
Applied Data Analysis

R-Laboratory 4

Model Parsimony – Testing in Linear Models – Analysis of Variance

Useful packages and functions:

- | | | |
|-------------------------------|----------------------------------|---------------------------------|
| • <code>set.seed()</code> | • <code>rgl::planes3d()</code> | • <code>TukeyHSD()</code> |
| • <code>runif()</code> | • <code>summary()</code> | • <code>par()</code> |
| • <code>lm()</code> | • <code>tapply()</code> | • <code>cooks.distance()</code> |
| • <code>shapiro.test()</code> | • <code>car</code> | • <code>anova()</code> |
| • <code>rgl</code> | • <code>car::leveneTest()</code> | |
| • <code>rgl::plot3d()</code> | • <code>aov()</code> | |

Task 13

For values of x in $[0, 100]$, suppose the linear model $(Y | X = x) \sim \mathcal{N}(\mu(x), \sigma^2)$ holds with

$$E(Y | X = x) = \mu(x) = 45 + 0.1x + 5 \cdot 10^{-4}x^2 + 5 \cdot 10^{-7}x^3 + 5 \cdot 10^{-11}x^4 + 5 \cdot 10^{-13}x^5$$

and $\sigma = 10$.

- Set a seed to 2020 and initialize two numeric vectors `vec.delta.simple` and `vec.delta.correct` of length 100.
- Repeat the following procedure 100 times using a loop.
 - Generate 25 observations from the model with X uniformly distributed on $[0, 100]$.
 - Fit a “simple” model with $\mu^{(0)}(x) = \beta_0 + \beta_1x$ and afterwards the “correct” model with $\mu^{(1)}(x) = \beta_0 + \beta_1x + \beta_2x^2 + \beta_3x^3 + \beta_4x^4 + \beta_5x^5$.
 - For the first five iterations construct plots showing the data, the true relationship, and both model fits.
 - For each model, summarize the quality of the model fit by the mean

$$\Delta_j = \frac{1}{25} \sum_{i=1}^{25} |\hat{\mu}^{(j)}(x_i) - \mu(x_i)|, \quad j \in \{0, 1\}. \quad (+)$$

Store the values of Δ_j , $j = 0, 1$, in (+) in the two numeric vectors `vec.delta.simple` and `vec.delta.correct`.

- By comparing the values of Δ_j , $j = 0, 1$, in the vectors `vec.delta.simple` and `vec.delta.correct` and the plots of (iii), which model do you prefer? Explain what this Task illustrates about model parsimony.

Task 14

- (a) Load the `.RData` file of the pre-processed data of *Survey1* (Task 7) into the R workspace.
- (b) Create a regression model with the approach

$$\text{DimSelf} = d + a \text{ DimEmotion} + b \text{ DimBody} \quad (++)$$

for parameters $a, b, d \in \mathbb{R}$.

- (c) Analyze, if the model assumptions are sufficiently satisfied:
 - (i) Create the following plots (you can directly apply the function `plot` to the fitted model for the first four plots) and interpret them:
 - i. Residuals versus fitted values
 - ii. $\sqrt{|\text{Standardized residuals}|}$ versus fitted values
 - iii. Quantiles of the standardized residuals versus the expected quantiles of the standard normal distribution (called QQ-Plot)
 - iv. Standardized residuals versus leverage
 - v. Cook's distance.
 - (ii) Test on level $\alpha = 0.05$, if there is evidence against the assumption of normally distributed residuals.
Hint: Use a Shapiro-Wilk-Test with the R function `shapiro.test`.
- (d) Create a 3d scatterplot with `DimEmotion` on the x-axis, `DimBody` on the y-axis and `DimSelf` on the z-axis. Add the regression surface of the model `(++)` to the plot.
Hint: Use the functions `plot3d` and `planes3d` from the package `rgl`.
- (e) In the model `(++)` test the hypotheses

$$H_0 : b = 0 \quad \text{versus} \quad H_1 : b \neq 0$$

on the significance level $\alpha = 0.05$. Is the null hypothesis rejected?

Task 15

- (a) Load the `.RData` file of the pre-processed data of *Solar* (Task 10) into the R workspace.
- (b) Create four boxplots for the attribute `Pmax`, one for each batch.
- (c) Carry out an analysis of variance for the attribute `Pmax` regarding the factor `batch`.
- (d) Analyze the model assumptions as in Task 14 (c). Additionally, test on level $\alpha = 0.05$, if there is evidence against the assumption of equal variance in each group of factor level.
Hint: Use a Levene-Test with the R function `leveneTest` from the package `car` to test the equality of the variances.
- (e) Test on the significance level $\alpha = 0.05$, if the null hypothesis of equal means of `Pmax` for the four batches is rejected.

Hint: You may call the function `summary` with the fitted model as argument.

- (f) Carry out a pairwise comparison of the batches regarding **Pmax** using a Tukey-Test on significance level $\alpha = 0.1$. Create a plot of the computed confidence intervals.

Task 16

- (a) Consider the data set **ToothGrowth** from the package **datasets** and transform the attribute **dose** to type **factor**.
- (b) Create a boxplot for the value of **len**, separated on all factor combinations of **supp** and **dose**. What is your impression?
- (c) Fit a linear model for **len**, where **supp** and **dose** (inclusive interaction) are explanatory variables.
- (d) Analyze the model assumptions as in Task 14 (c). Additionally, test on level $\alpha = 0.05$, if there is evidence against the assumption of equal variance in each group of factor combination.
- (e) If the model assumptions are sufficiently satisfied, test on level $\alpha = 0.05$, if there is any influence of the explanatory variables on the value of **len**.
- (f) If there is any influence of explanatory variables, analyze it concretely: Test on overall $\alpha = 0.05$, if the interaction of **supp** and **dose** and possibly their main effect has an influence on the value of **len**.

Hint: Use a Bonferroni correction to ensure that all tests together satisfy the significance level α . This means that you can compare each p-value with an adapted significance level $\tilde{\alpha} = \frac{\alpha}{k}$, where $k \in \mathbb{N}$ is the number of tests.

- (g) If some effects are not significantly different from zero, fit a new model with the removed terms to get the final model for interpretation.

```
#####
#
# Task 13
#
#####

# (a)
set.seed(2020)

# (b)
N=25
vec.delta.simple=rep(0,100)
vec.delta.correct=rep(0,100)
vec.delta.correct.poly=rep(0,100)
for(i in 1:100){
  x=runif(N,0,100)

  mu=45+0.1*x+0.0005*x^2+5e-7*x^3+5e-11*x^4+5e-13*x^5
  y=mu+rnorm(N,sd=10)
  model.correct=lm(y~x+l(x^2)+l(x^3)+l(x^4)+l(x^5))

  # better use poly
  model.correct.poly=lm(y~poly(x,degree=5))
  fitted.vals.poly=predict(model.correct.poly,newdata=data.frame(x=x))

  model.simple=lm(y~x)

  if(i<6){
    # data
    plot(x,y)
    param1=model.correct$coefficients
    param2=model.simple$coefficients
    # true relationship
    curve(45+0.1*x+0.0005*x^2+5e-7*x^3+5e-11*x^4+5e-13*x^5,add=TRUE,col="blue")
    # correct model
    curve(param1[1]+param1[2]*x+param1[3]*x^2+param1[4]*x^3+param1[5]*x^4+param1[6]*x^5,add=TRUE,col="red")
    # simple model
    curve(param2[1]+param2[2]*x,add=TRUE,col="green")
    # correct model fitted with poly
    x.grid=seq(min(x),max(x),length.out = 100)
    y.pred=predict(model.correct.poly,newdata=data.frame(x=x.grid))
    lines(x.grid,y.pred, col="orange")
  }
  vec.delta.correct[i]=mean(abs(model.correct$fitted.values-mu))
  vec.delta.correct.poly[i]=mean(abs(fitted.vals.poly-mu))
  vec.delta.simple[i]=mean(abs(model.simple$fitted.values-mu))
}
```

```
#####
#
# Task 14
#
#####
library(rgl)

# (a)
load("Survey1.RData")

# (b)
model.survey=lm(DimSelf~DimEmotion+DimBody, data = data.survey)

# (c)
# check the fit of the model
par(mfrow=c(2,2))
plot(model.survey)
par(mfrow=c(1,1))
plot(cooks.distance(model.survey))

# test of normality
shapiro.test(model.survey$residuals)

# (d)
plot3d(x=data.survey$DimEmotion,y=data.survey$DimBody,z=data.survey$DimSelf,xlab="DimEmotion",ylab="DimBody",zlab="DimSelf")
planes3d(a=model.survey$coefficient[2],b=model.survey$coefficient[3],c=-1,d=model.survey$coefficients[1],alpha=0.5)

# (e)
summary(model.survey)
```

```
boxplot(solar$Pmax ~ solar$batch)
```

```
# (c)
```

```
# analysis of variance
```

```
solar.aov = aov(solar$Pmax ~ solar$batch)
```

```
# (d)
```

```
# check the fit of the model
```

```
par(mfrow=c(2,2))
```

```
plot(solar.aov)
```

```
par(mfrow=c(1,1))
```

```
plot(cooks.distance(solar.aov))
```

```
#test of normality
```

```
shapiro.test(residuals(solar.aov))
```

```
#Levene-Test of equal variances
```

```
leveneTest(solar.aov)
```

```
# alternative: Levene-Test "by hand"
```

```
Median.Grp = tapply(solar$Pmax,solar$batch,median)
```

```
Z = abs(solar$Pmax - Median.Grp[solar$batch])
```

```
summary(aov(Z ~ solar$batch))
```

```
# (e)
```

```
summary(solar.aov)
```

```
# (f)
```

```
# pairwise comparison with Tukey-Test
```

```
# since the model is balanced (each group of a factor level has the same length)
```

```
solar.Tuk = TukeyHSD(solar.aov,conf.level=0.9)
```

```
solar.Tuk
```

```
# plot of the computed confidence intervals
```

```
plot(solar.Tuk)
```

```
#####
```

```
#
```

```
# Task 16
```

```
#
```

```
#####
```

```
# (a)
```

```
ToothGrowth
```

```
len=ToothGrowth$len
```

```
supp=ToothGrowth$supp
```

```
dose=as.factor(ToothGrowth$dose)
```

```
# (b)
```

```
boxplot(len~supp*dose)
```

```
# (c)
```

```
model=lm(len~supp*dose)
```

```
# (d)
```

```
# check the fit of the model
```

```
par(mfrow=c(2,2))
```

```
plot(model)
```

```
par(mfrow=c(1,1))
```

```
plot(cooks.distance(model))
```

```
shapiro.test(residuals(model))
```

```
leveneTest(model)
```

```
# (e)
```

```
summary(model)
```

```
# (f)
```

```
anova(model)
```

```
# (g)
```

```
model.new=lm(len~dose+supp)
```