

BIOSTATYSTYKA – LABORATORIUM 2

```
library("foreign")
library("survival")
library("rms")

nsclc <- read.dta("C:\\Users\\Marta\\Desktop\\Marta\\studia\\rok4\\Biostatystyka\\2\\nsclc_eng.dta"),
-1]
head(nsclc, 2)

##      mutation survtime survind tnm expression
## 1          1     24.51         1   2          1
## 2          1     27.13         1   2          1

nsclc.PH.P53e <- coxph(Surv(survtime, survind) ~ expression, data = nsclc)
print(nsclc.PH.P53e)

## Call:
## coxph(formula = Surv(survtime, survind) ~ expression, data = nsclc)
##
##
##              coef exp(coef) se(coef)      z      p
## expression 0.786      2.19    0.302 2.6 0.0093
##
## Likelihood ratio test=7.15 on 1 df, p=0.00749 n= 102, number of events= 49

# test score:

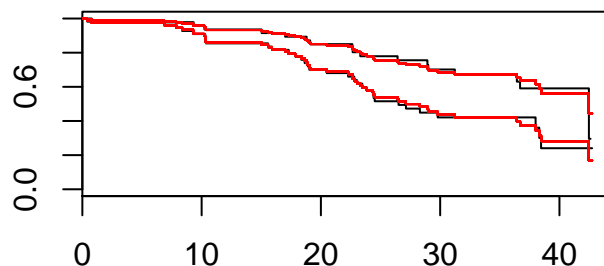
1 - pchisq(nsclc.PH.P53e$score, 1) # male, czyli expression istotne

## [1] 0.007687

# bazowa funkcja przezywania (porownanie):

nsclc.pKM.P53e <- survfit(nsclc.PH.P53e, newdata = nsclc) # PH
nsclc.KM.P53e <- survfit(Surv(survtime, survind) ~ expression, data = nsclc) # KM

plot(nsclc.KM.P53e, conf.int = FALSE, mark.time = FALSE)
lines(nsclc.pKM.P53e, col = "red", mark.time = FALSE) # bardzo podobne
```



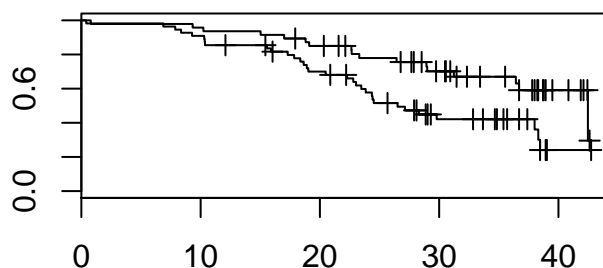
```
# model z dwiema zmiennymi:

nsclcl.PH.P53em <- coxph(Surv(survtime, survind) ~ mutation + expression, data = nsclcl)
print(nsclcl.PH.P53em)

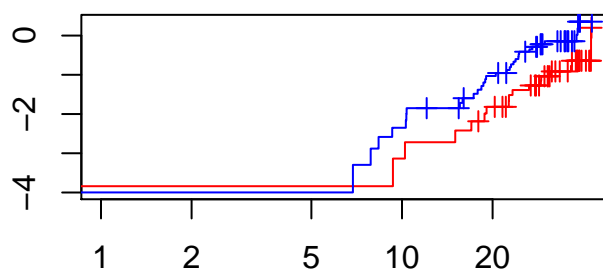
## Call:
## coxph(formula = Surv(survtime, survind) ~ mutation + expression,
##       data = nsclcl)
##
##
##              coef exp(coef) se(coef)      z      p
## mutation      1.735      5.671   0.407  4.262 0.00002
## expression    -0.199      0.819   0.371 -0.538 0.59000
##
## Likelihood ratio test=27.5 on 2 df, p=1.07e-06 n= 102, number of events= 49

# ocena zalozen dla pierwszego modelu:

plot(nsclcl.KM.P53e, conf.int = FALSE) # krzywe przezycia nie przecinaja sie
```



```
plot(nsclcl.KM.P53e, col = c("red", "blue"), fun = function(x) log(-log(x)),
     log = "x", firstx = 1) # sa rownolegle
```

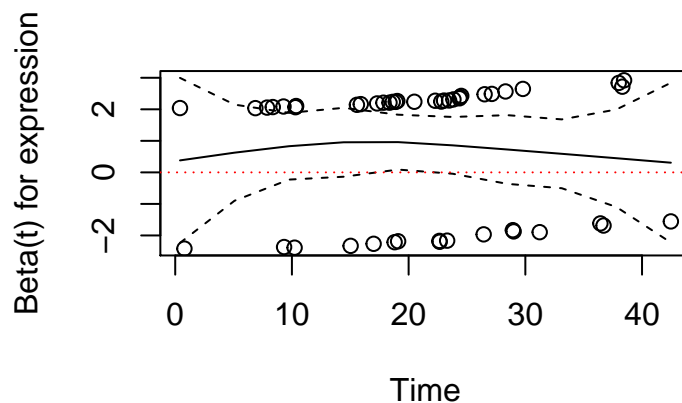


```
# test Schoenfelda:

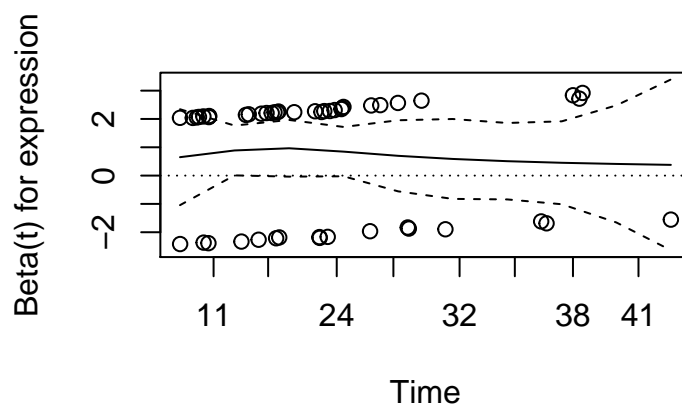
nsclcl.PHfit.P53e <- cox.zph(nsclcl.PH.P53e, transform = "identity")
print(nsclcl.PHfit.P53e) # przyjmujemy hipoteze, czyli zalozenie spelnione

##              rho  chisq      p
## expression -0.033 0.0524 0.819

plot(nsclcl.PHfit.P53e, df = 4, nsmo = 10, se = TRUE)
abline(0, 0, lty = 3, col = "red")
```



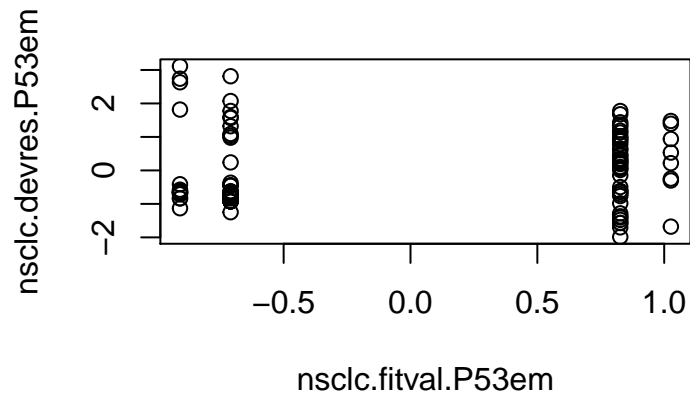
```
nsclcl.PHfit1.P53e <- cox.zph(nsclcl.PH.P53e, transform = function(x) x^2)
plot(nsclcl.PHfit1.P53e, df = 4, nsmo = 10, se = TRUE)
abline(0, 0, lty = 3)
```



```
# ocena zalozen dla drugiego modelu:

nsclcl.devres.P53em <- residuals(nsclcl.PH.P53em, type = "deviance")
nsclcl.fitval.P53em <- predict(nsclcl.PH.P53em, type = "lp")

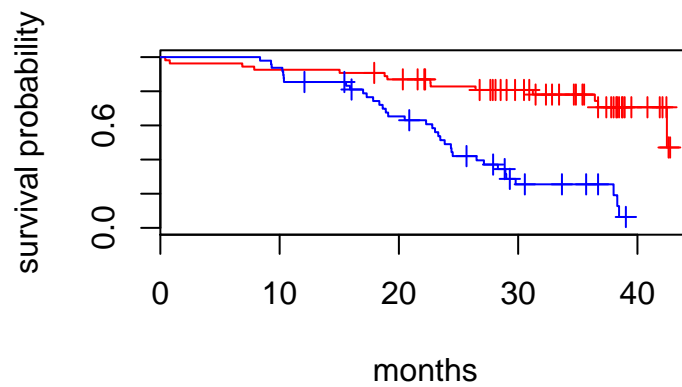
plot(nsclcl.fitval.P53em, nsclcl.devres.P53em)
```



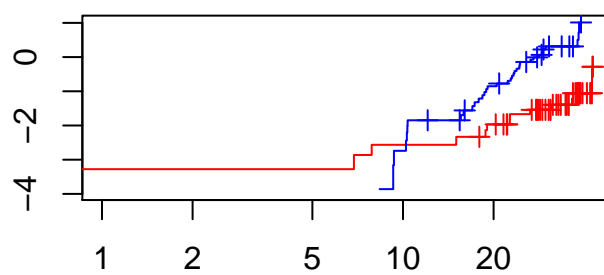
```
# dla mutation:
```

```
nsclc.KM.P53m <- survfit(Surv(survtime, survind) ~ mutation, data = nsclc)
```

```
plot(nsclc.KM.P53m, col = c("red", "blue"), xlab = "months", ylab = "survival probability")
```



```
plot(nsclc.KM.P53m, col = c("red", "blue"), fun = function(x) log(-log(x)),  
      log = "x", firstx = 1) # raczej zalozenia niespełnione
```

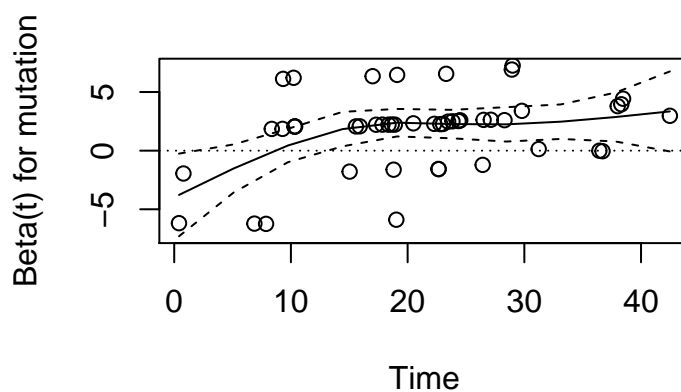


```
# test formalny:

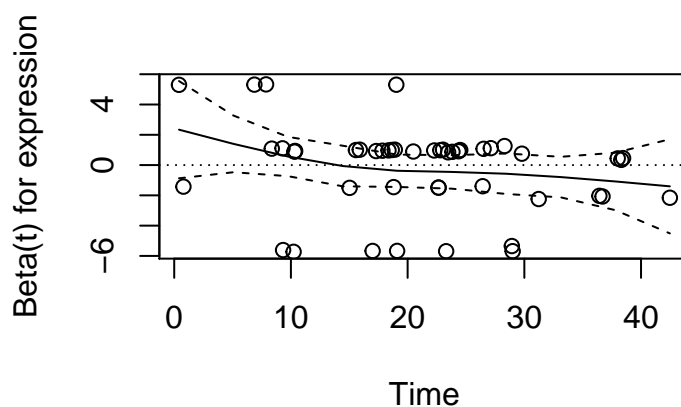
nsclcl.PHfit.P53em <- cox.zph(nsclcl.PH.P53em, transform = "identity")
print(nsclcl.PHfit.P53em) # mutation nie spelnia zalozen

##               rho chisq      p
## mutation      0.349   7.75 0.00538
## expression    -0.239   3.29 0.06967
## GLOBAL         NA    7.81 0.02010

plot(nsclcl.PHfit.P53em, df = 4, nsmo = 10, se = TRUE, var = 1)
abline(0, 0, lty = 3)
```



```
plot(nsclcl.PHfit.P53em, df = 4, nsmo = 10, se = TRUE, var = 2)
abline(0, 0, lty = 3)
```



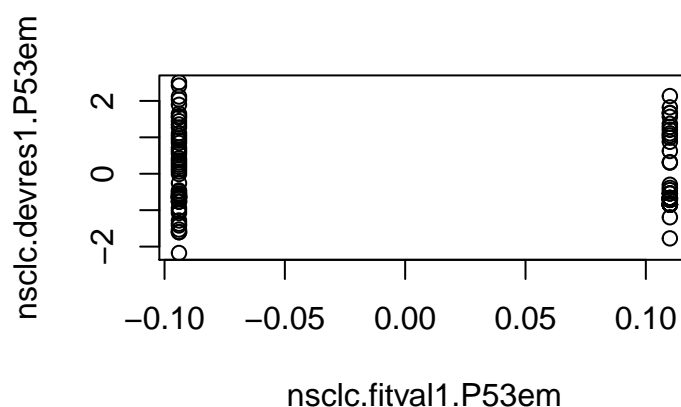
```
# model warstwowy:

nsclcl.strPH.P53em <- coxph(Surv(survtime, survind) ~ expression + strata(mutation),
  data = nsclcl)
print(nsclcl.strPH.P53em)

## Call:
## coxph(formula = Surv(survtime, survind) ~ expression + strata(mutation),
```

```
##      data = nsclc)
##
##
##           coef exp(coef) se(coef)      z    p
## expression -0.204      0.815    0.372 -0.548 0.58
##
## Likelihood ratio test=0.3  on 1 df, p=0.586  n= 102, number of events= 49

nsclc.devres1.P53em <- residuals(nsclc.strPH.P53em, type = "deviance")
nsclc.fitval1.P53em <- nsclc.strPH.P53em$linear.predictors
plot(nsclc.fitval1.P53em, nsclc.devres1.P53em)
```



```
# inne dane:

data("ovarian")
head(ovarian, 1)

##      futime fustat   age resid.ds rx ecog.ps
## 1      59      1 72.33      2  1      1

ovar.PH <- coxph(Surv(futime, fustat) ~ 1, data = ovarian)
mart <- resid(ovar.PH)
plot(ovarian$age, mart)
lines(lowess(ovarian$age, mart, iter = 0, f = 0.6))
```

