Cox-ph model

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```r
library(tidyverse)
library(survival)
library(survminer)
```

```r
data(cancer, package="survival")
```

data preparation

```r
# data preparation
bladder1 <-
  bladder1 %>%
  mutate(recurr = if_else(status == 1, 1, 0),
         time = stop - start,
         rtumor = as.numeric(na_if(rtumor, ".")),
         rsize = as.numeric(na_if(rsize, "."))) %>%
  filter(start == 0)
```

```r
#skimr::skim(bladder1) %>% knitr::kable()
```

Fit cox-ph model

```r
# fit univariate coxph model
bladder1.cox.1 <- coxph(Surv(time, recurr) ~ treatment, data = bladder1)
summary(bladder1.cox.1)
```

```
## Call:
## coxph(formula = Surv(time, recurr) ~ treatment, data = bladder1)
##
##   n= 118, number of events= 62
##
##                       coef exp(coef) se(coef)      z Pr(>|z|)
## treatmentpyridoxine -0.3532    0.7024   0.3202 -1.103    0.270
## treatmentthiotepa   -0.3830    0.6818   0.3025 -1.266    0.205
##
##                     exp(coef) exp(-coef) lower .95 upper .95
## treatmentpyridoxine    0.7024      1.424    0.3750     1.316
## treatmentthiotepa      0.6818      1.467    0.3769     1.234
```
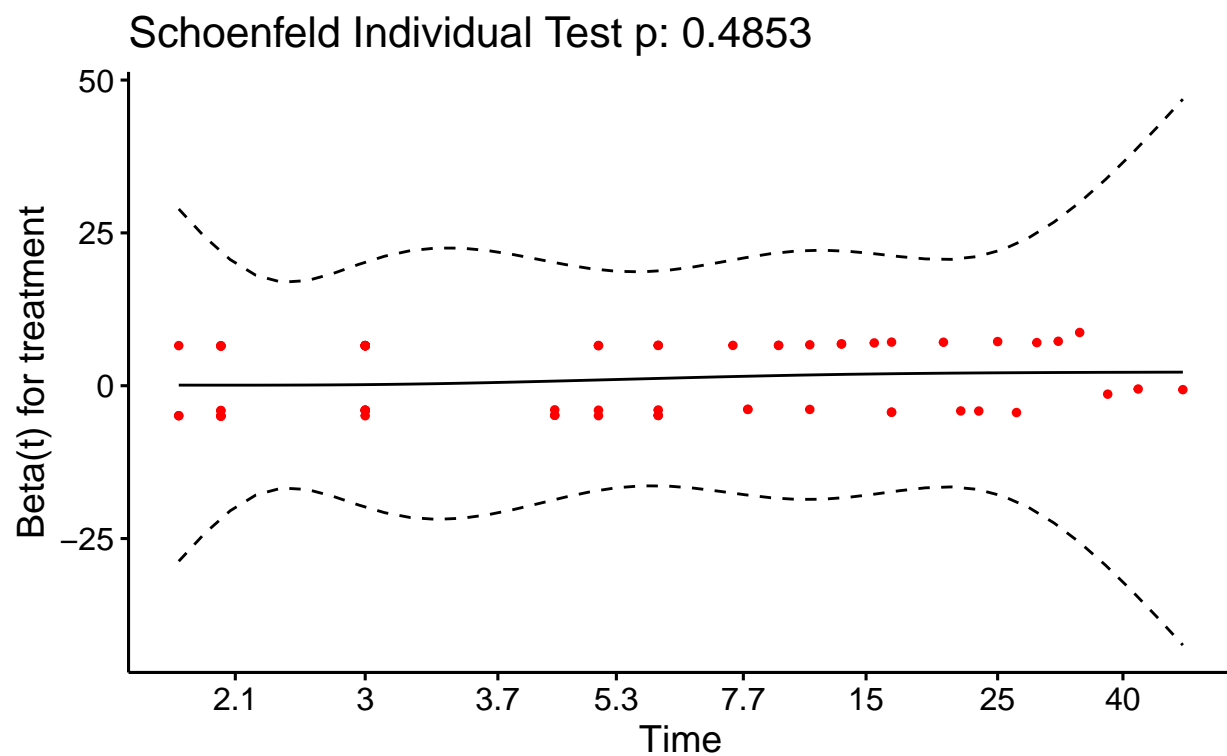
```
## 
## Concordance= 0.533  (se = 0.038 )
## Likelihood ratio test= 2.05  on 2 df,   p=0.4
## Wald test            = 2.07  on 2 df,   p=0.4
## Score (logrank) test = 2.09  on 2 df,   p=0.4
```

```
# check assumption
test.ph.1 <- cox.zph(bladder1.cox.1, transform = "km")
print(test.ph.1)
```

```
##            chisq df    p
## treatment   1.45  2 0.49
## GLOBAL      1.45  2 0.49
```

```
ggcoxzph(test.ph.1)
```

Global Schoenfeld Test p: 0.4853

Schoenfeld Individual Test p: 0.4853

```
bladder1.cox.2 <- coxph(Surv(time, recurr) ~ treatment + number + size, data = bladder1)
summary(bladder1.cox.2)
```

```
## Call:
## coxph(formula = Surv(time, recurr) ~ treatment + number + size,
##     data = bladder1)
## 
##   n= 118, number of events= 62
```
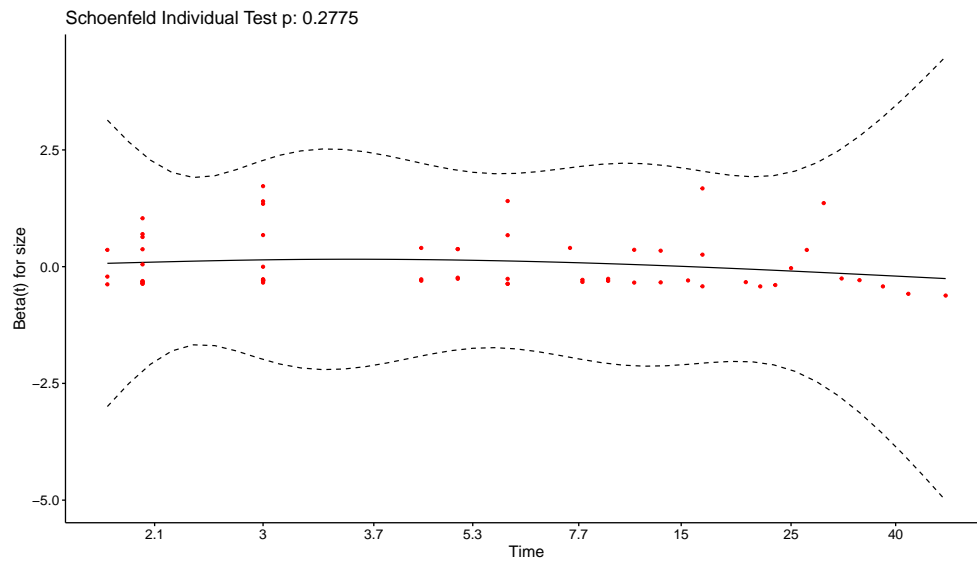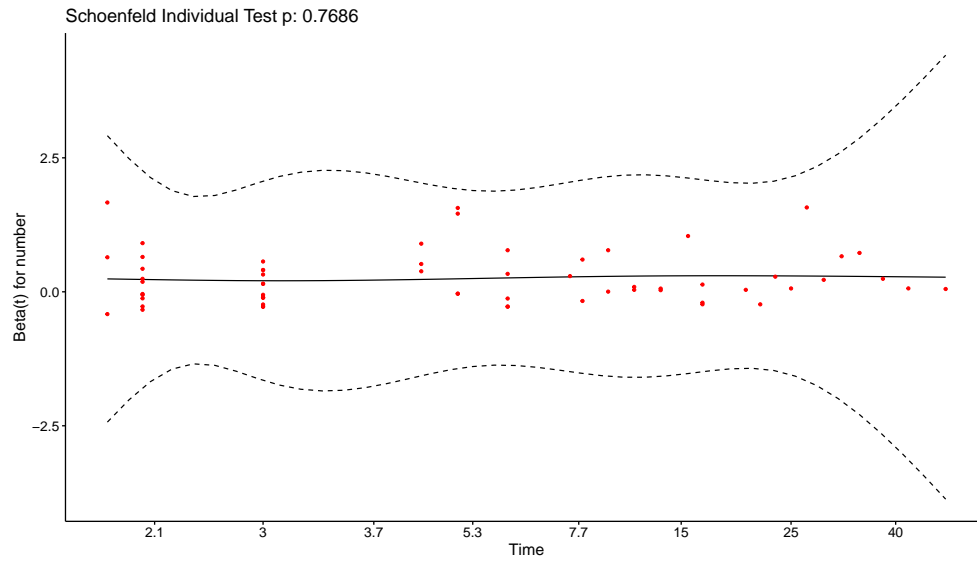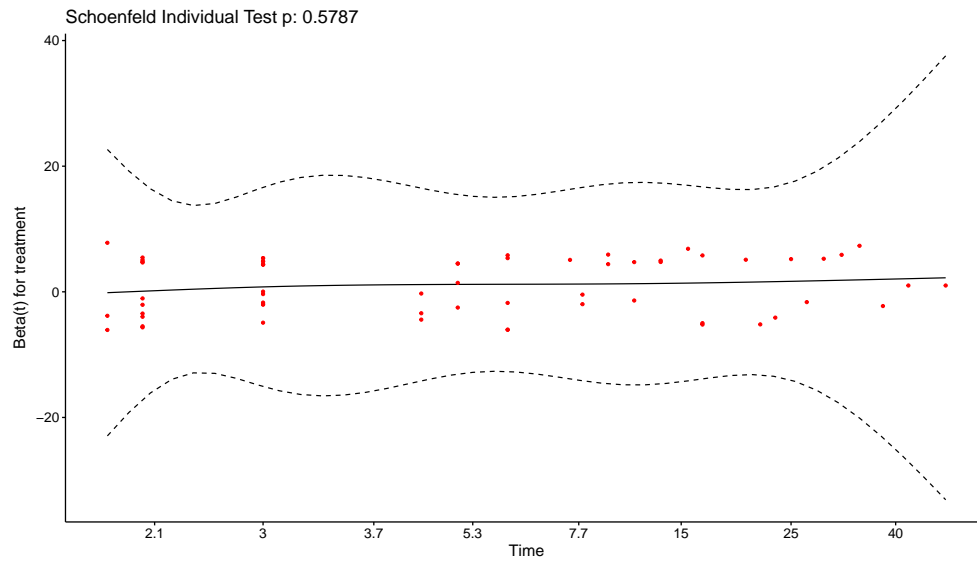
```
## 
##                    coef exp(coef) se(coef)      z Pr(>|z|)
## treatmentpyridoxine -0.34130   0.71085  0.32227 -1.059 0.289585
## treatmentthiotepa   -0.55105   0.57634  0.31257 -1.763 0.077904 .
## number               0.25249   1.28723  0.06498  3.886 0.000102 ***
## size                 0.05892   1.06069  0.07414  0.795 0.426761
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
##                    exp(coef) exp(-coef) lower .95 upper .95
## treatmentpyridoxine    0.7108     1.4068    0.3780     1.337
## treatmentthiotepa      0.5763     1.7351    0.3123     1.064
## number                 1.2872     0.7769    1.1333     1.462
## size                   1.0607     0.9428    0.9172     1.227
## 
## Concordance= 0.642  (se = 0.038 )
## Likelihood ratio test= 14.94  on 4 df,   p=0.005
## Wald test            = 16.55  on 4 df,   p=0.002
## Score (logrank) test = 17.75  on 4 df,   p=0.001
```

```
test.ph.2 <- cox.zph(bladder1.cox.2)
print(test.ph.2)
```
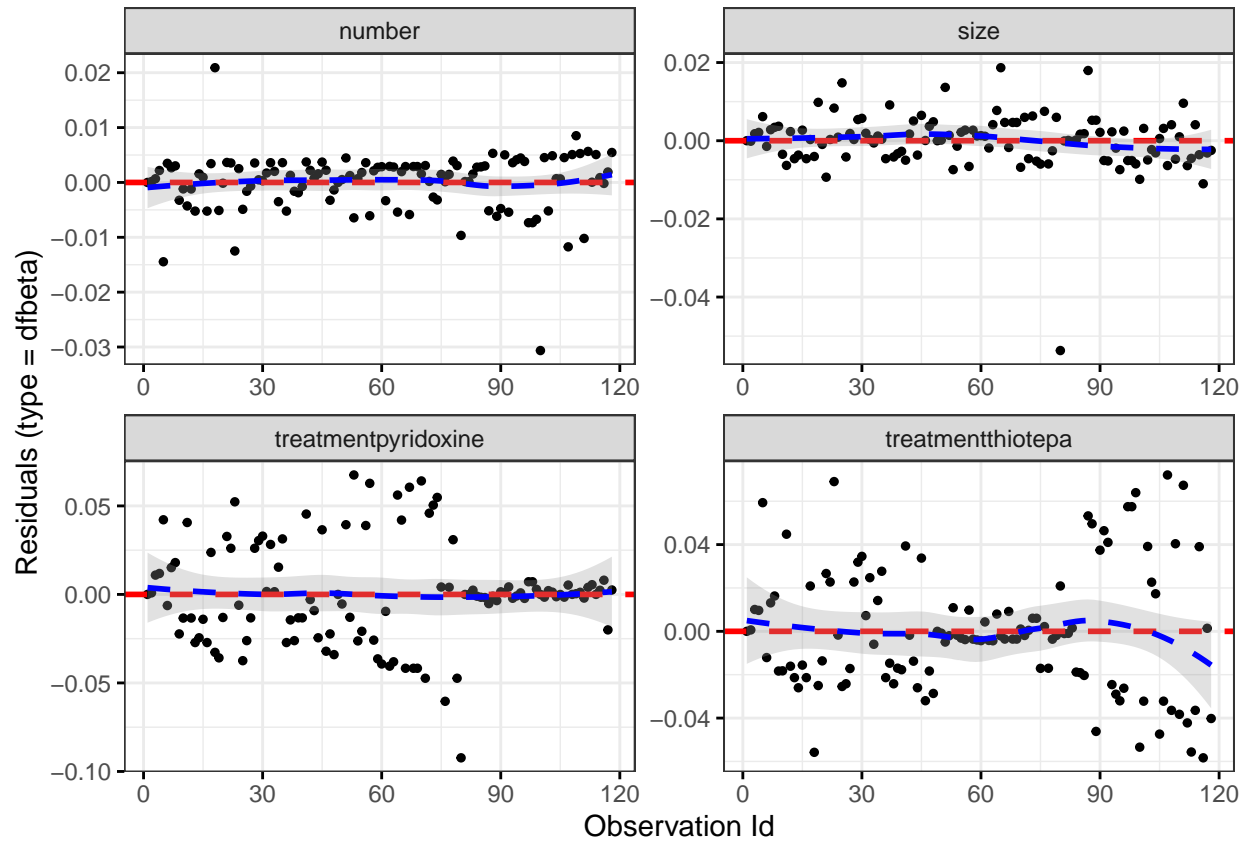
```
##            chisq df    p
## treatment 1.0940  2 0.58
## number    0.0865  1 0.77
## size      1.1794  1 0.28
## GLOBAL    2.4600  4 0.65
```

```
ggcoxzph(test.ph.2)
```

Global Schoenfeld Test p: 0.6518

Schoenfeld Individual Test p: 0.5787

Schoenfeld Individual Test p: 0.7686

Schoenfeld Individual Test p: 0.2775

```
# Testing influential observations
ggcoxdiagnostics(
  bladder1.cox.2,
  type = "dfbeta"
)
```


Testing non linearity

```
# Testing non linearity
ggcoxfunctional(Surv(time, recurr) ~  number + log(number) + sqrt(number), data = bladder1)
```

```
## Warning: arguments formula is deprecated; will be removed in the next version;
## please use fit instead.
```
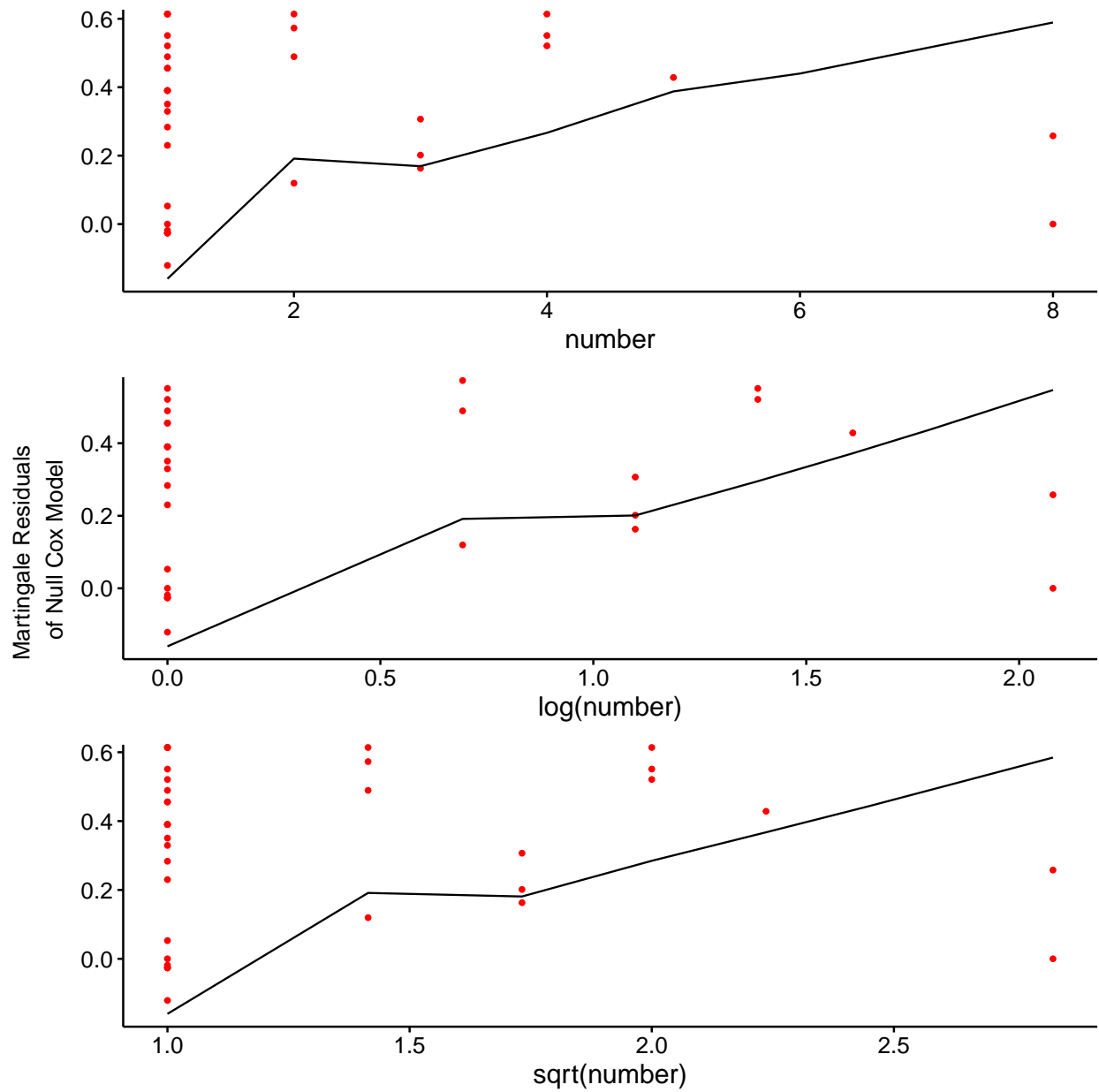
```
ggcoxfunctional(Surv(time, recurr) ~  size + log(size) + sqrt(size), data = bladder1)
```

```
## Warning: arguments formula is deprecated; will be removed in the next version;
## please use fit instead.
```
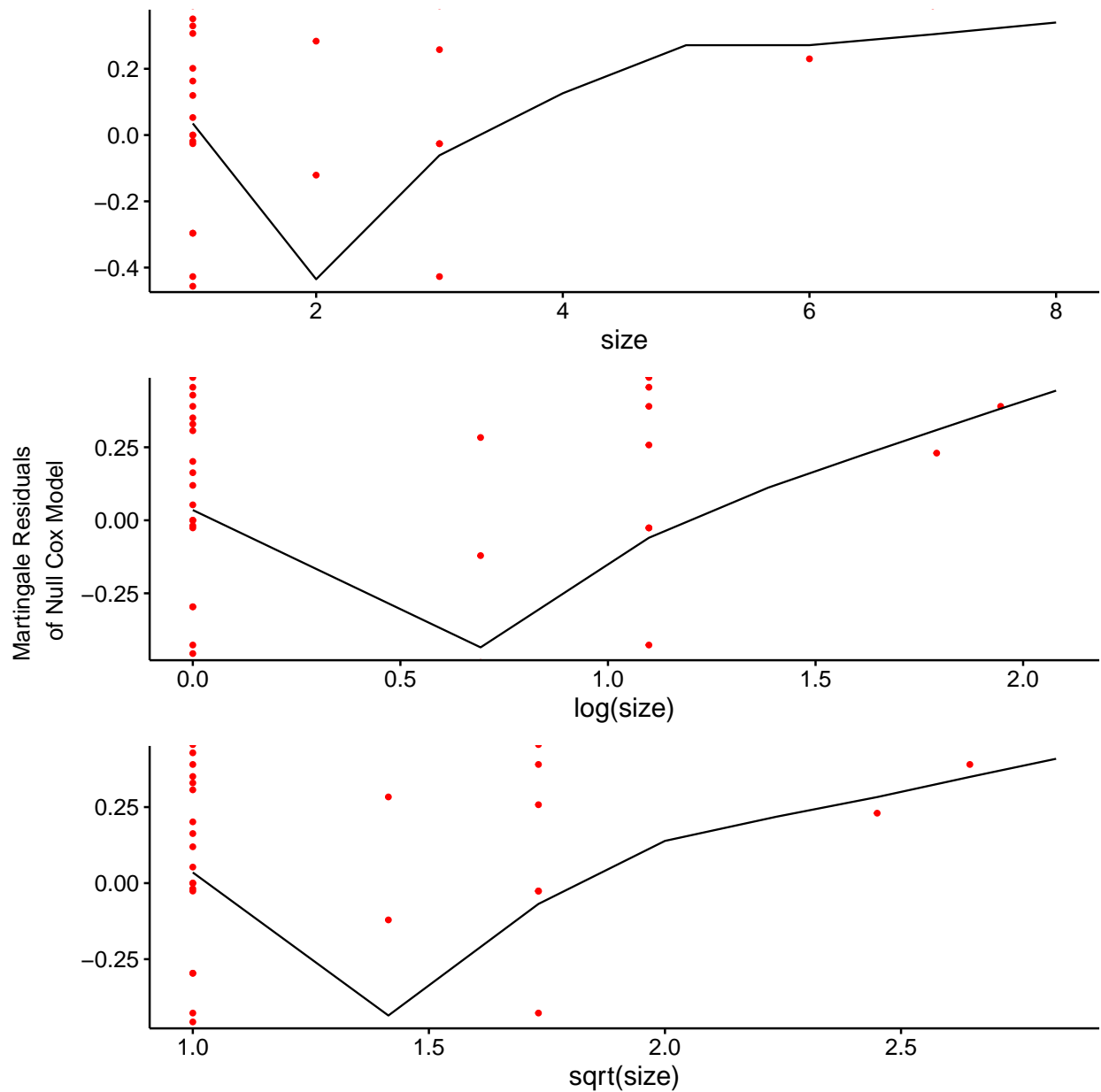
```
bladder1.cox.3 <- coxph(Surv(time, recurr) ~ treatment + number, data = bladder1)
summary(bladder1.cox.3)
```

```
## Call:
## coxph(formula = Surv(time, recurr) ~ treatment + number, data = bladder1)
##
##   n= 118, number of events= 62
##
##                        coef exp(coef) se(coef)      z Pr(>|z|)
## treatmentpyridoxine -0.32570   0.72202  0.32095 -1.015  0.31020
## treatmentthiotepa   -0.54309   0.58095  0.31116 -1.745  0.08092 .
## number               0.25037   1.28451  0.06475  3.867  0.00011 ***
## ---
```

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```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##                     exp(coef) exp(-coef) lower .95 upper .95
## treatmentpyridoxine    0.7220     1.3850    0.3849      1.354
## treatmentthiotepa      0.5809     1.7213    0.3157      1.069
## number                 1.2845     0.7785    1.1314      1.458
##
## Concordance= 0.646  (se = 0.038 )
## Likelihood ratio test= 14.34  on 3 df,   p=0.002
## Wald test            = 16.19  on 3 df,   p=0.001
## Score (logrank) test = 17.34  on 3 df,   p=6e-04
```

```
test.ph.3 <- cox.zph(bladder1.cox.3)
print(test.ph.3)
```

```
##            chisq df    p
## treatment 1.044  2 0.59
## number    0.158  1 0.69
## GLOBAL    1.413  3 0.70
```

```
ggcoxzph(test.ph.3)
```

Global Schoenfeld Test p: 0.7024

Schoenfeld Individual Test p: 0.5932

Schoenfeld Individual Test p: 0.691
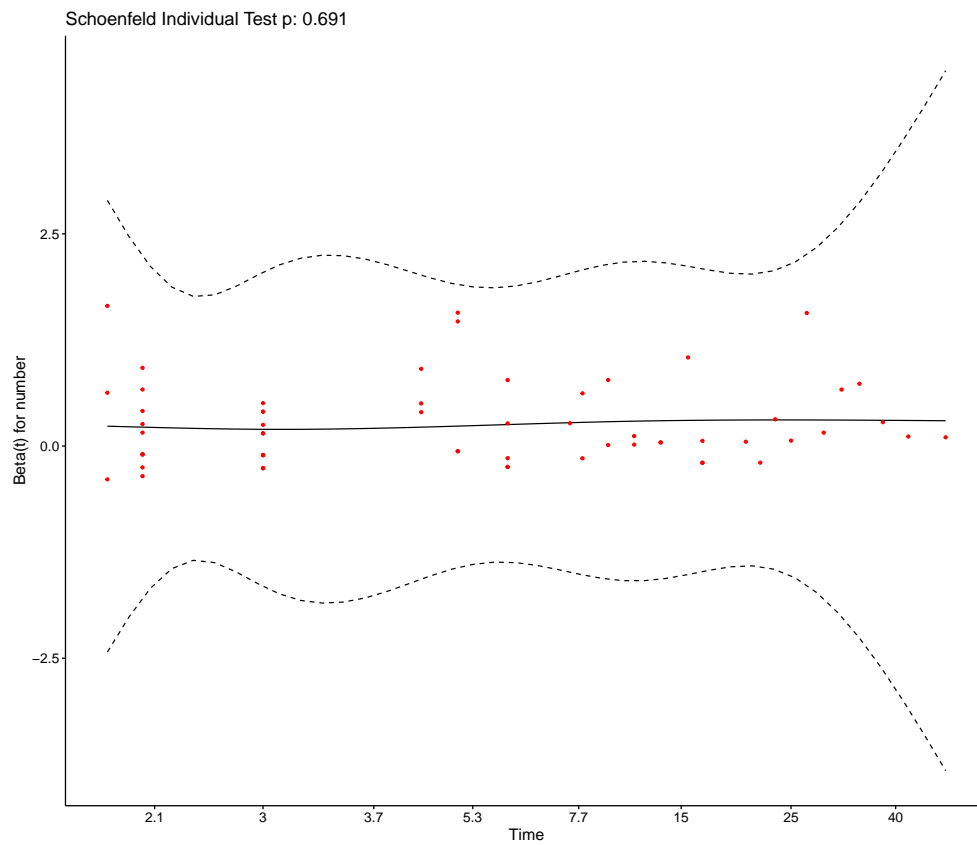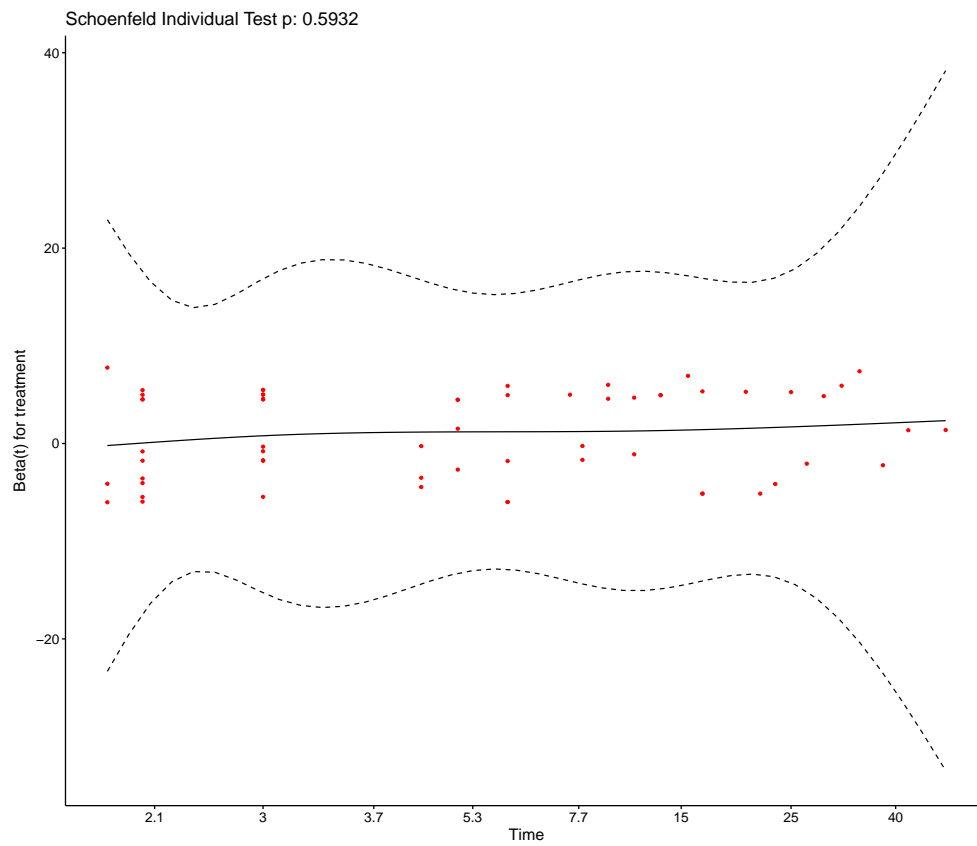
```
# Testing influential observations
ggcoxdiagnostics(
  bladder1.cox.3,
  type = "dfbeta"
)
```