

# Module 8 - Analysis of variance (ANOVA). Analysis of covariance (ANCOVA).

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## Exercise 1.

(One-way ANOVA) File pszen.txt contains data on harvest rates (variable plon) for 32 fields each of which was fertilized with nitrogen in one of four doses (factor azot ). Each dose of nitrogen was applied to 8 fields.

```
> #load data
> pszen <- read.table(file="pszen.txt",header=T)
```

- Check if the assumptions of one-way analysis of variance hold. Assumptions:

- Continuously distributed response variable and nominal factor:

```
> class(pszen$plon)
```

```
[1] "numeric"
```

```
> class(pszen$azot)
```

```
[1] "factor"
```

- Response variable is normally distributed with a constant variance  $\sigma^2$  which does not depend on the level of the factor.

From the Figure-10 we see the the variance does not depend on the level of the nitrogen. We cannot see either any outliers on boxplots.

```
> boxplot(plon~azot, pszen,col="blue")
```

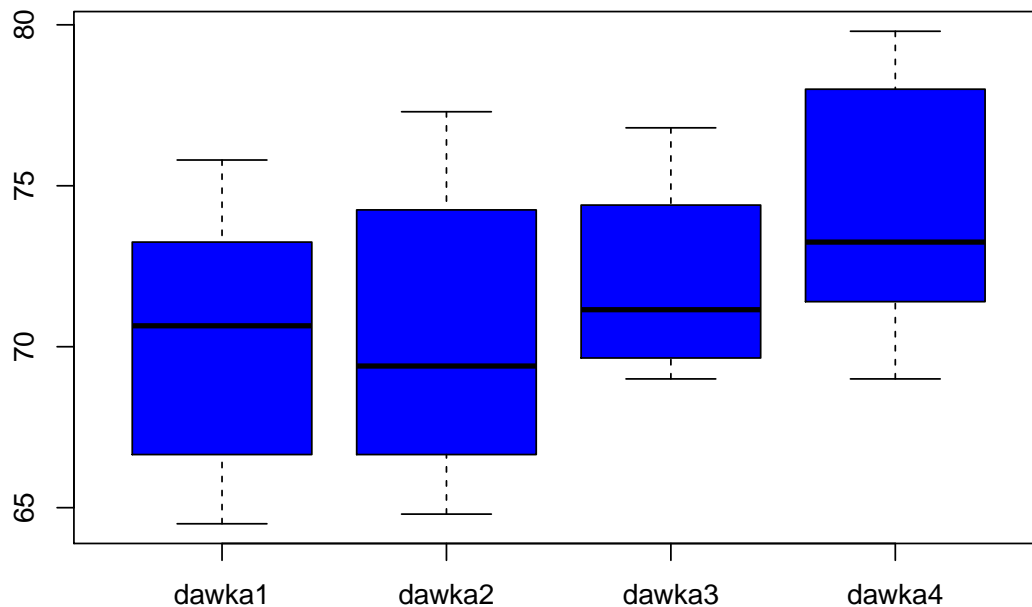


Figure 1: Boxplots of plon for differnt levels of azot

We can also perform statistical tests:

```
> library(car)
> leveneTest(plon~azot,pszen)
```

```

Levene's Test for Homogeneity of Variance (center = median)
  Df F value Pr(>F)
group 3  0.9384 0.4353
    28

```

```

> bartlett.test(plon~azot, data=pszen)

Bartlett test of homogeneity of variances

```

```

data:  plon by azot
Bartlett's K-squared = 1.0934, df = 3, p-value = 0.7787

```

```

> fligner.test(plon~azot, data=pszen)

Fligner-Killeen test of homogeneity of variances

```

```

data:  plon by azot
Fligner-Killeen:med chi-squared = 2.7323, df = 3, p-value = 0.4348

```

which conclude our visual findings that we cannot reject assumption about homogeneity of variance across groups. Figure-2 depicts normally shaped distribution.

```

> hist(pszzen$plon, xlab="plon",main="",col="blue")

```

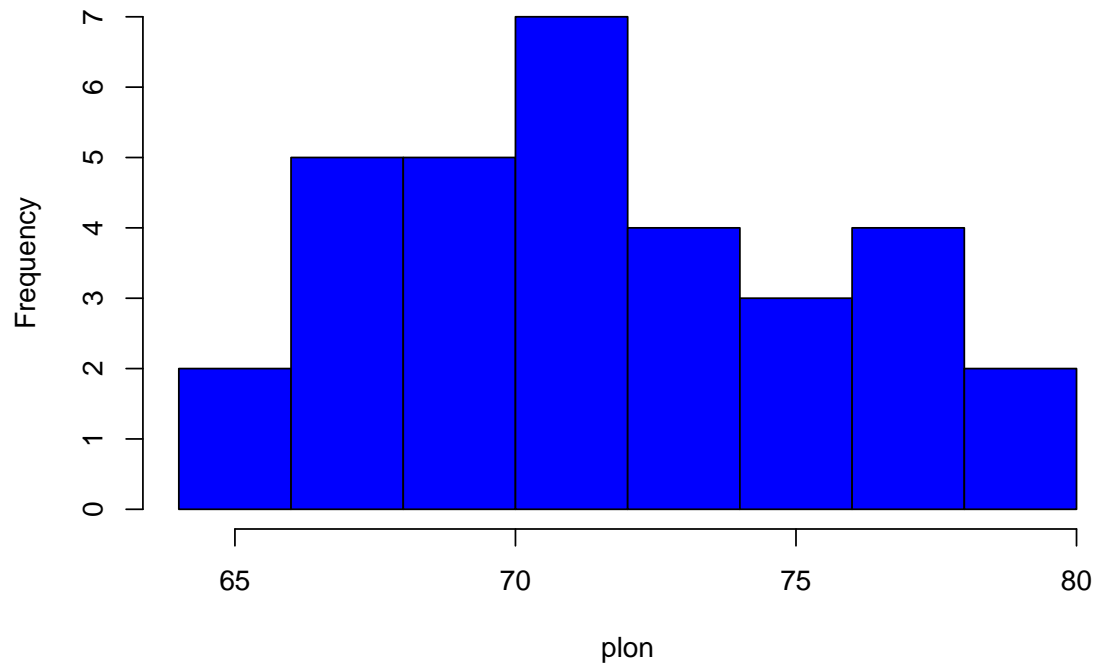


Figure 2: Histogram of response variable

The Figure-3 also confirms the normality assumption.

```
> qqnorm(pszan$plon,main="qq plot of plon",)
> qqline(pszan$plon)
```

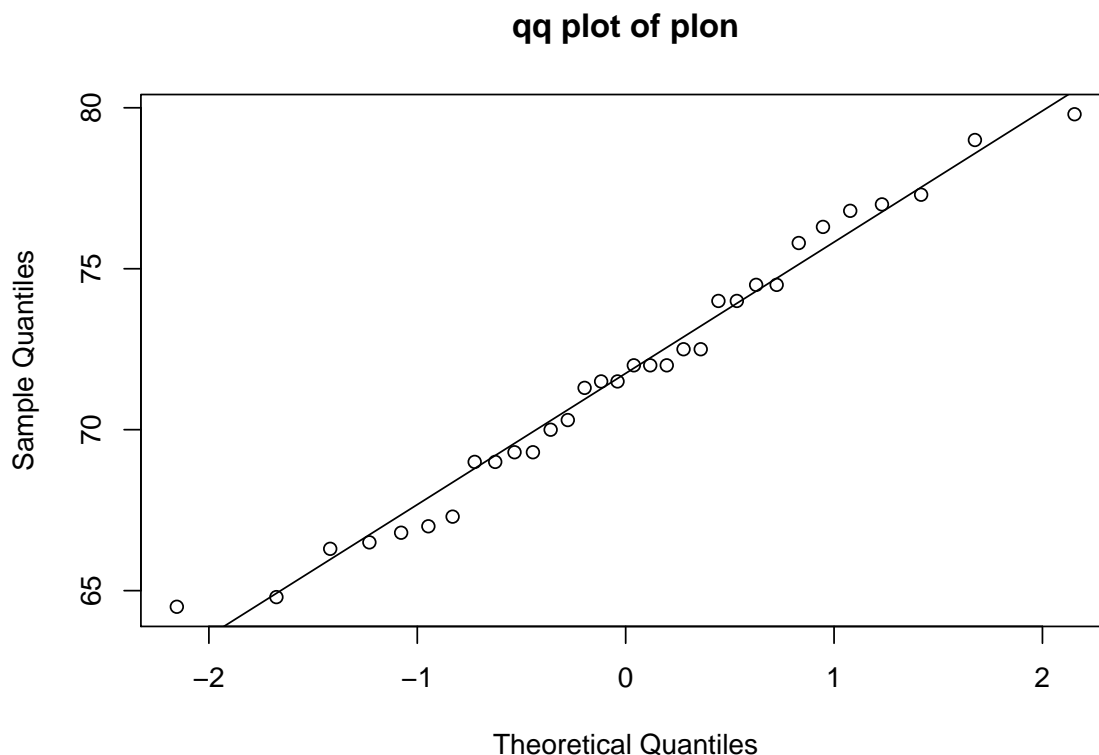


Figure 3: QQ plot for plon variable

– Balanced samples

We have balanced samples i.e. each level has been assigned the same number of

```
> table(pszan$azot)
```

```
dawka1 dawka2 dawka3 dawka4
      8      8      8      8
```

- Perform analysis of variance to decide whether the mean value of harvest depends on the dose of nitrogen used as fertilizer.

```
> (plon.azon.lm <- lm(plon~azot,pszan))
```

Call:

```
lm(formula = plon ~ azot, data = pszan)
```

Coefficients:

```
(Intercept)  azotdawka2  azotdawka3  azotdawka4
    70.1750     0.1625     1.8500     4.0875
```

```
> (plon.azon.lm.sum <- summary(lm(plon~azot,pszan)))
```

Call:

```
lm(formula = plon ~ azot, data = pszan)
```

Residuals:

```
    Min      1Q  Median      3Q     Max
-5.675 -3.028 -0.450  3.703  6.963
```

Coefficients:

```
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  70.1750     1.3945  50.322  <2e-16 ***
azotdawka2    0.1625     1.9721   0.082  0.9349
azotdawka3    1.8500     1.9721   0.938  0.3562
azotdawka4    4.0875     1.9721   2.073  0.0475 *
```

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 3.944 on 28 degrees of freedom  
 Multiple R-squared: 0.1662, Adjusted R-squared: 0.07687  
 F-statistic: 1.86 on 3 and 28 DF, p-value: 0.1592

To test whether the mean value of harvest depends on the dose of nitrogen used as fertilizer test:

$$H_0 : \text{azotdawka}_1 = \text{azotdawka}_2 = \text{azotdawka}_3 = \text{azotdawka}_4$$

$$H_1 : \text{there exists } i \text{ and } j \text{ such that } \text{azotdawka}_i \neq \text{azotdawka}_j$$

From the p-value 0.1592 we cannot reject  $H_0$  that all means are equal. So we cannot say that mean value of harvest depends on the dose of nitrogen used as fertilizer provided the data. Looking at the plots we see that there is a difference for different means but possibly we need more data to reject null hypothesis.

## Exercise 2.

(Two-way ANOVA) File `truczny.txt` contains data on survival times of 48 rats which were cured after being poisoned.

```
> truczny <- read.table(file="truczny.txt",header=T)
```

The following factors are considered:

`truczna` - dose of poison applied: low (A), medium (B), high (C),

`kuracja` - treatment method (one of four).

For every level of `truczna` and `kuracja` the survival times for four rats chosen at random were measured.

- Present the mean values of survival times graphically. Is an interaction visible in the plots?

There is possibly an interaction on the first plot when lines for A and B cross. However a formal test is needed to draw a statistically valid conclusion.

```
> par(mfrow=c(1,2))
> with(truczny,interaction.plot(kuracja, truczna, wyczas))
> with(truczny,interaction.plot(truczna,kuracja, wyczas))
```

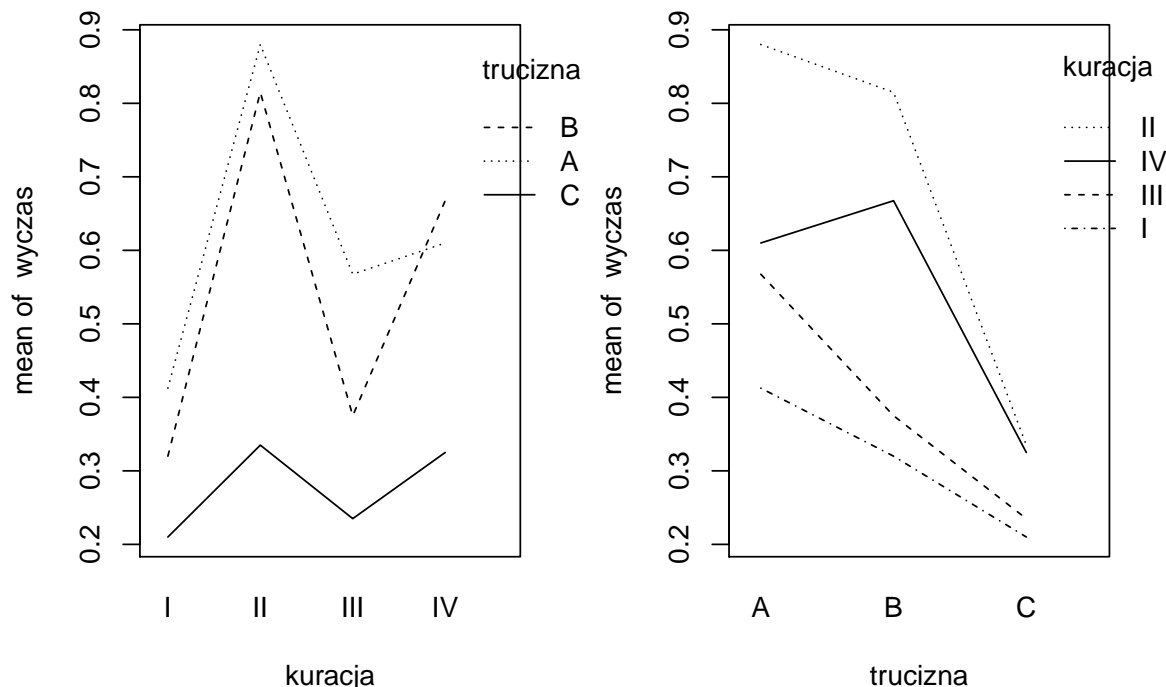


Figure 4: Profile plots of the mean responses

- Fit two-way ANOVA model and perform appropriate test to decide whether the interaction is present.

```
> truczny.lm <- lm(wyczas~kuracja*truczna,truczny)
> anova(truczny.lm)
```

## Analysis of Variance Table

Response: wyczas

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
kuracja	3	0.92121	0.30707	13.8056	3.777e-06 ***
trucizna	2	1.03301	0.51651	23.2217	3.331e-07 ***
kuracja:trucizna	6	0.25014	0.04169	1.8743	0.1123
Residuals	36	0.80073	0.02224		

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

We conclude that interaction between factors (kuracja and trucizna) is not statistically significant.

- Check if the model assumptions hold. In particular analyze residual plot.

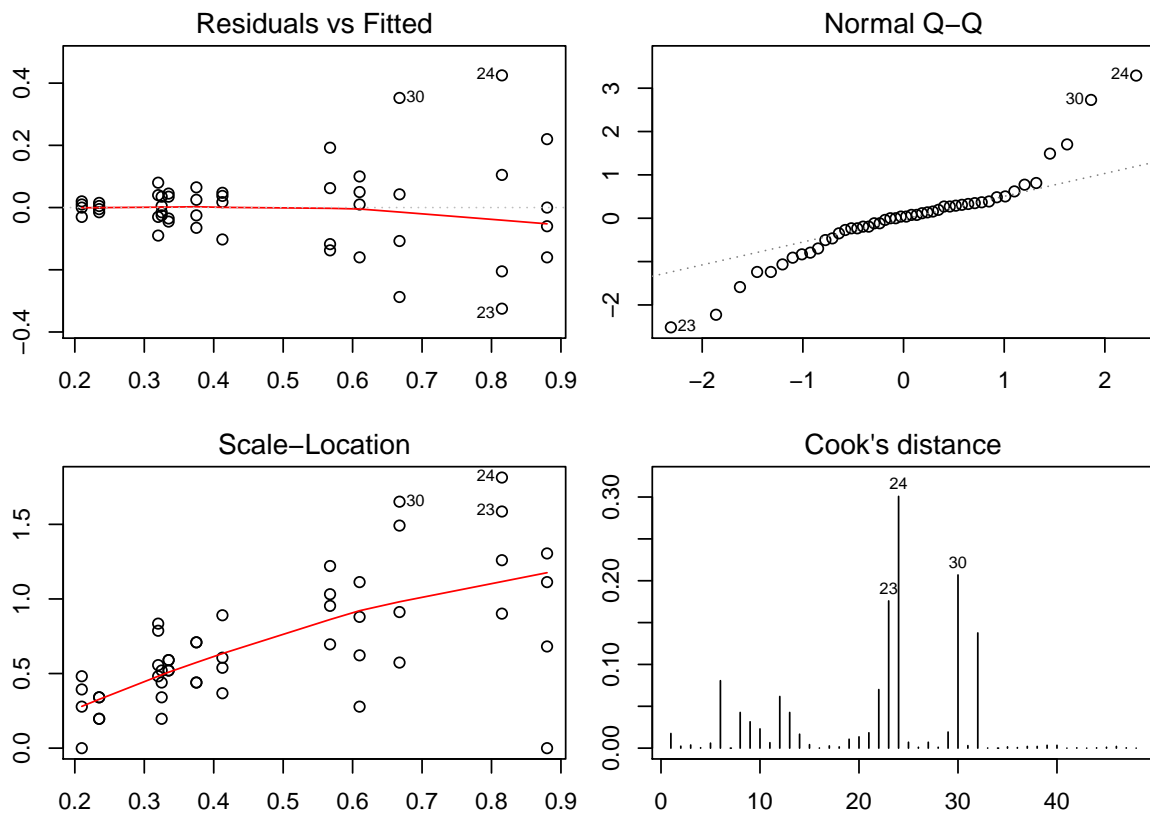


Figure 5: Diagnostic plots for trucizny model with interactions

From diagnostics plot it can be seen that model doesn't meet model assumptions:

- variance is not constant

We can also check variance per each combination of factors where we see that variance is not constant across groupings:

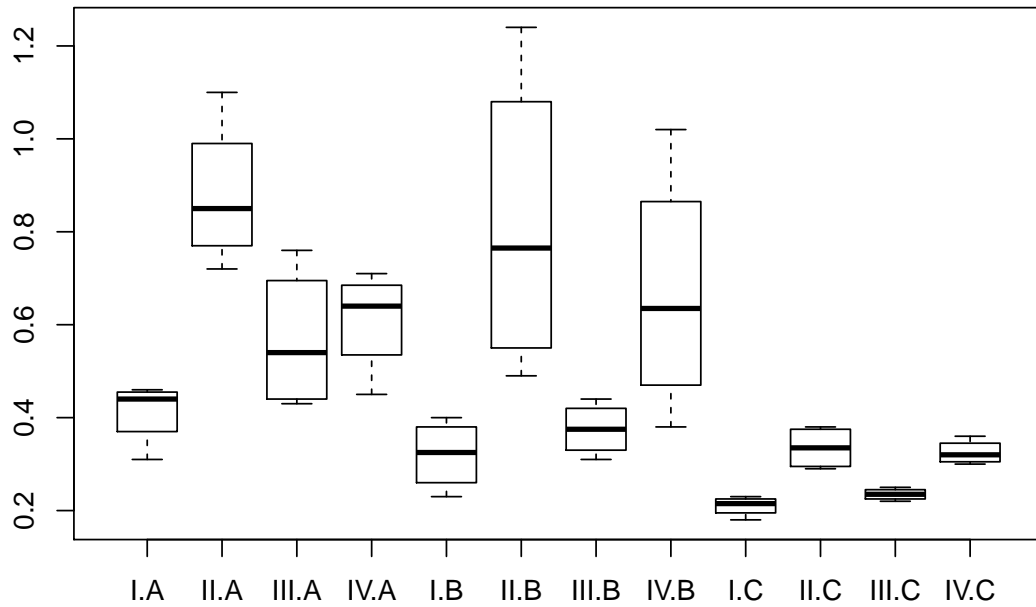


Figure 6: Distribution of wyczas for each combination of kuracja and trucizna

- residuals diverge from normal distribution (residuals have leptokurtic distribution)
  - Propose a new model which fits the data better.
- To find new model we can use Box-Cox procedure to find model with the biggest likelihood:

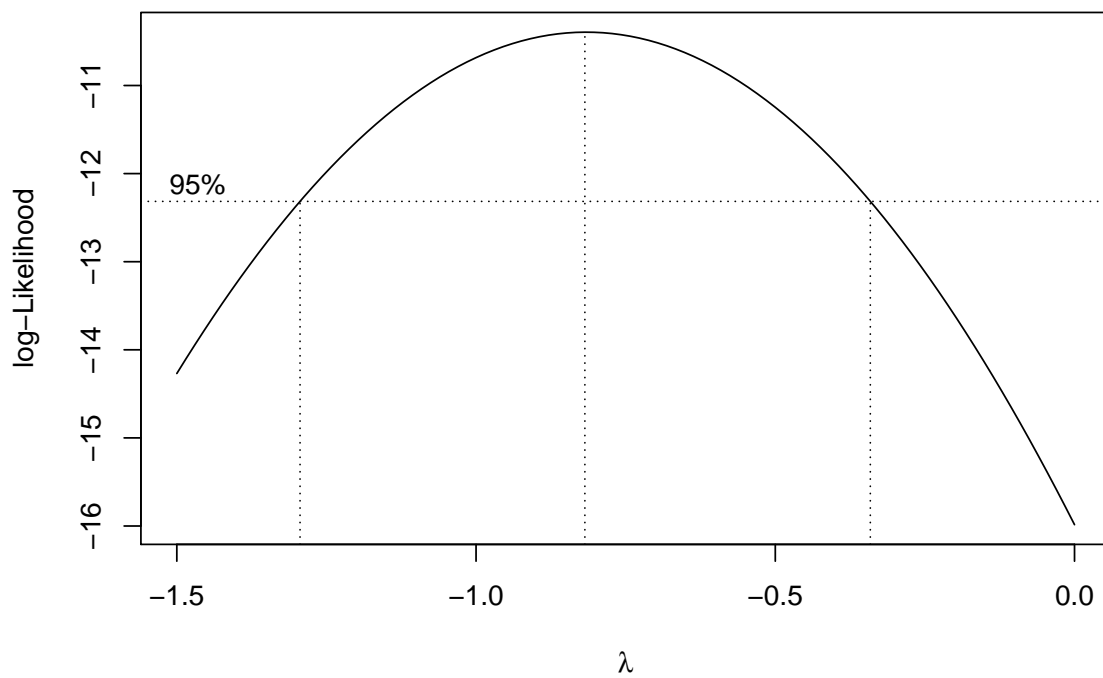


Figure 7: Box-Cox procedure to find best model for given data

We see that model with reciprocal of response variable is contained in 95% interval for model for which data is most

probable so using this transformation (without interaction because interaction is still nonsignificant):

```
> truczny.transformed.lm <- lm(1/wyczas~kuracja+truczna,truczny)
> anova(truczny.transformed.lm)
```

#### Analysis of Variance Table

Response: 1/wyczas

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
kuracja	3	20.414	6.8048	27.982	4.192e-10 ***
truczna	2	34.877	17.4386	71.708	2.865e-14 ***
Residuals	42	10.214	0.2432		

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

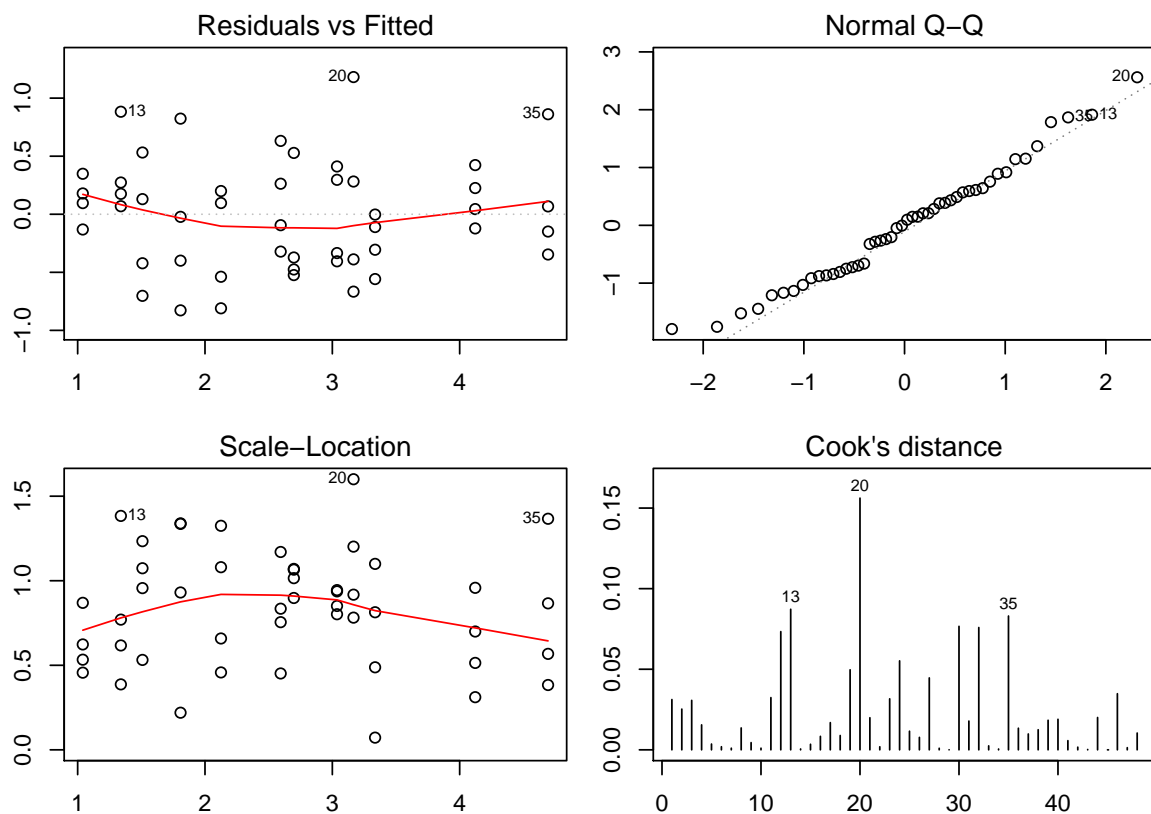


Figure 8: Diagnostic plots for transformed truczny model with interactions

Now we can see that normality and homogeneity of variance are adhered. The boxplot also depicts the variance which look visually much more homogenous than before:

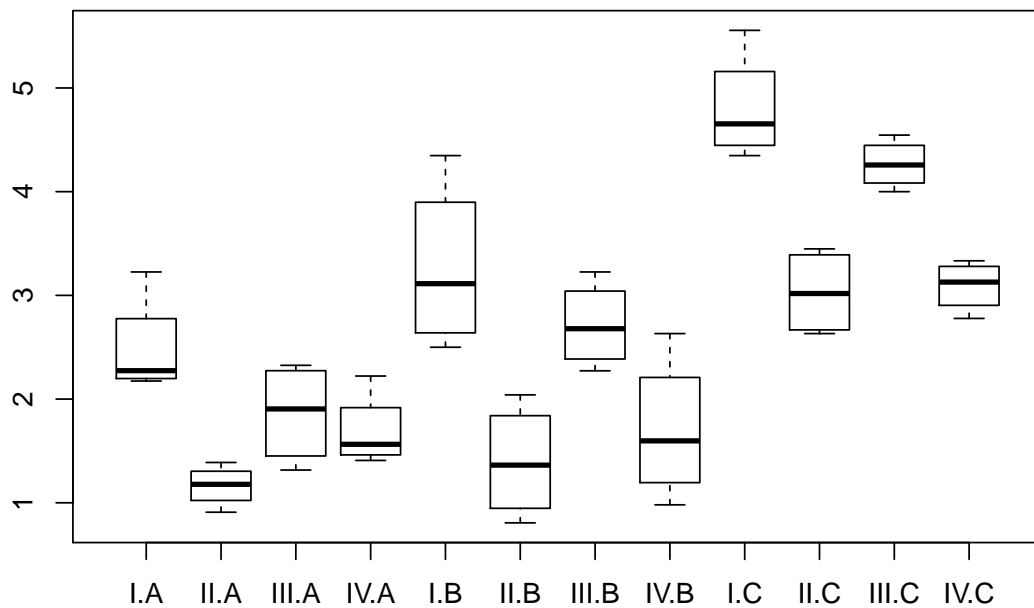


Figure 9: Distribution of  $1/\text{wyczas}$  for each combination of *kuracja* and *trucizna*

- In the new model test the significance of interaction and the presence of the main effects of the two factors. The interaction is not significant:

```
> trucizny.transformed.interaction.lm <- lm(1/wyczas~kuracja*trucizna, trucizny)
> anova(trucizny.transformed.interaction.lm)
```

Analysis of Variance Table

Response:  $1/\text{wyczas}$

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
kuracja	3	20.414	6.8048	28.3431	1.376e-09 ***
trucizna	2	34.877	17.4386	72.6347	2.310e-13 ***
kuracja:trucizna	6	1.571	0.2618	1.0904	0.3867
Residuals	36	8.643	0.2401		

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

But both main effects are significant:

```
> anova(trucizny.transformed.lm)
```

Analysis of Variance Table

Response:  $1/\text{wyczas}$

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
kuracja	3	20.414	6.8048	27.982	4.192e-10 ***
trucizna	2	34.877	17.4386	71.708	2.865e-14 ***
Residuals	42	10.214	0.2432		

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

- Interpret the results on the main effects' existence as well as the results of multiple comparisons.

From the selected model:

```
> trucizny.transformed.lm
```



Call:

```
lm(formula = 1/wyczas ~ kuracja + trucizna, data = trucizny)
```

Coefficients:

(Intercept)	kuracjaII	kuracjaIII	kuracjaIV	truciznaB	truciznaC
2.6977	-1.6574	-0.5721	-1.3583	0.4686	1.9964

we can conclude:

- When truciznaA and kuracjaI applied then wyczas is  $\frac{1}{2.6977}=0.370686140045224$
- When truciznaA and kuracjaII applied then wyczas is  $\frac{1}{2.6977-1.6574}=0.961261174661155$
- When truciznaA and kuracjaIII applied then wyczas is  $\frac{1}{2.6977-0.5721}=0.470455400828001$
- When truciznaA and kuracjaIV applied then wyczas is  $\frac{1}{2.6977-1.3583}=0.746602956547708$
- When truciznaB and kuracjaI applied then wyczas is  $\frac{1}{2.6977+0.4686}=0.315826043015507$
- When truciznaC and kuracjaI applied then wyczas is  $\frac{1}{2.6977+1.9964}=0.213033382331011$

Using Tukey's HSD test (conclusions at 0.05 level):

```
> TukeyHSD(aov(1/wyczas~kuracja+trucizna, trucizny))
```

Tukey multiple comparisons of means  
95% family-wise confidence level

```
Fit: aov(formula = 1/wyczas ~ kuracja + trucizna, data = trucizny)
```

\$kuracja

	diff	lwr	upr	p adj
II-I	-1.6574024	-2.1959343	-1.11887050	0.0000000
III-I	-0.5721354	-1.1106673	-0.03360355	0.0335202
IV-I	-1.3583383	-1.8968702	-0.81980640	0.0000002
III-II	1.0852669	0.5467351	1.62379883	0.0000172
IV-II	0.2990641	-0.2394678	0.83759598	0.4550931
IV-III	-0.7862029	-1.3247347	-0.24767096	0.0018399

\$trucizna

	diff	lwr	upr	p adj
B-A	0.4686413	0.04505584	0.8922267	0.0271587
C-A	1.9964249	1.57283950	2.4200103	0.0000000
C-B	1.5277837	1.10419824	1.9513691	0.0000000

- The differences between all levels of kuracja are significant but not the one between IV-II.
- The differences between all levels of trucizna are significant.

### Exercise 3.

(ANCOVA) Data set fuelprices.txt gives information about fuel prices in six Australian cities.

```
> fuelprices <- read.table(file="fuelprices.txt",header=T)
```

- Fit one-way ANOVA model taking price as an output variable and city as a factor to check whether there are any differences in fuel prices between the given cities.

```
> fuelprices.price.vs.city.lm <- lm(price ~ city, fuelprices)
> summary(fuelprices.price.vs.city.lm)
```

Call:

```
lm(formula = price ~ city, data = fuelprices)
```

Residuals:

Min	1Q	Median	3Q	Max
-8.3667	-5.1667	0.5917	4.2583	10.0000

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	90.2333	2.3706	38.063	<2e-16 ***
cityCairns	2.7167	3.3526	0.810	0.424
cityGold.Coast	-2.0667	3.3526	-0.616	0.542

citySunshine.Coast	0.5333	3.3526	0.159	0.875
cityToowoomba	1.6667	3.3526	0.497	0.623
cityTownsville	1.3333	3.3526	0.398	0.694

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 5.807 on 30 degrees of freedom

Multiple R-squared: 0.07452, Adjusted R-squared: -0.07973

F-statistic: 0.4831 on 5 and 30 DF, p-value: 0.786

We see that the differences in fuel prices between cities are not significant.

- Analyze all the diagnostics for the fitted model. What can we say about the dispersion of observations in each group and what may this imply?

```
> boxplot(price ~ city, fuelprices,col="blue")
```

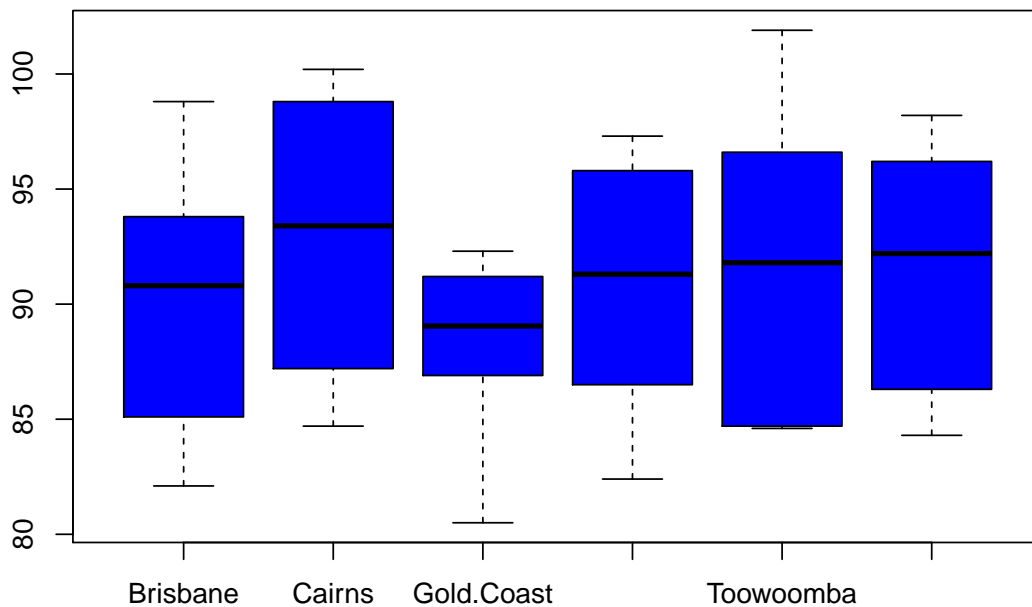


Figure 10: Boxplots of price for differnt cities

We see that dispersion for Gold.Coast differs noticeably from the rest. We can also notice that for all groups IQR overlap which can mean that the means do not differ significantly. The data is also skewed (for some groups quite visibly).

Using statistical tests to check homogeneity of variance:

```
> leveneTest(price ~ city,fuelprices)
```

Levene's Test for Homogeneity of Variance (center = median)

	Df	F value	Pr(>F)
group	5	0.4371	0.819
	30		

```
> bartlett.test(price ~ city, data=fuelprices)
```

Bartlett test of homogeneity of variances

data: price by city

Bartlett's K-squared = 1.1097, df = 5, p-value = 0.9532

```
> fligner.test(price ~ city, data=fuelprices)
```

## Fligner-Killeen test of homogeneity of variances

data: price by city

Fligner-Killeen:med chi-squared = 2.4346, df = 5, p-value = 0.7863

Statistical tests lack power to reject hypothesis about homogeneity of variance.

We see that the QQ plot of residuals doesn't resemble normal distribution.

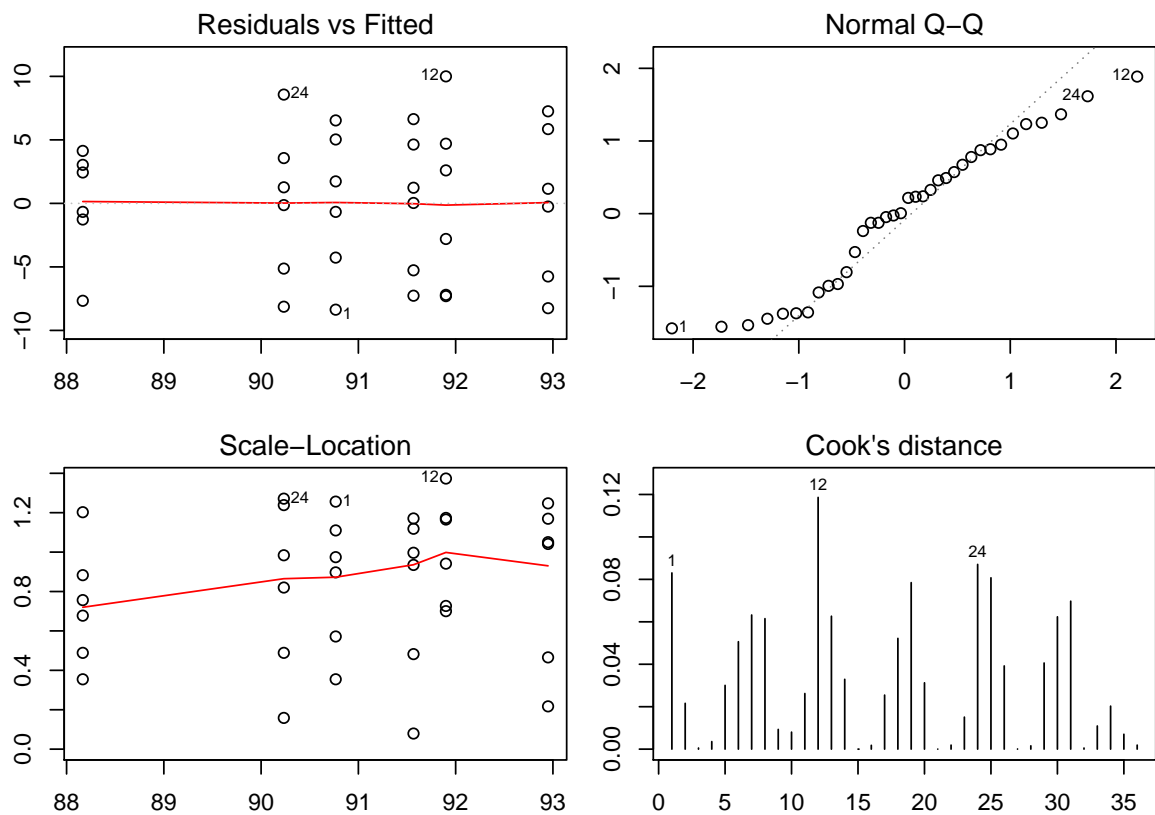


Figure 11: Diagnostic plots for model  $\text{price} \sim \text{city}$

- The data was collected within couple of months. Make a plot of the price against variable month for every city. What can we say about the dispersion of the data now?

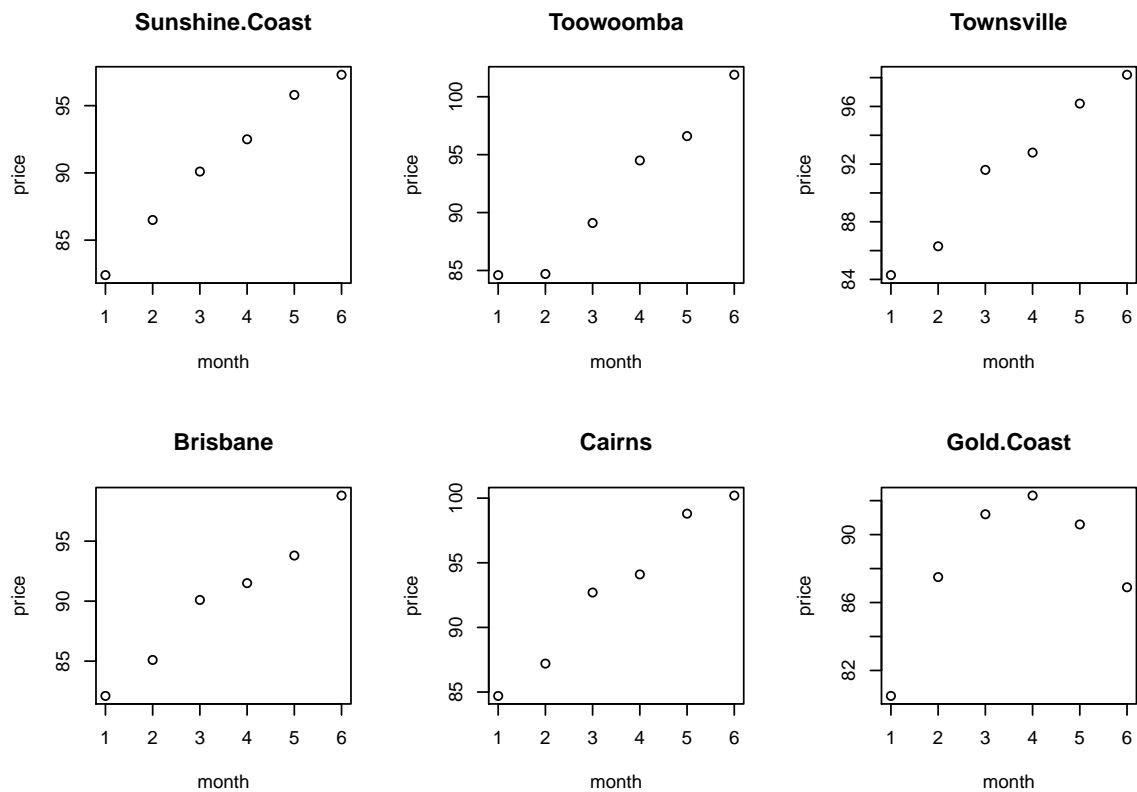


Figure 12: Price against variable month for every city

The price of the fuel depends not only on city but also on time (it increases with time). We see the price  $\sim$  time relation is similar for all cities but not for Gold.Coast for which it looks quadratic and not linear.

- Fit ANCOVA model taking month as a continuous predictor.

```
> (fuelprices.price.vs.city.month.lm <- lm(price ~ city*month, fuelprices))
```

Call:

```
lm(formula = price ~ city * month, data = fuelprices)
```

Coefficients:

	(Intercept)	cityCairns	cityGold.Coast
	79.133333	2.446667	4.793333
citySunshine.Coast		cityToowoomba	cityTownsville
	1.153333	0.006667	2.393333
month		cityCairns:month	cityGold.Coast:month
	3.171429	0.077143	-1.960000
citySunshine.Coast:month		cityToowoomba:month	cityTownsville:month
	-0.177143	0.474286	-0.302857

- Is the interaction between two predictors significant in this model?

```
> summary(fuelprices.price.vs.city.month.lm)
```

Call:

```
lm(formula = price ~ city * month, data = fuelprices)
```

Residuals:

Min	1Q	Median	3Q	Max
-4.6381	-0.8729	-0.1119	0.8443	3.6390

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	79.133333	1.819832	43.484	< 2e-16 ***
cityCairns	2.446667	2.573631	0.951	0.35125
cityGold.Coast	4.793333	2.573631	1.862	0.07482 .
citySunshine.Coast	1.153333	2.573631	0.448	0.65808
cityToowoomba	0.006667	2.573631	0.003	0.99795

```

cityTownsville      2.393333  2.573631  0.930  0.36166
month               3.171429  0.467290  6.787  5.09e-07 ***
cityCairns:month     0.077143  0.660847  0.117  0.90804
cityGold.Coast:month -1.960000  0.660847 -2.966  0.00673 **
citySunshine.Coast:month -0.177143  0.660847 -0.268  0.79095
cityToowoomba:month  0.474286  0.660847  0.718  0.47987
cityTownsville:month -0.302857  0.660847 -0.458  0.65087
---

```

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 1.955 on 24 degrees of freedom

Multiple R-squared: 0.9161, Adjusted R-squared: 0.8776

F-statistic: 23.82 on 11 and 24 DF, p-value: 2.894e-10

The interaction between two predictors is significant (Gold.Coast has different slope for month than reference city Brisbane).

- Analyze diagnostic plots for this model.

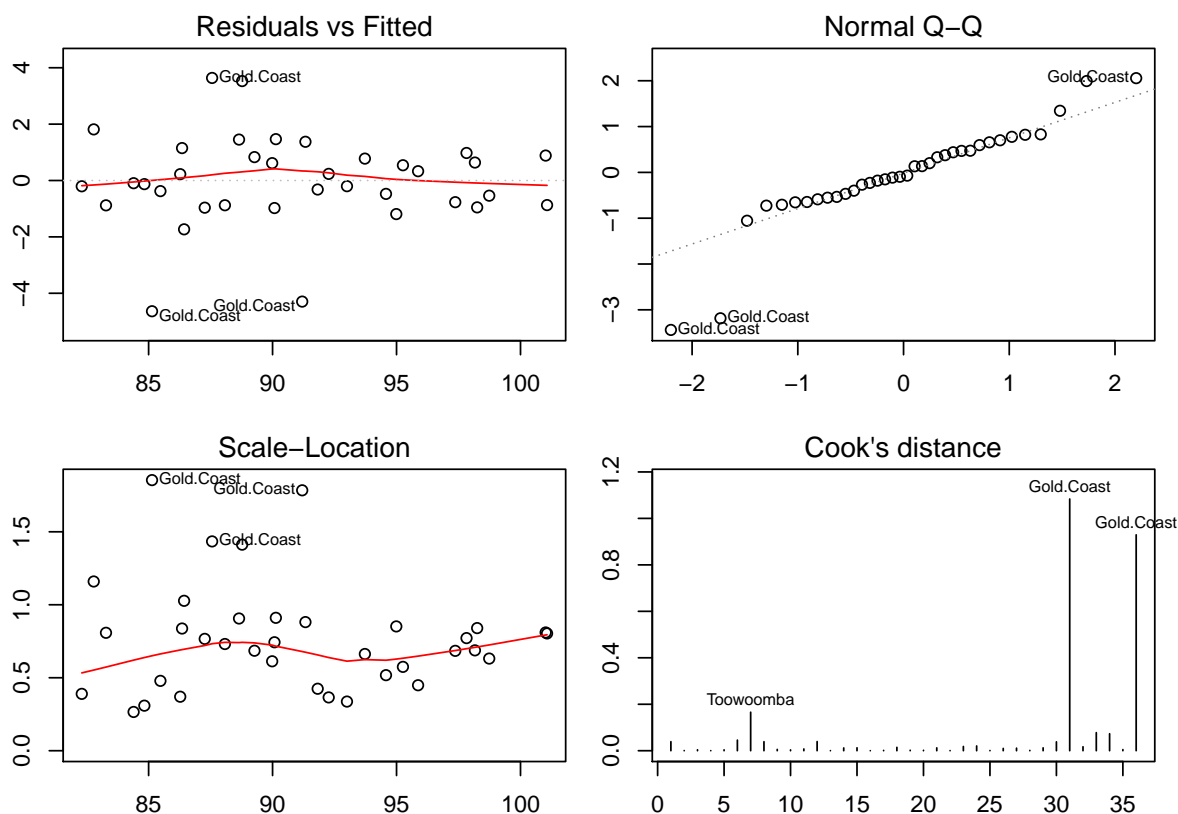


Figure 13: Diagnostic plots for  $\text{price} \sim \text{city} * \text{month}$  model

We see that variance doesn't seem constant, the residual plot shows divergence from normality and we see some potential influential observations with Cook's distance greater than 1. We see (observer earlier) that Gold.Coast doesn't fit into the model.

- Does the assumption of linear dependence between price and month hold for every city? If not, exclude the respective city from the analysis and refit ANCOVA model.

We have seen on Figure-12 that  $\text{price} \sim \text{month}$  shows quadratic dependence for Gold.Coast city (other cities show linear relationship). Removing this city from data and refitting the model:

```

> fuelprices <- fuelprices[fuelprices$city!="Gold.Coast",]
> (fuelprices.price.vs.city.month.lm <- lm(price ~ city*month, fuelprices))

```

Call:

```
lm(formula = price ~ city * month, data = fuelprices)
```

Coefficients:

(Intercept)	cityCairns	citySunshine.Coast
79.133333	2.446667	1.153333

cityToowoomba	cityTownsville	month
0.006667	2.393333	3.171429
cityCairns:month	citySunshine.Coast:month	cityToowoomba:month
0.077143	-0.177143	0.474286
cityTownsville:month		
-0.302857		

- Analyze the fit of the resulting model (check diagnostics). If possible simplify the model.

Now the interaction term is insignificant:

```
> summary(fuelprices.price.vs.city.month.lm)
```

Call:

```
lm(formula = price ~ city * month, data = fuelprices)
```

Residuals:

Min	1Q	Median	3Q	Max
-1.7314	-0.8457	-0.1648	0.7424	1.8143

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	79.133333	1.027424	77.021	< 2e-16 ***
cityCairns	2.446667	1.452997	1.684	0.108
citySunshine.Coast	1.153333	1.452997	0.794	0.437
cityToowoomba	0.006667	1.452997	0.005	0.996
cityTownsville	2.393333	1.452997	1.647	0.115
month	3.171429	0.263818	12.021	1.32e-10 ***
cityCairns:month	0.077143	0.373095	0.207	0.838
citySunshine.Coast:month	-0.177143	0.373095	-0.475	0.640
cityToowoomba:month	0.474286	0.373095	1.271	0.218
cityTownsville:month	-0.302857	0.373095	-0.812	0.426

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 1.104 on 20 degrees of freedom

Multiple R-squared: 0.9742, Adjusted R-squared: 0.9626

F-statistic: 83.98 on 9 and 20 DF, p-value: 6.523e-14

So we simplify the model to model without interaction term (now we see significant differences between means):

```
> fuelprices.price.vs.city.month.lm <- lm(price ~ city+month, fuelprices)
> summary(fuelprices.price.vs.city.month.lm)
```

Call:

```
lm(formula = price ~ city + month, data = fuelprices)
```

Residuals:

Min	1Q	Median	3Q	Max
-2.4214	-0.4768	-0.1571	0.6893	2.0357

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	79.0833	0.6247	126.603	< 2e-16 ***
cityCairns	2.7167	0.6513	4.171	0.000341 ***
citySunshine.Coast	0.5333	0.6513	0.819	0.420880
cityToowoomba	1.6667	0.6513	2.559	0.017218 *
cityTownsville	1.3333	0.6513	2.047	0.051722 .
month	3.1857	0.1206	26.418	< 2e-16 ***

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 1.128 on 24 degrees of freedom

Multiple R-squared: 0.9677, Adjusted R-squared: 0.961

F-statistic: 143.7 on 5 and 24 DF, p-value: < 2.2e-16

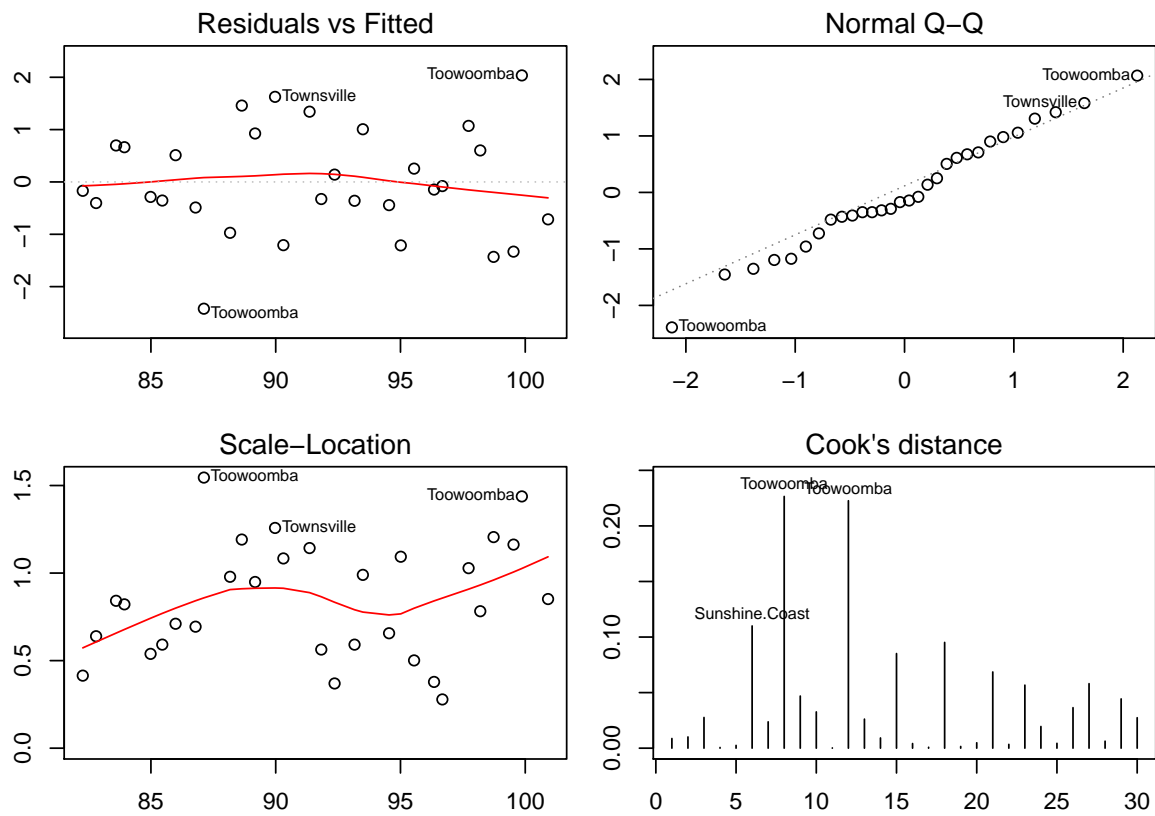


Figure 14: Diagnostic plots for  $\text{price} \sim \text{city} + \text{month}$  model without Gold.Coast city

This model meets model assumptions much better than previous one.

- Draw and interpret the fitted lines. Which city is the cheapest and which is the most expensive with respect to fuel prices? How much the prices grow per month? Compare the results with the initial ANOVA model.

All the lines have the same slope but different coefficients. The most expensive city is Cairns (the biggest mean which differs from the reference city Brisbane significantly). The Brisbane, Sunshine.Coast, Townsville mean prices does not differ significantly from each other so they are the cheapest cities. We see that Toowoomba is more expensive than Brisbane but we from this model we cannot compare Toowoomba and Cairns (to compare them we would have to fit model with reference city set to one of them).

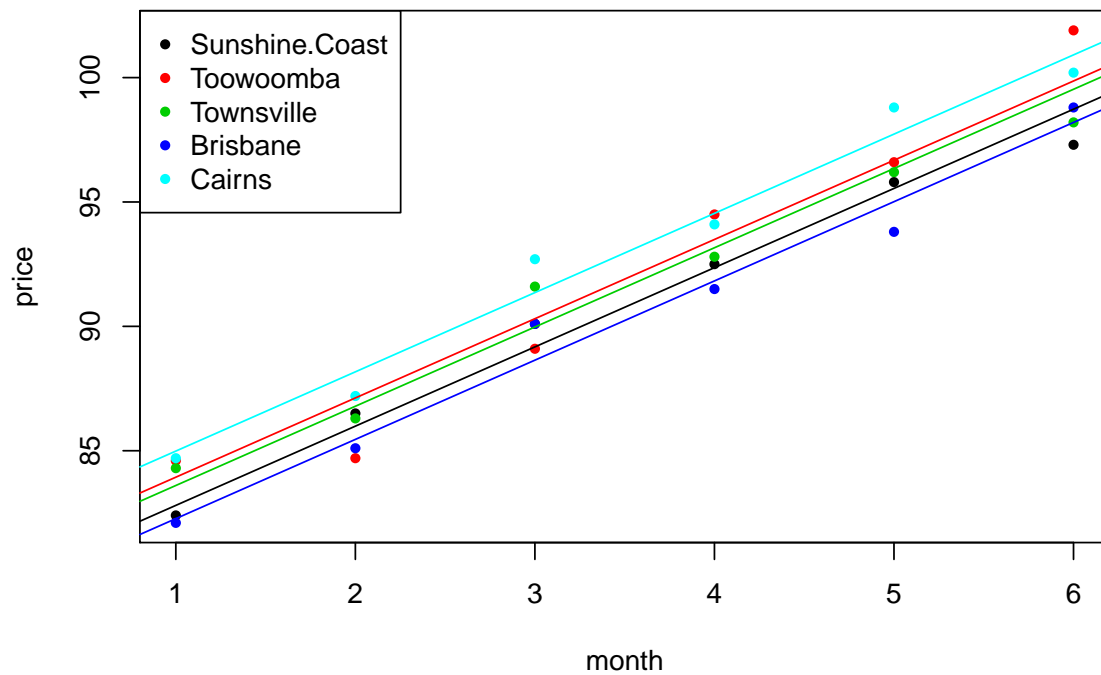


Figure 15: Fitted lines for cities

#### Exercise 4.

(ANCOVA) The file `twins.txt` contains data collected during the study aiming to examine whether intelligence is inherent or rather dependent on education.

```
> twins <- read.table(file="twins.txt",header=T)
```

Level of IQ was measured for monozygotic twins one of which was raised by foster parents. The data includes the following variables:

FosterIQ - IQ level for the twin raised by foster parents,  
 BiolIQ - IQ level of the twin raised by biological parents,  
 Social - social status of biological parents.

We are interested in examining the dependence between variables FosterIQ and BiolIQ including the social status of biological parents.

- Plot variable FosterIQ against BiolIQ and mark the social status for each observation.



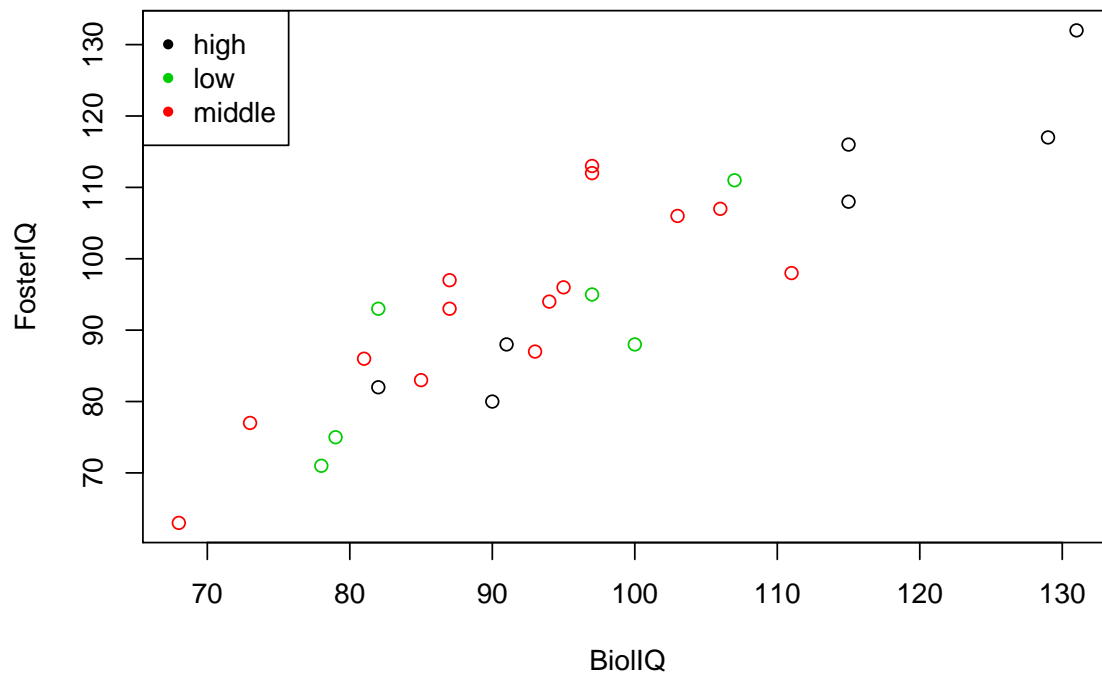


Figure 16: FosterIQ against BiolIQ with marked the social status for each observation

- Fit ANCOVA model with interactions and simplify it if possible.

We can see that interaction is not significant in the model:

```
> twins.interaction.lm <- lm(FosterIQ~BiolIQ*Social,twins)
> summary(twins.interaction.lm)
```

Call:

```
lm(formula = FosterIQ ~ BiolIQ * Social, data = twins)
```

Residuals:

Min	1Q	Median	3Q	Max
-14.479	-5.248	-0.155	4.582	13.798

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	-1.872044	17.808264	-0.105	0.917
BiolIQ	0.977562	0.163192	5.990	6.04e-06 ***
Socialallow	9.076654	24.448704	0.371	0.714
Socialmiddle	2.688068	31.604178	0.085	0.933
BiolIQ:Socialallow	-0.029140	0.244580	-0.119	0.906
BiolIQ:Socialmiddle	-0.004995	0.329525	-0.015	0.988

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 7.921 on 21 degrees of freedom

Multiple R-squared: 0.8041, Adjusted R-squared: 0.7574

F-statistic: 17.24 on 5 and 21 DF, p-value: 8.31e-07

So simplifying it to the model without interaction:

```
> twins.lm <- lm(FosterIQ~BiolIQ+Social,twins)
> summary(twins.lm)
```

Call:

```
lm(formula = FosterIQ ~ BiolIQ + Social, data = twins)
```

Residuals:

	Min	1Q	Median	3Q	Max
	-14.8235	-5.2366	-0.1111	4.4755	13.6978

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	-0.6076	11.8551	-0.051	0.960
BiolIQ	0.9658	0.1069	9.031	5.05e-09 ***
Sociallow	6.2264	3.9171	1.590	0.126
Socialmiddle	2.0353	4.5908	0.443	0.662

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 7.571 on 23 degrees of freedom

Multiple R-squared: 0.8039, Adjusted R-squared: 0.7784

F-statistic: 31.44 on 3 and 23 DF, p-value: 2.604e-08

- Analyse diagnostics for the model.

We see that model fulfills assumptions i.e. constant variance, normal distribution of residuals, no influential values, no outliers.

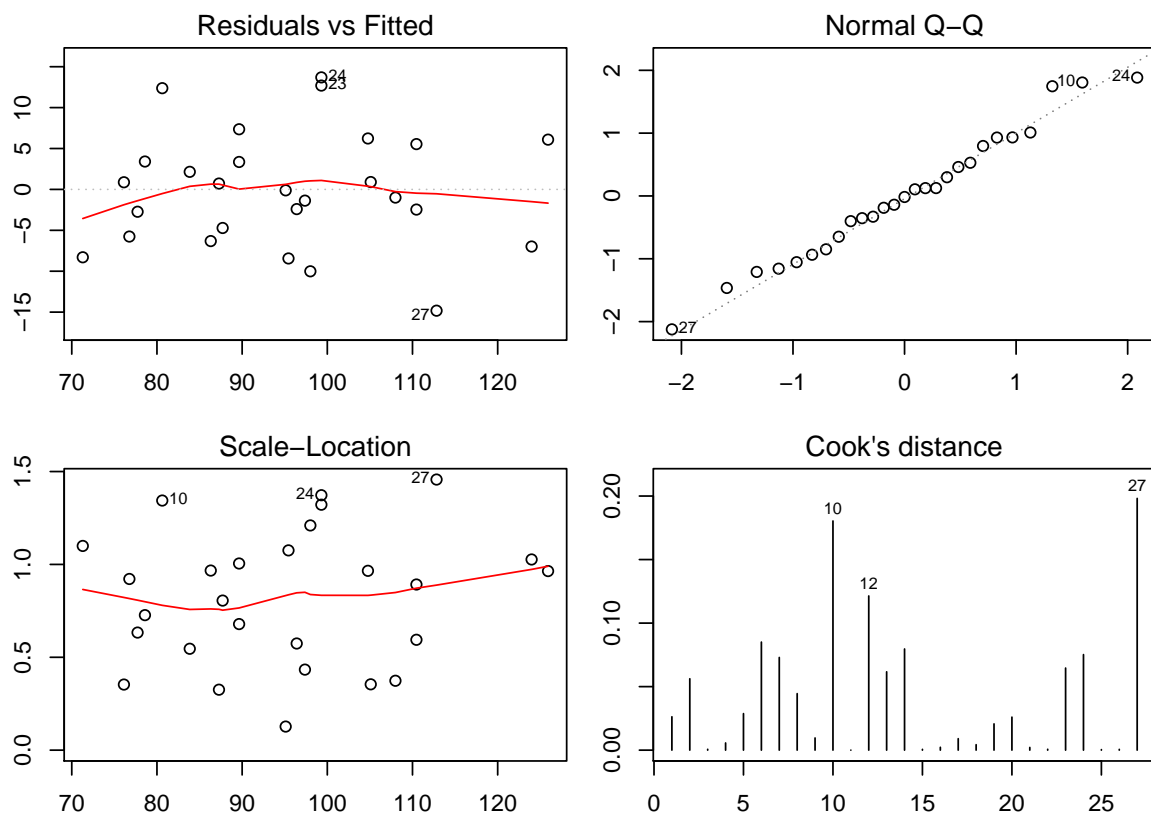


Figure 17: Diagnostic plots for twins model without interactions

- Interpret the results. Base on the model:

```
> summary(twins.lm)
```

Call:

```
lm(formula = FosterIQ ~ BiolIQ + Social, data = twins)
```

Residuals:

	Min	1Q	Median	3Q	Max
	-14.8235	-5.2366	-0.1111	4.4755	13.6978

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	-0.6076	11.8551	-0.051	0.960
BiolIQ	0.9658	0.1069	9.031	5.05e-09 ***
Sociallow	6.2264	3.9171	1.590	0.126

```
Socialmiddle  2.0353    4.5908    0.443    0.662
```

```
---
```

```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
Residual standard error: 7.571 on 23 degrees of freedom
```

```
Multiple R-squared:  0.8039,    Adjusted R-squared:  0.7784
```

```
F-statistic: 31.44 on 3 and 23 DF,  p-value: 2.604e-08
```

we can conclude:

- there is linear dependence between FosterIQ and BiolIQ with slope 0.9658 which is significant (i.e. 1 additional IQ for BiolIQ gives 1 additional IQ for FosterIQ for one of the twins)
- the slope doesn't differ across social classes.
- there is no significant difference between means among social classes.