

Cox-ph model

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

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

data preparation

```
# 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)
```

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

Fit cox-ph model

```
# 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
```

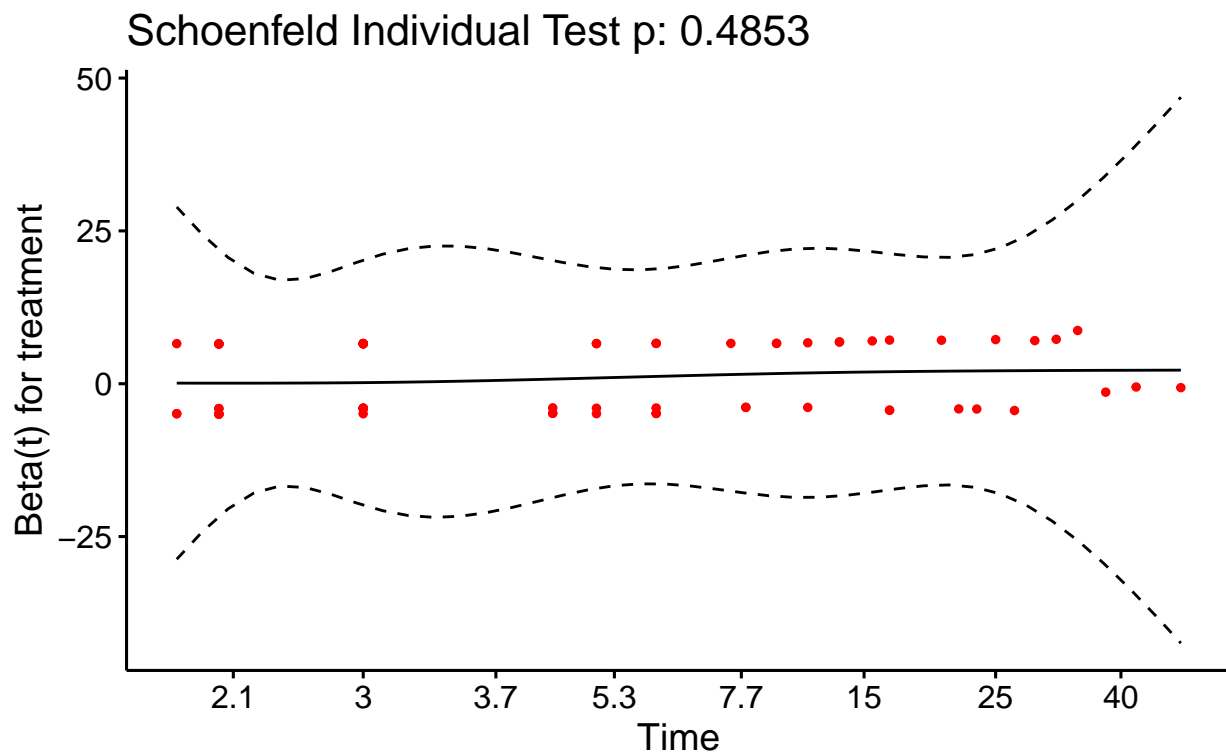
```
##
## Concordance= 0.533 (se = 0.038 )
## Likelihood ratio test= 2.05 on 2 df, p=0.4
## Wald test = 2.07 on 2 df, p=0.4
## Score (logrank) test = 2.09 on 2 df, p=0.4

# 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



```
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
```

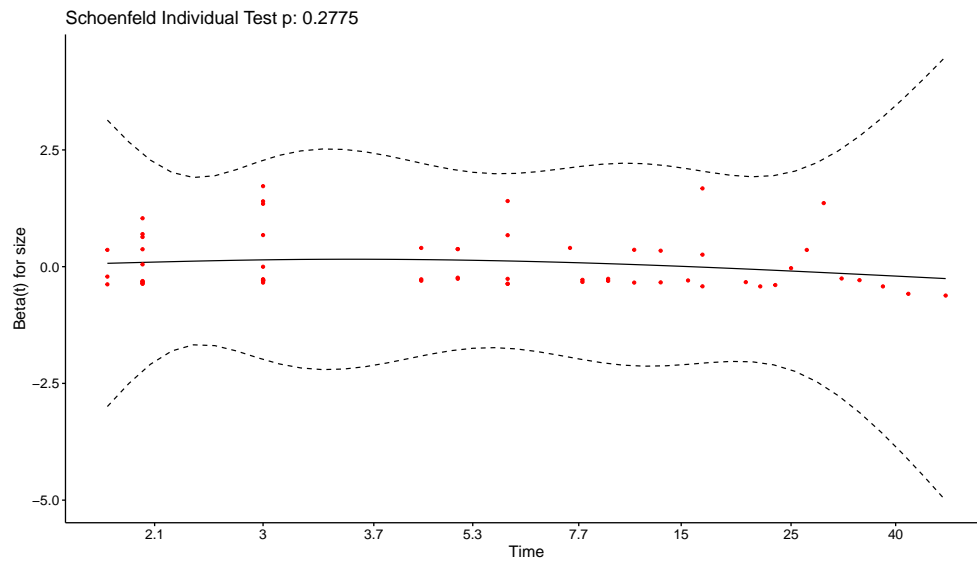
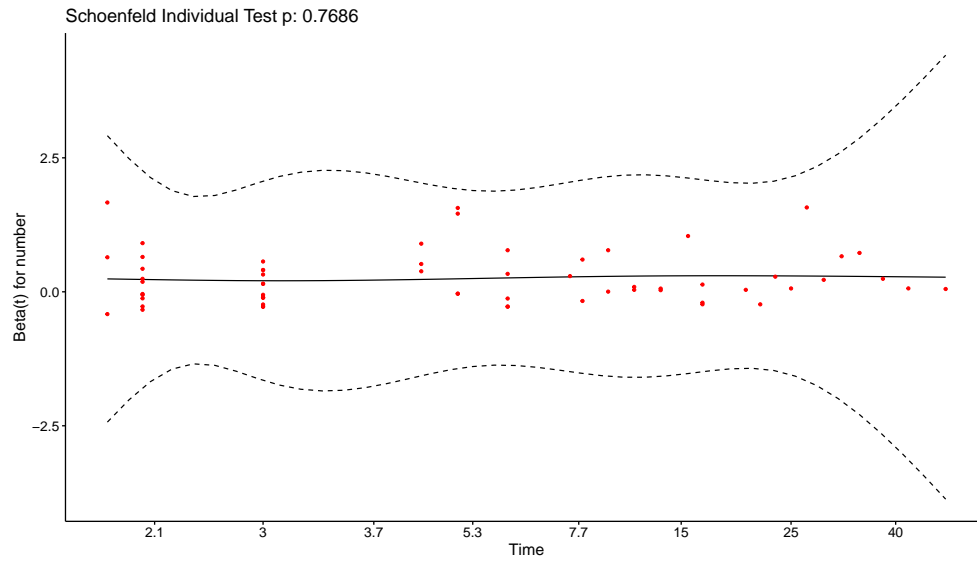
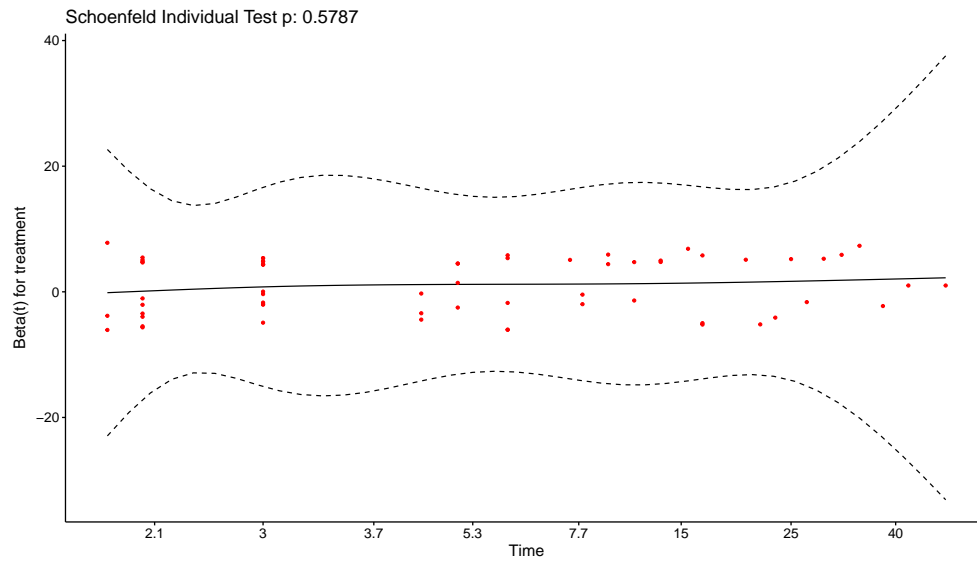
```
##
##               coef exp(coef) se(coef)      z Pr(>|z|)
## treatmentpyridoxine -0.34130  0.71085  0.32227 -1.059 0.289585
## treatmentthiotepa  -0.55105  0.57634  0.31257 -1.763 0.077904 .
## number              0.25249  1.28723  0.06498  3.886 0.000102 ***
## size                0.05892  1.06069  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
```

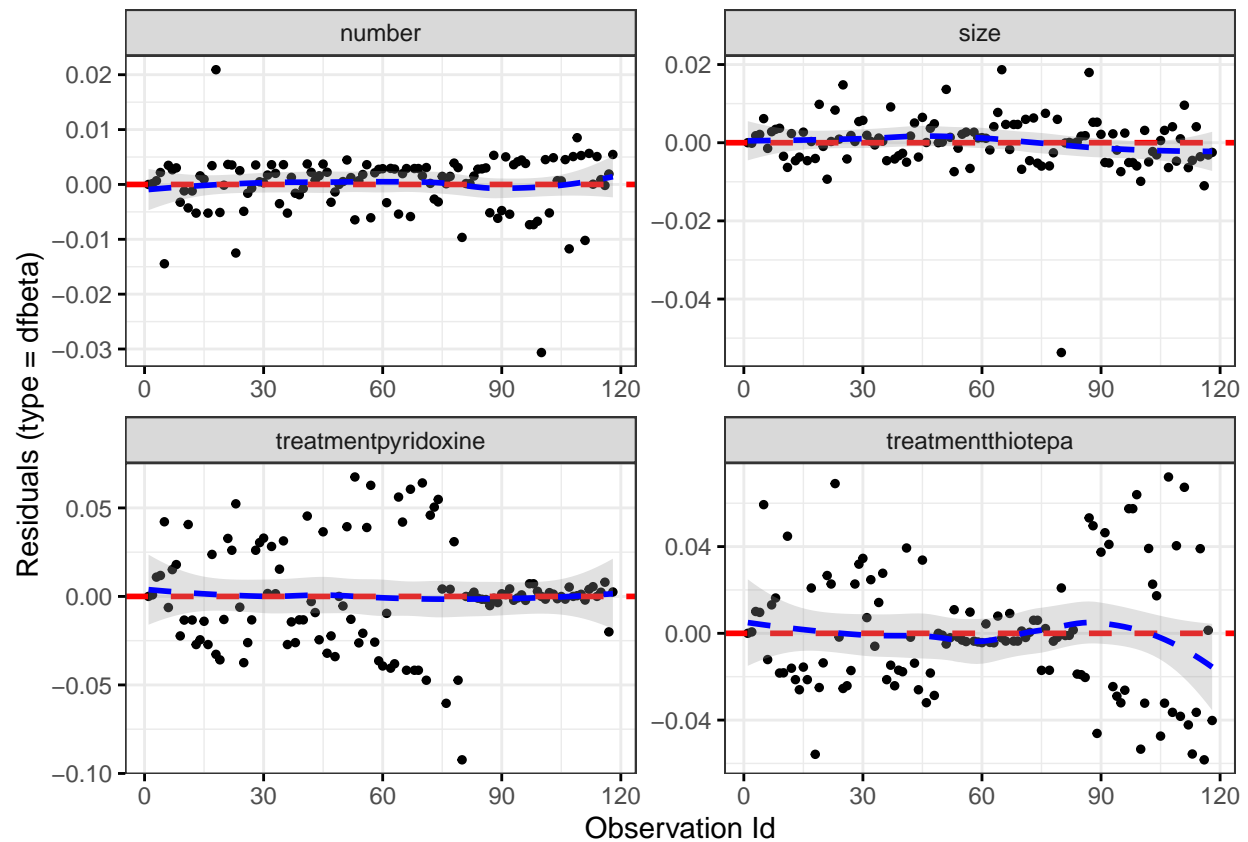
```
ggcoxzph(test.ph.2)
```

Global Schoenfeld Test p: 0.6518



```
# Testing influential observations
```

```
ggcoxdiagnostics(  
  bladder1.cox.2,  
  type = "dfbeta"  
)
```



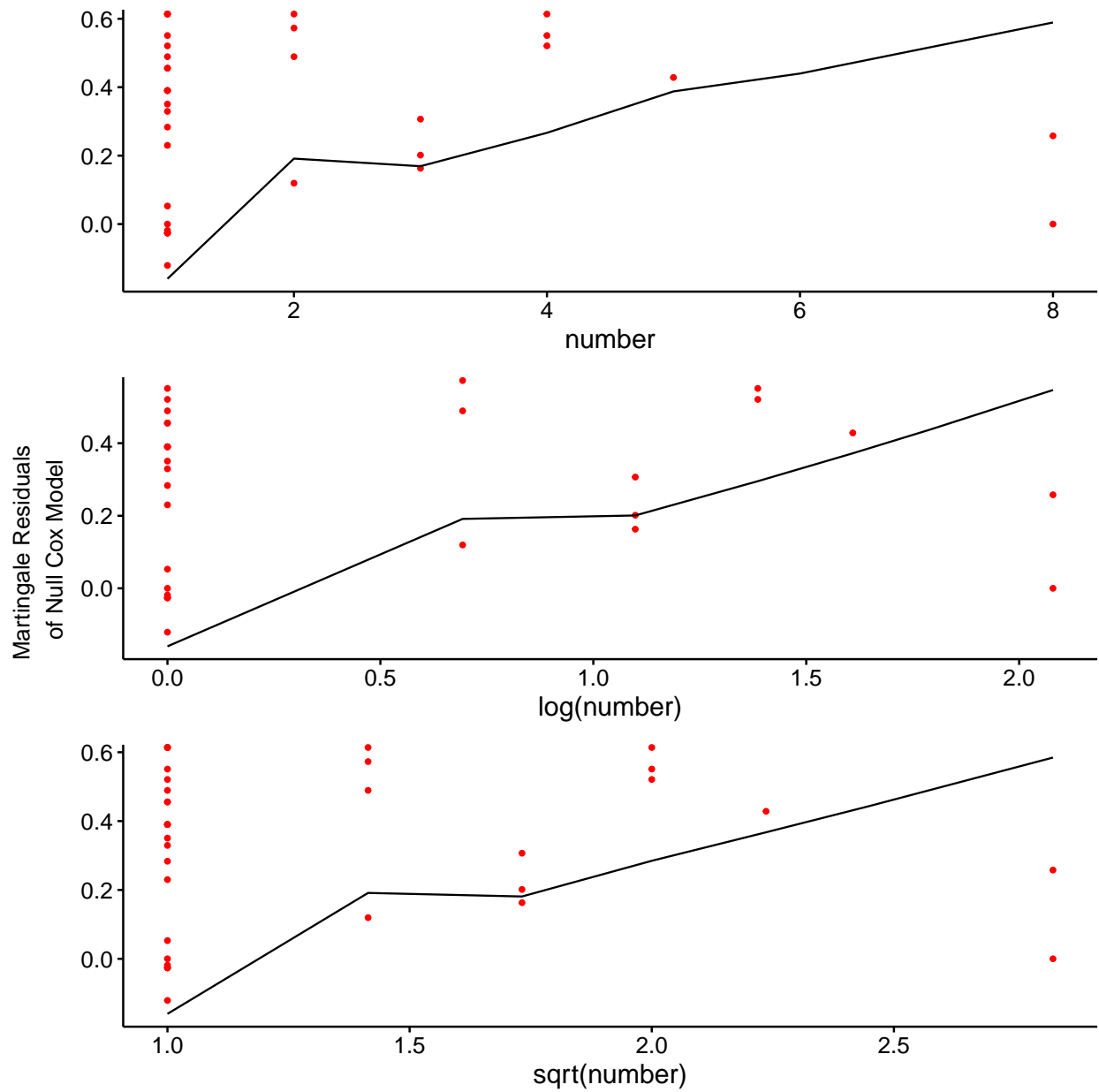
```
### Testing non linearity
```

```
# Testing non linearity
```

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

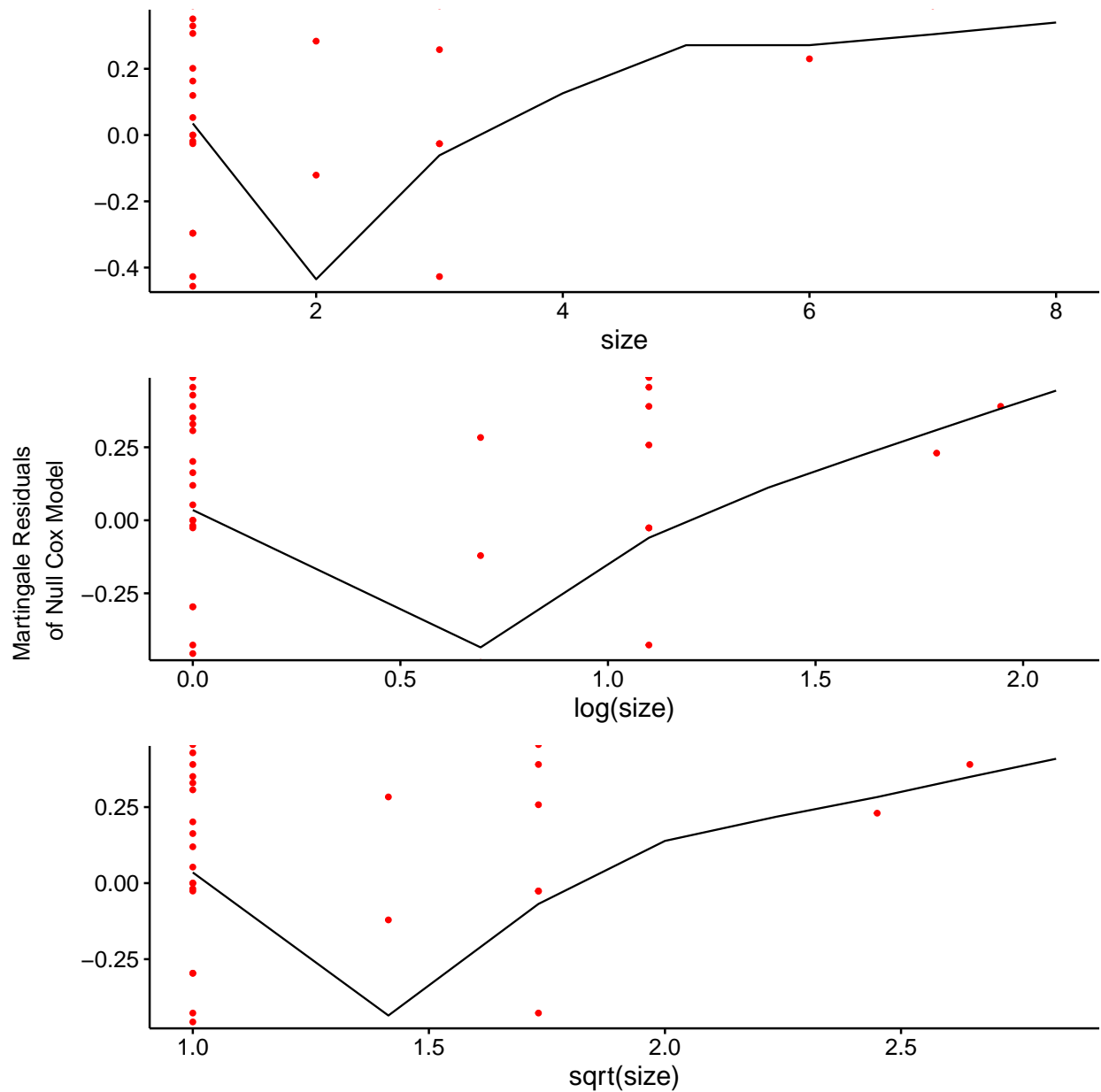
```
## Warning: arguments formula is deprecated; will be removed in the next version;
```

```
## 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 ***
## ---
```

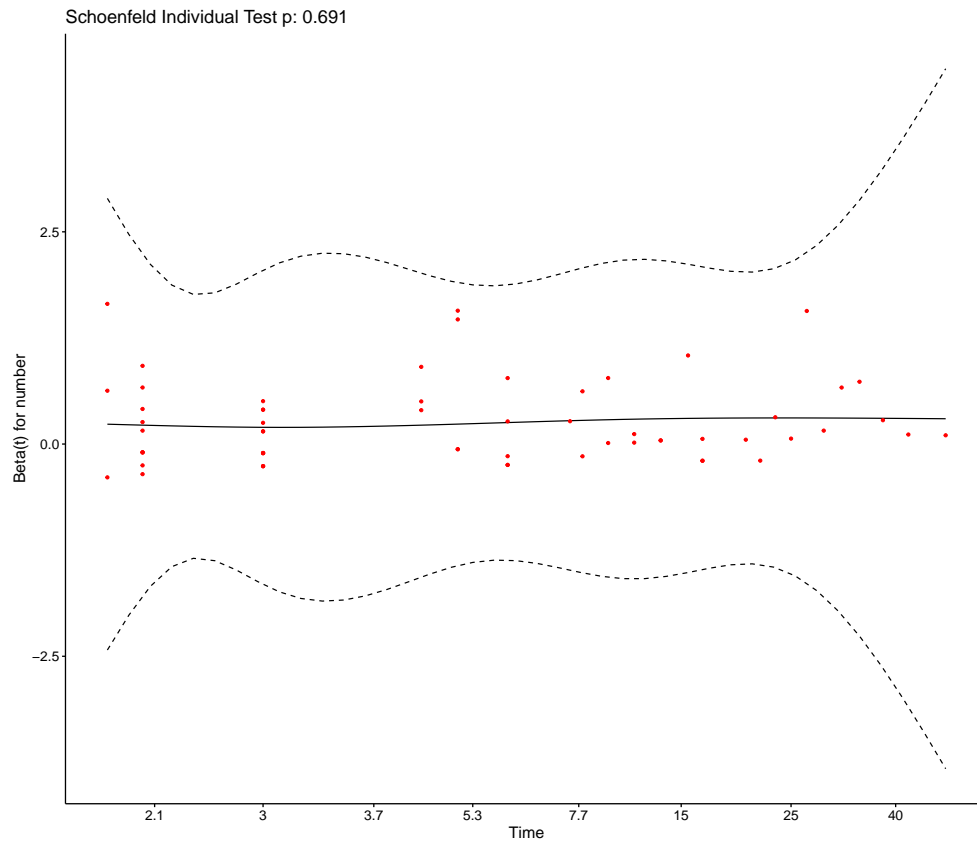
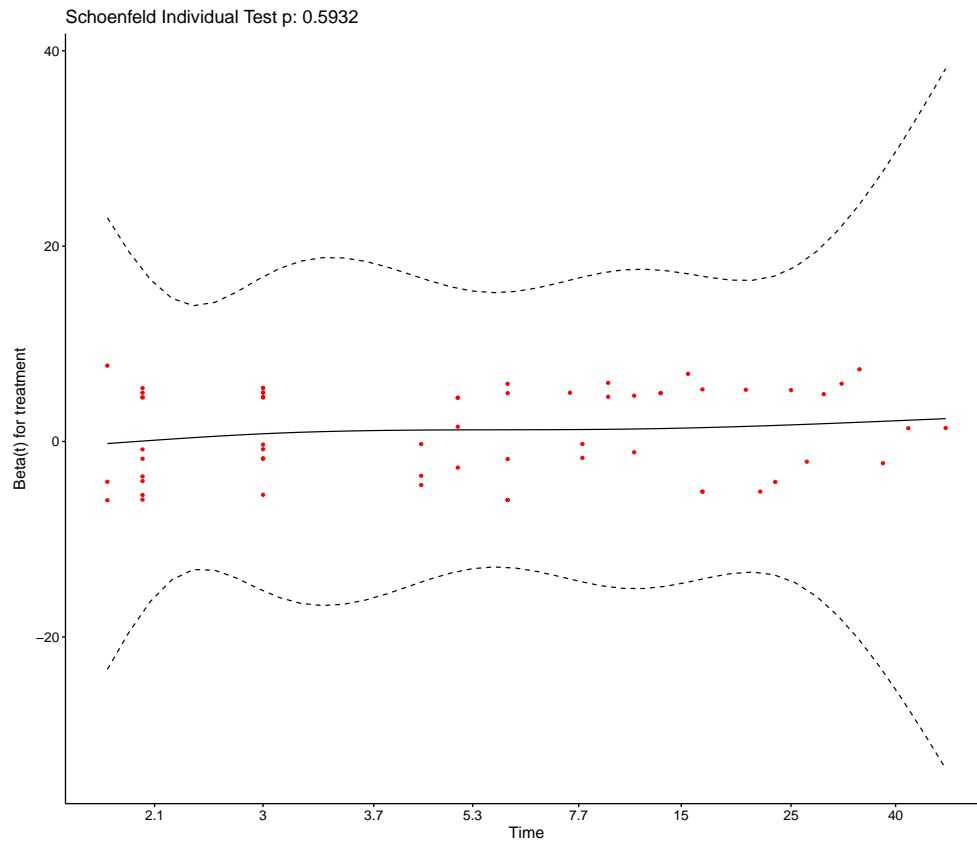
```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##               exp(coef) exp(-coef) lower .95 upper .95
## treatmentpyridoxine    0.7220    1.3850    0.3849    1.354
## treatmentthiotepa     0.5809    1.7213    0.3157    1.069
## number                 1.2845    0.7785    1.1314    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



```
# Testing influential observations
ggcoxdiagnostics(
  bladder1.cox.3,
  type = "dfbeta"
)
```

