/3 * poisonII:treatC + 1/3 * poisonIII:treatC == 0
treatD + 1/3 * poisonII:treatD + 1/3 * poisonIII:treatD == 0
treatC + 1/3 * poisonII:treatC + 1/3 * poisonIII:treatC - treatB - 1/3 * poisonII:treatB - 1/3 * poison
treatD + 1/3 * poisonII:treatD + 1/3 * poisonIII:treatD - treatB - 1/3 * poisonII:treatB - 1/3 * poison
treatD + 1/3 * poisonII:treatD + 1/3 * poisonIII:treatD - treatC - 1/3 * poisonII:treatC - 1/3 * poison

poisonII + 1/4 * poisonII:treatB + 1/4 * poisonII:treatC + 1/4 * poisonII:treatD == 0
poisonIII + 1/4 * poisonIII:treatB + 1/4 * poisonIII:treatC + 1/4 * poisonIII:treatD == 0
poisonIII + 1/4 * poisonIII:treatB + 1/4 * poisonIII:treatC + 1/4 * poisonIII:treatD - poisonII - 1/4 *
treatB + 1/3 * poisonII:treatB + 1/3 * poisonIII:treatB == 0
treatC + 1/3 * poisonII:treatC + 1/3 * poisonIII:treatC == 0
treatD + 1/3 * poisonII:treatD + 1/3 * poisonIII:treatD == 0
treatC + 1/3 * poisonII:treatC + 1/3 * poisonIII:treatC - treatB - 1/3 * poisonII:treatB - 1/3 * poison
treatD + 1/3 * poisonII:treatD + 1/3 * poisonIII:treatD - treatB - 1/3 * poisonII:treatB - 1/3 * poison
treatD + 1/3 * poisonII:treatD + 1/3 * poisonIII:treatD - treatC - 1/3 * poisonII:treatC - 1/3 * poison

poisonII + 1/4 * poisonII:treatB + 1/4 * poisonII:treatC + 1/4 * poisonII:treatD == 0
poisonIII + 1/4 * poisonIII:treatB + 1/4 * poisonIII:treatC + 1/4 * poisonIII:treatD == 0
poisonIII + 1/4 * poisonIII:treatB + 1/4 * poisonIII:treatC + 1/4 * poisonIII:treatD - poisonII - 1/4 *
treatB + 1/3 * poisonII:treatB + 1/3 * poisonIII:treatB == 0
treatC + 1/3 * poisonII:treatC + 1/3 * poisonIII:treatC == 0
treatD + 1/3 * poisonII:treatD + 1/3 * poisonIII:treatD == 0
treatC + 1/3 * poisonII:treatC + 1/3 * poisonIII:treatC - treatB - 1/3 * poisonII:treatB - 1/3 * poison
treatD + 1/3 * poisonII:treatD + 1/3 * poisonIII:treatD - treatB - 1/3 * poisonII:treatB - 1/3 * poison
treatD + 1/3 * poisonII:treatD + 1/3 * poisonIII:treatD - treatC - 1/3 * poisonII:treatC - 1/3 * poison

poisonII + 1/4 * poisonII:treatB + 1/4 * poisonII:treatC + 1/4 * poisonII:treatD == 0
poisonIII + 1/4 * poisonIII:treatB + 1/4 * poisonIII:treatC + 1/4 * poisonIII:treatD == 0
poisonIII + 1/4 * poisonIII:treatB + 1/4 * poisonIII:treatC + 1/4 * poisonIII:treatD - poisonII - 1/4 *
treatB + 1/3 * poisonII:treatB + 1/3 * poisonIII:treatB == 0
treatC + 1/3 * poisonII:treatC + 1/3 * poisonIII:treatC == 0
treatD + 1/3 * poisonII:treatD + 1/3 * poisonIII:treatD == 0
treatC + 1/3 * poisonII:treatC + 1/3 * poisonIII:treatC - treatB - 1/3 * poisonII:treatB - 1/3 * poison
treatD + 1/3 * poisonII:treatD + 1/3 * poisonIII:treatD - treatB - 1/3 * poisonII:treatB - 1/3 * poison
treatD + 1/3 * poisonII:treatD + 1/3 * poisonIII:treatD - treatC - 1/3 * poisonII:treatC - 1/3 * poison

poisonII + 1/4 * poisonII:treatB + 1/4 * poisonII:treatC + 1/4 * poisonII:treatD == 0
poisonIII + 1/4 * poisonIII:treatB + 1/4 * poisonIII:treatC + 1/4 * poisonIII:treatD == 0
poisonIII + 1/4 * poisonIII:treatB + 1/4 * poisonIII:treatC + 1/4 * poisonIII:treatD - poisonII - 1/4 *
treatB + 1/3 * poisonII:treatB + 1/3 * poisonIII:treatB == 0
treatC + 1/3 * poisonII:treatC + 1/3 * poisonIII:treatC == 0
treatD + 1/3 * poisonII:treatD + 1/3 * poisonIII:treatD == 0
treatC + 1/3 * poisonII:treatC + 1/3 * poisonIII:treatC - treatB - 1/3 * poisonII:treatB - 1/3 * poison
treatD + 1/3 * poisonII:treatD + 1/3 * poisonIII:treatD - treatB - 1/3 * poisonII:treatB - 1/3 * poison
```

treatD + 1/3 * poisonII:treatD + 1/3 * poisonIII:treatD - treatC - 1/3 * poisonII:treatC - 1/3 * poison
---
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
(Adjusted p values reported -- single-step method)

confint(comparisonsInt)

      Simultaneous Confidence Intervals

Fit: lm(formula = 1/time ~ poison * treat, data = rats)

Quantile = 2.871
95% family-wise confidence level

Linear Hypotheses:

poisonII + 1/4 * poisonII:treatB + 1/4 * poisonII:treatC + 1/4 * poisonII:treatD == 0
poisonIII + 1/4 * poisonIII:treatB + 1/4 * poisonIII:treatC + 1/4 * poisonIII:treatD == 0
poisonIII + 1/4 * poisonIII:treatB + 1/4 * poisonIII:treatC + 1/4 * poisonIII:treatD - poisonII - 1/4 *
treatB + 1/3 * poisonII:treatB + 1/3 * poisonIII:treatB == 0
treatC + 1/3 * poisonII:treatC + 1/3 * poisonIII:treatC == 0
treatD + 1/3 * poisonII:treatD + 1/3 * poisonIII:treatD == 0
treatC + 1/3 * poisonII:treatC + 1/3 * poisonIII:treatC - treatB - 1/3 * poisonII:treatB - 1/3 * poison
treatD + 1/3 * poisonII:treatD + 1/3 * poisonIII:treatD - treatB - 1/3 * poisonII:treatB - 1/3 * poison
treatD + 1/3 * poisonII:treatD + 1/3 * poisonIII:treatD - treatC - 1/3 * poisonII:treatC - 1/3 * poison

poisonII + 1/4 * poisonII:treatB + 1/4 * poisonII:treatC + 1/4 * poisonII:treatD == 0
poisonIII + 1/4 * poisonIII:treatB + 1/4 * poisonIII:treatC + 1/4 * poisonIII:treatD == 0
poisonIII + 1/4 * poisonIII:treatB + 1/4 * poisonIII:treatC + 1/4 * poisonIII:treatD - poisonII - 1/4 *
treatB + 1/3 * poisonII:treatB + 1/3 * poisonIII:treatB == 0
treatC + 1/3 * poisonII:treatC + 1/3 * poisonIII:treatC == 0
treatD + 1/3 * poisonII:treatD + 1/3 * poisonIII:treatD == 0
treatC + 1/3 * poisonII:treatC + 1/3 * poisonIII:treatC - treatB - 1/3 * poisonII:treatB - 1/3 * poison
treatD + 1/3 * poisonII:treatD + 1/3 * poisonIII:treatD - treatB - 1/3 * poisonII:treatB - 1/3 * poison
treatD + 1/3 * poisonII:treatD + 1/3 * poisonIII:treatD - treatC - 1/3 * poisonII:treatC - 1/3 * poison

poisonII + 1/4 * poisonII:treatB + 1/4 * poisonII:treatC + 1/4 * poisonII:treatD == 0
poisonIII + 1/4 * poisonIII:treatB + 1/4 * poisonIII:treatC + 1/4 * poisonIII:treatD == 0
poisonIII + 1/4 * poisonIII:treatB + 1/4 * poisonIII:treatC + 1/4 * poisonIII:treatD - poisonII - 1/4 *
treatB + 1/3 * poisonII:treatB + 1/3 * poisonIII:treatB == 0
treatC + 1/3 * poisonII:treatC + 1/3 * poisonIII:treatC == 0
treatD + 1/3 * poisonII:treatD + 1/3 * poisonIII:treatD == 0
treatC + 1/3 * poisonII:treatC + 1/3 * poisonIII:treatC - treatB - 1/3 * poisonII:treatB - 1/3 * poison
treatD + 1/3 * poisonII:treatD + 1/3 * poisonIII:treatD - treatB - 1/3 * poisonII:treatB - 1/3 * poison
treatD + 1/3 * poisonII:treatD + 1/3 * poisonIII:treatD - treatC - 1/3 * poisonII:treatC - 1/3 * poison

```
plot(comparisonsInt)
```

95% family−wise confidence level