project2

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Libraries

```
library(tidyverse)
library(readr)
library(boot)
library(table1)
library(gridExtra)
library(MASS)
library(car)
library(dplyr)
library(leaps)
library(corrplot)
library(survival)
```

Data Clean

```
breastcancer_data =
  read_csv("Project_2_data.csv") |>
  janitor::clean_names()
```

```
## Rows: 4024 Columns: 16
## -- Column specification --------------------------------------------------------
## Delimiter: ","
## chr (11): Race, Marital Status, T Stage, N Stage, 6th Stage, differentiate, ...
## dbl  (5): Age, Tumor Size, Regional Node Examined, Reginol Node Positive, Su...
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```
summary(breastcancer_data)
```

```
##       age            race           marital_status       t_stage
##  Min.   :30.00   Length:4024        Length:4024        Length:4024
##  1st Qu.:47.00   Class :character   Class :character   Class :character
##  Median :54.00   Mode  :character   Mode  :character   Mode  :character
##  Mean   :53.97
##  3rd Qu.:61.00
```

```
##  Max.   :69.00
##    n_stage           x6th_stage        differentiate         grade
##  Length:4024        Length:4024        Length:4024        Length:4024
##  Class :character   Class :character   Class :character   Class :character
##  Mode  :character   Mode  :character   Mode  :character   Mode  :character
##
##
##
##    a_stage            tumor_size     estrogen_status    progesterone_status
##  Length:4024        Min.   :  1.00   Length:4024        Length:4024
##  Class :character   1st Qu.: 16.00   Class :character   Class :character
##  Mode  :character   Median : 25.00   Mode  :character   Mode  :character
##                     Mean   : 30.47
##                     3rd Qu.: 38.00
##                     Max.   :140.00
##  regional_node_examined reginol_node_positive survival_months
##  Min.   : 1.00          Min.   : 1.000        Min.   :  1.0
##  1st Qu.: 9.00          1st Qu.: 1.000        1st Qu.: 56.0
##  Median :14.00          Median : 2.000        Median : 73.0
##  Mean   :14.36          Mean   : 4.158        Mean   : 71.3
##  3rd Qu.:19.00          3rd Qu.: 5.000        3rd Qu.: 90.0
##  Max.   :61.00          Max.   :46.000        Max.   :107.0
##     status
##  Length:4024
##  Class :character
##  Mode  :character
##
##
##
```

```r
bc = breastcancer_data |>
  mutate(
    race = factor(race, levels = c("White", "Black", "Other")),
    marital_status = factor(marital_status, levels = c("Married", "Divorced",
                                                       "Single", "Widowed",
                                                       "Separated")),
    t_stage = factor(t_stage, levels = c("T1", "T2", "T3", "T4")),
    n_stage = factor(n_stage, levels = c("N1", "N2", "N3")),
    x6th_stage = factor(x6th_stage, levels = c("IIA", "IIIA", "IIIC", "IIB", "IIIB")),
    differentiate = factor(differentiate, levels = c("Poorly differentiated",
                                                     "Moderately differentiated",
                                                     "Well differentiated",
                                                     "Undifferentiated")),
    grade = factor(grade, levels = c("1", "2", "3", "anaplastic; Grade IV")),
    a_stage = factor(a_stage, levels = c("Distant", "Regional")),
    estrogen_status = factor(estrogen_status, levels = c("Negative", "Positive")),
    progesterone_status = factor(progesterone_status,
                                 levels = c("Negative", "Positive")),
    status = factor(status, levels = c("Dead", "Alive"))
  )
```

Descriptive statistics for all variables

```
summary(bc)
```

```
##       age           race        marital_status t_stage   n_stage   x6th_stage
##  Min.   :30.00   White:3413   Married  :2643   T1:1603   N1:2732   IIA :1305
##  1st Qu.:47.00   Black: 291   Divorced : 486   T2:1786   N2: 820   IIIA:1050
##  Median :54.00   Other: 320   Single   : 615   T3: 533   N3: 472   IIIC: 472
##  Mean   :53.97                Widowed  : 235   T4: 102             IIB :1130
##  3rd Qu.:61.00                Separated:  45                       IIIB:  67
##  Max.   :69.00
##                    differentiate                    grade          a_stage
##  Poorly differentiated    :1111   1                   : 543   Distant :  92
##  Moderately differentiated:2351   2                   :2351   Regional:3932
##  Well differentiated      : 543   3                   :1111
##  Undifferentiated         :  19   anaplastic; Grade IV:  19
##
##
##    tumor_size     estrogen_status progesterone_status regional_node_examined
##  Min.   :  1.00   Negative: 269   Negative: 698       Min.   : 1.00
##  1st Qu.: 16.00   Positive:3755   Positive:3326       1st Qu.: 9.00
##  Median : 25.00                                       Median :14.00
##  Mean   : 30.47                                       Mean   :14.36
##  3rd Qu.: 38.00                                       3rd Qu.:19.00
##  Max.   :140.00                                       Max.   :61.00
##  reginol_node_positive survival_months   status
##  Min.   : 1.000        Min.   :  1.0   Dead : 616
##  1st Qu.: 1.000        1st Qu.: 56.0   Alive:3408
##  Median : 2.000        Median : 73.0
##  Mean   : 4.158        Mean   : 71.3
##  3rd Qu.: 5.000        3rd Qu.: 90.0
##  Max.   :46.000        Max.   :107.0
```

Fit a Cox Proportional Hazards Model

```
bc$survival_months <- as.numeric(bc$survival_months)
bc$status <- as.numeric(bc$status)
surv_obj <- Surv(time = bc$survival_months, event = bc$status)

# Fit the Cox model
cox_model <- coxph(surv_obj ~ age + race + marital_status + t_stage + n_stage + x6th_stage +
                     differentiate + grade + a_stage + tumor_size + estrogen_status +
                     progesterone_status + regional_node_examined + reginol_node_positive, data = bc)
summary(cox_model)
```

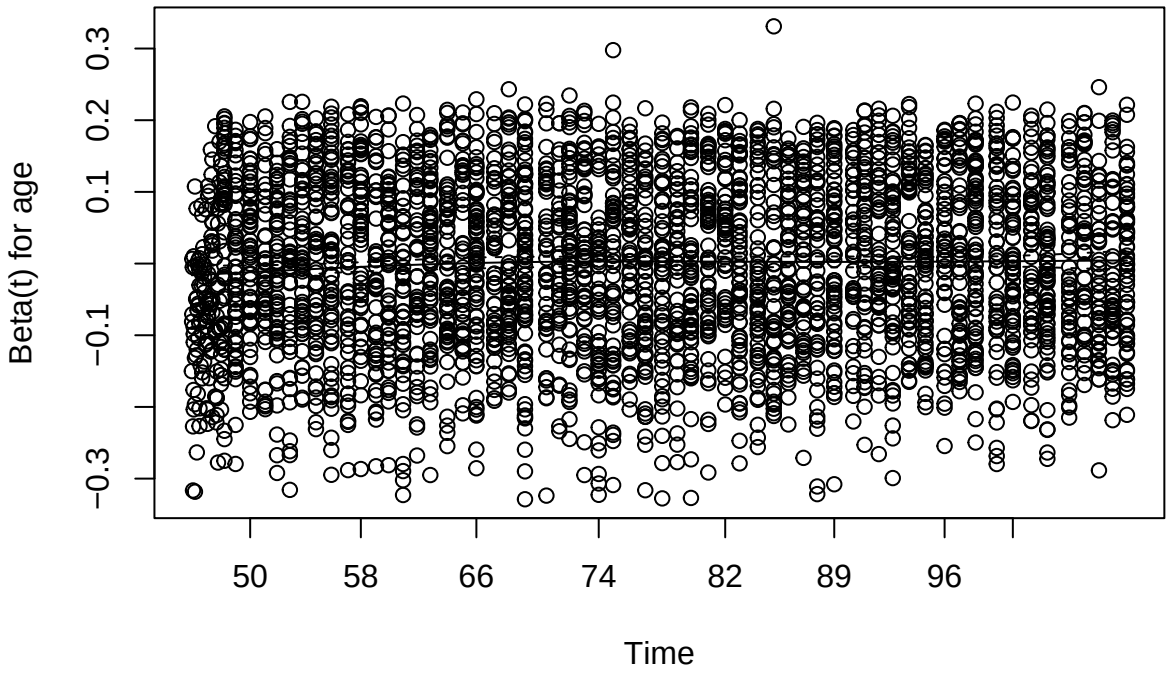
```
## Call:
## coxph(formula = surv_obj ~ age + race + marital_status + t_stage +
##     n_stage + x6th_stage + differentiate + grade + a_stage +
##     tumor_size + estrogen_status + progesterone_status + regional_node_examined +
##     reginol_node_positive, data = bc)
```

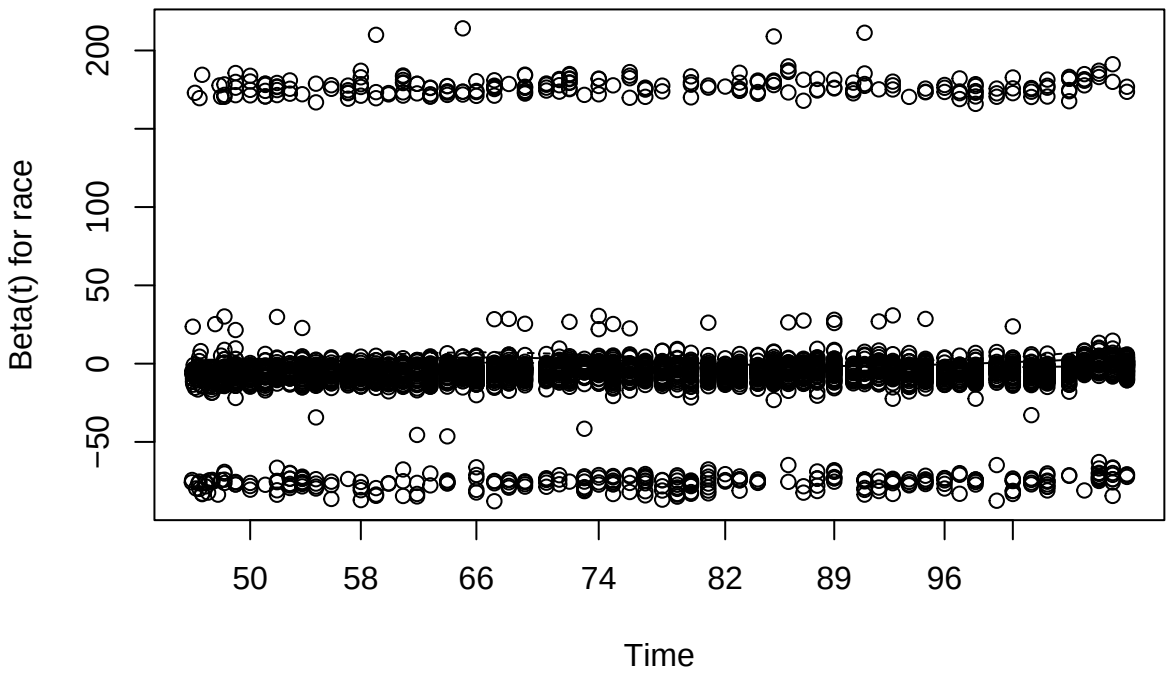
```
##
##   n= 4024, number of events= 3408
##
##                                          coef  exp(coef)   se(coef)      z
## age                                   -0.0004124  0.9995877  0.0020594 -0.200
## raceBlack                              0.0725419  1.0752378  0.0713977  1.016
## raceOther                             -0.0282799  0.9721162  0.0623962 -0.453
## marital_statusDivorced                -0.0604365  0.9413536  0.0549382 -1.100
## marital_statusSingle                  -0.0482234  0.9529209  0.0496924 -0.970
## marital_statusWidowed                 -0.0303772  0.9700795  0.0782217 -0.388
## marital_statusSeparated                0.2309519  1.2597987  0.1848733  1.249
## t_stageT2                              0.0125409  1.0126199  0.0857679  0.146
## t_stageT3                             -0.0847136  0.9187754  0.1434176 -0.591
## t_stageT4                             -0.3011978  0.7399314  0.2924931 -1.030
## n_stageN2                             -0.1666794  0.8464709  0.1012458 -1.646
## n_stageN3                             -0.0261531  0.9741859  0.1405331 -0.186
## x6th_stageIIIA                         0.1632452  1.1773253  0.1182755  1.380
## x6th_stageIIIC                                NA         NA  0.0000000     NA
## x6th_stageIIB                         -0.0071028  0.9929224  0.0905328 -0.078
## x6th_stageIIIB                         0.1569403  1.1699257  0.3163929  0.496
## differentiateModerately differentiated 0.0557485  1.0573318  0.0419336  1.329
## differentiateWell differentiated       0.1215000  1.1291894  0.0580404  2.093
## differentiateUndifferentiated         -0.3997794  0.6704679  0.3199544 -1.249
## grade2                                        NA         NA  0.0000000     NA
## grade3                                        NA         NA  0.0000000     NA
## gradeanaplastic; Grade IV                     NA         NA  0.0000000     NA
## a_stageRegional                       -0.0051530  0.9948603  0.1508261 -0.034
## tumor_size                             0.0009129  1.0009133  0.0018429  0.495
## estrogen_statusPositive                0.0915971  1.0959232  0.0909893  1.007
## progesterone_statusPositive            0.1628328  1.1768400  0.0545896  2.983
## regional_node_examined                 0.0025479  1.0025511  0.0023305  1.093
## reginol_node_positive                 -0.0032452  0.9967601  0.0080101 -0.405
##                                       Pr(>|z|)
## age                                    0.84127
## raceBlack                              0.30962
## raceOther                              0.65038
## marital_statusDivorced                 0.27130
## marital_statusSingle                   0.33183
## marital_statusWidowed                  0.69776
## marital_statusSeparated                0.21158
## t_stageT2                              0.88375
## t_stageT3                              0.55474
## t_stageT4                              0.30312
## n_stageN2                              0.09970 .
## n_stageN3                              0.85237
## x6th_stageIIIA                         0.16752
## x6th_stageIIIC                              NA
## x6th_stageIIB                          0.93747
## x6th_stageIIIB                         0.61987
## differentiateModerately differentiated 0.18370
## differentiateWell differentiated       0.03632 *
## differentiateUndifferentiated          0.21149
## grade2                                      NA
## grade3                                      NA
```

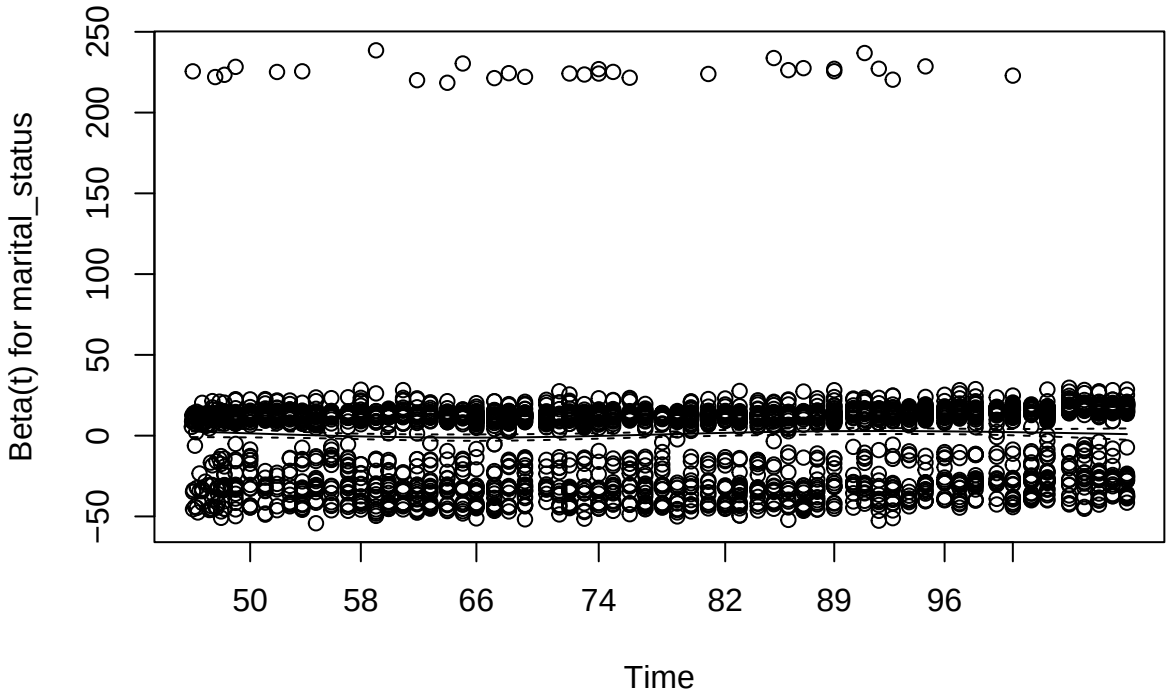
```
## gradeanaplastic; Grade IV                    NA
## a_stageRegional                           0.97275
## tumor_size                                0.62035
## estrogen_statusPositive                   0.31409
## progesterone_statusPositive               0.00286 **
## regional_node_examined                    0.27428
## reginol_node_positive                     0.68538
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##                                        exp(coef) exp(-coef) lower .95 upper .95
## age                                       0.9996     1.0004    0.9956     1.004
## raceBlack                                 1.0752     0.9300    0.9348     1.237
## raceOther                                 0.9721     1.0287    0.8602     1.099
## marital_statusDivorced                    0.9414     1.0623    0.8453     1.048
## marital_statusSingle                      0.9529     1.0494    0.8645     1.050
## marital_statusWidowed                     0.9701     1.0308    0.8322     1.131
## marital_statusSeparated                   1.2598     0.7938    0.8769     1.810
## t_stageT2                                 1.0126     0.9875    0.8559     1.198
## t_stageT3                                 0.9188     1.0884    0.6936     1.217
## t_stageT4                                 0.7399     1.3515    0.4171     1.313
## n_stageN2                                 0.8465     1.1814    0.6941     1.032
## n_stageN3                                 0.9742     1.0265    0.7396     1.283
## x6th_stageIIIA                            1.1773     0.8494    0.9337     1.484
## x6th_stageIIIC                               NA         NA        NA        NA
## x6th_stageIIB                             0.9929     1.0071    0.8315     1.186
## x6th_stageIIIB                            1.1699     0.8548    0.6293     2.175
## differentiateModerately differentiated    1.0573     0.9458    0.9739     1.148
## differentiateWell differentiated          1.1292     0.8856    1.0078     1.265
## differentiateUndifferentiated             0.6705     1.4915    0.3581     1.255
## grade2                                       NA         NA        NA        NA
## grade3                                       NA         NA        NA        NA
## gradeanaplastic; Grade IV                    NA         NA        NA        NA
## a_stageRegional                           0.9949     1.0052    0.7403     1.337
## tumor_size                                1.0009     0.9991    0.9973     1.005
## estrogen_statusPositive                   1.0959     0.9125    0.9169     1.310
## progesterone_statusPositive               1.1768     0.8497    1.0574     1.310
## regional_node_examined                    1.0026     0.9975    0.9980     1.007
## reginol_node_positive                     0.9968     1.0033    0.9812     1.013
##
## Concordance= 0.538  (se = 0.006 )
## Likelihood ratio test= 39.61  on 24 df,   p=0.02
## Wald test            = 38.29  on 24 df,   p=0.03
## Score (logrank) test = 38.42  on 24 df,   p=0.03
```

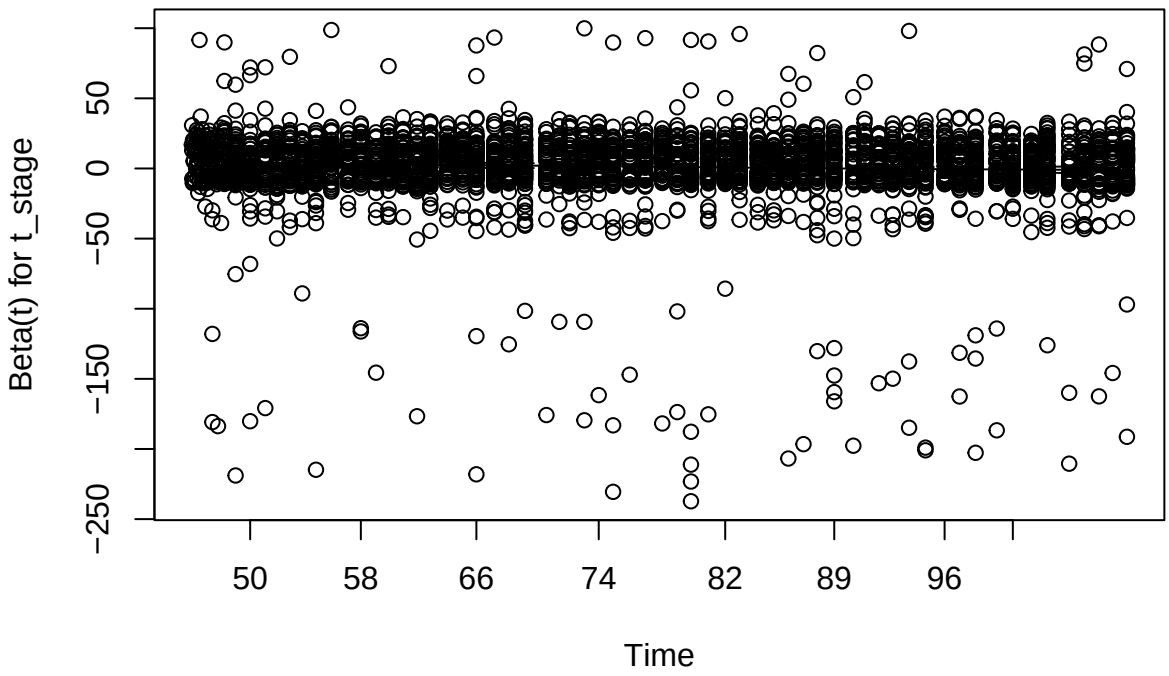
Check Proportional Hazards Assumption

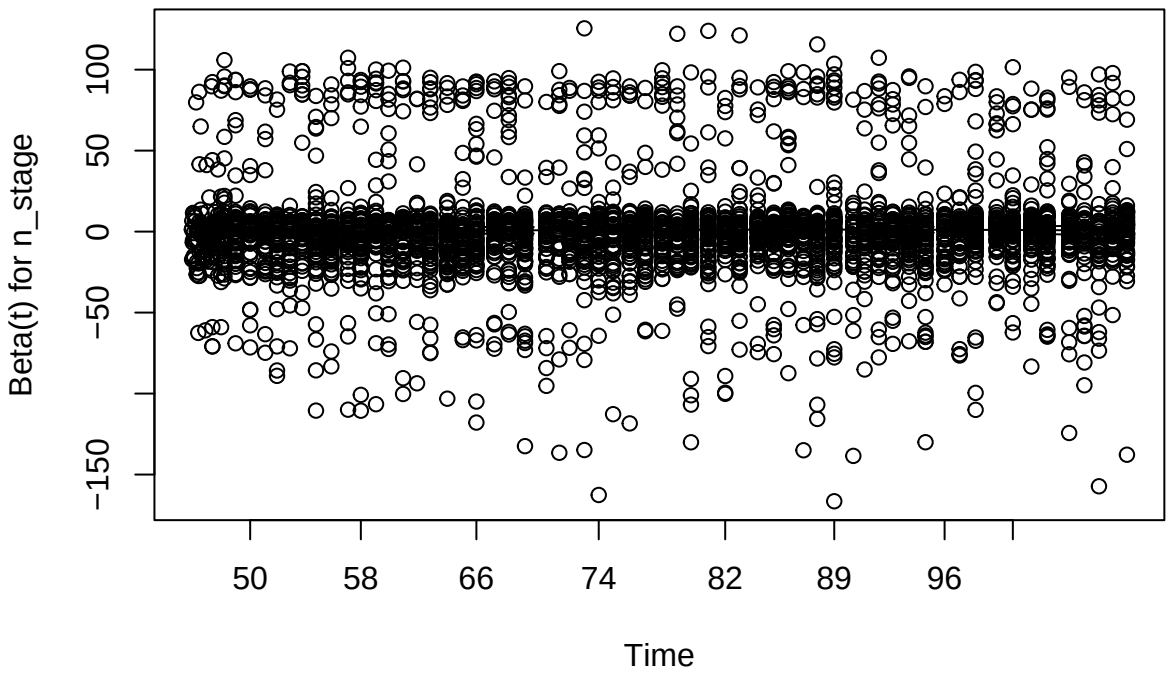
```
zph <- cox.zph(cox_model)
plot(zph)
```

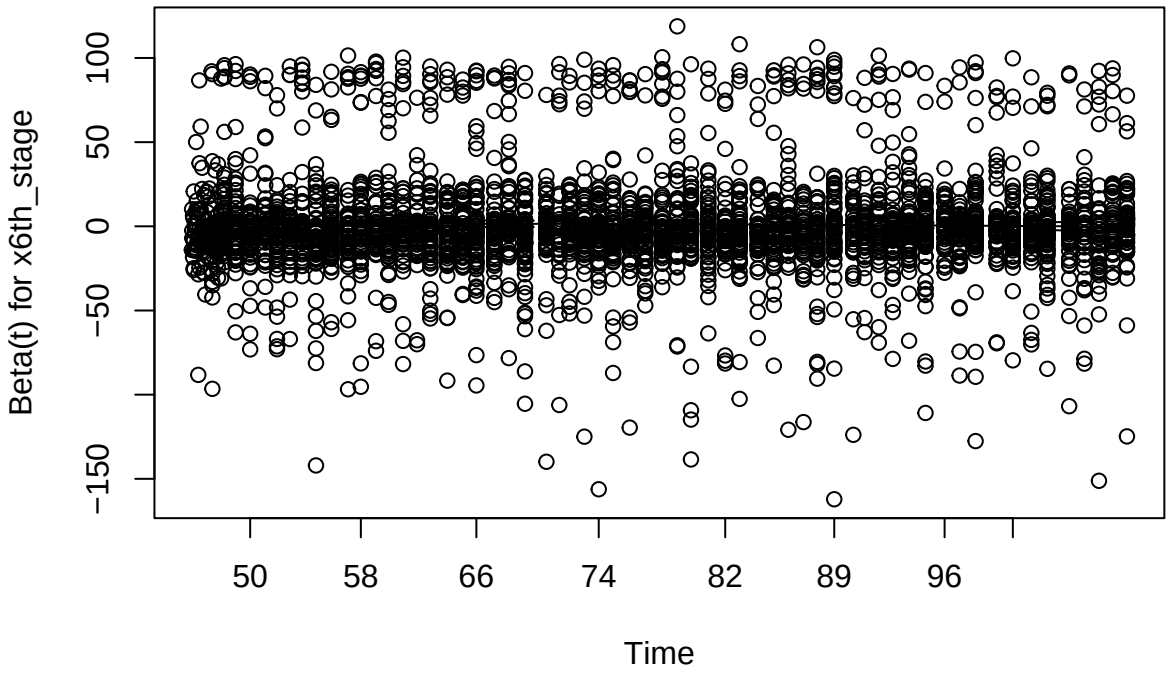

Beta(t) for age
−0.3
−0.1
0.1
0.2
0.3
50
58
66
74
82
89
96
Time

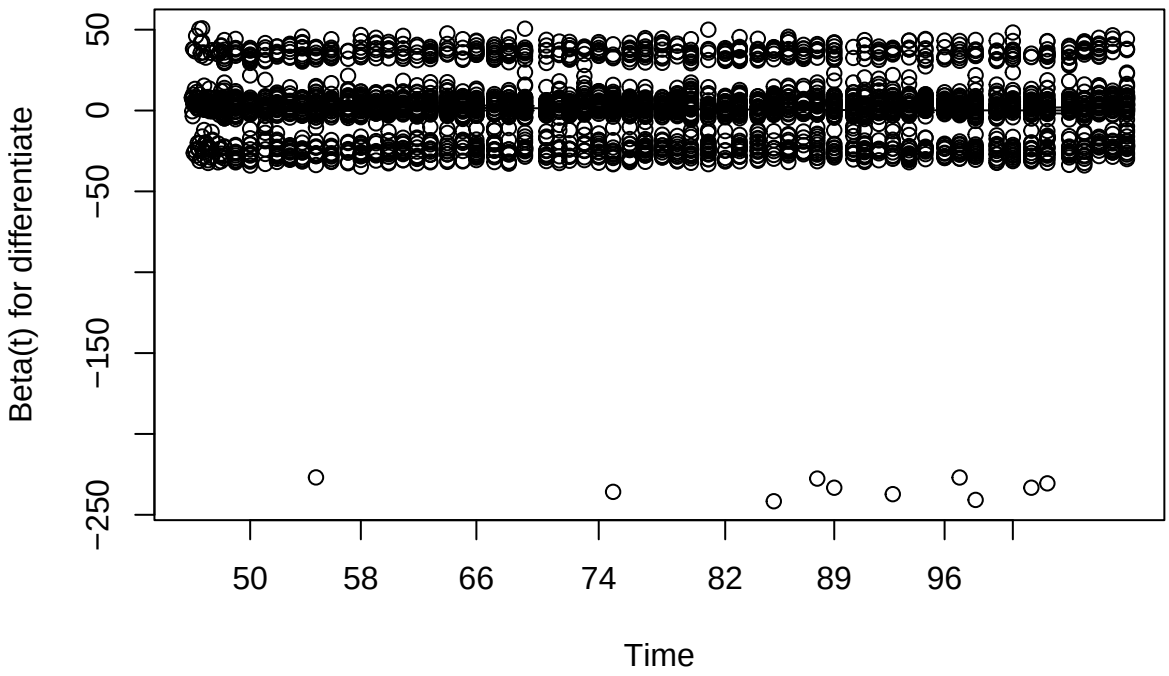

Beta(t) for race
200
100
50
0
−50
50
58
66
74
82
89
96
Time

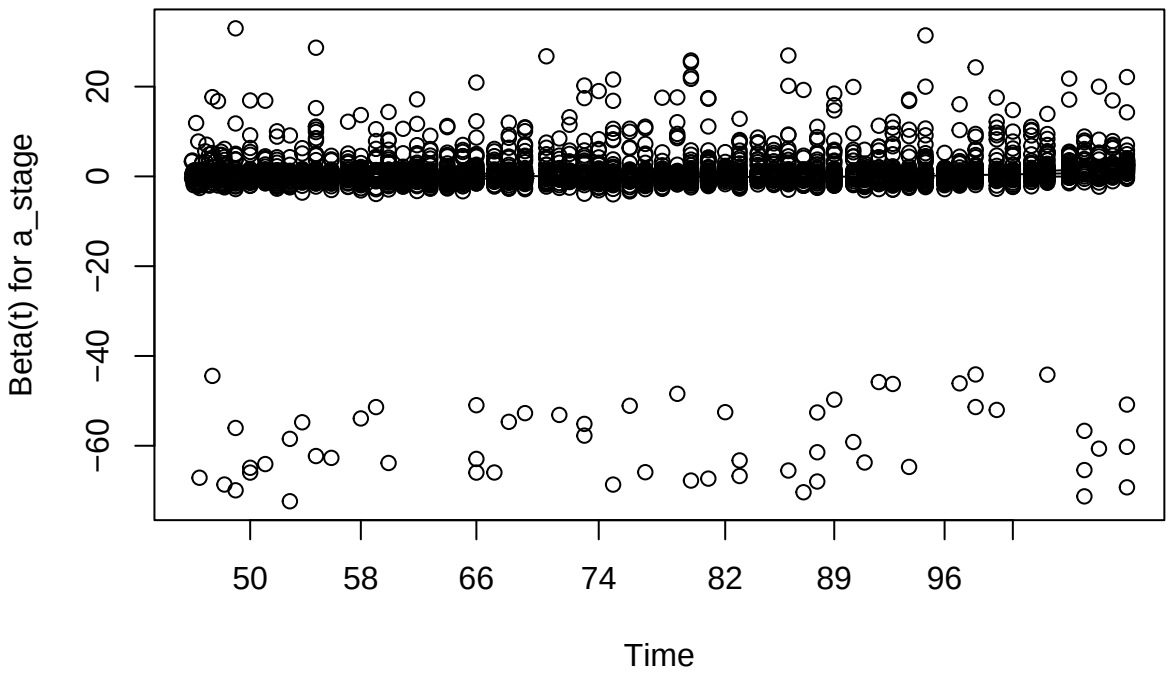

Beta(t) for marital_status
250
200
150
100
50
0
−50
50
58
66
74
82
89
96
Time

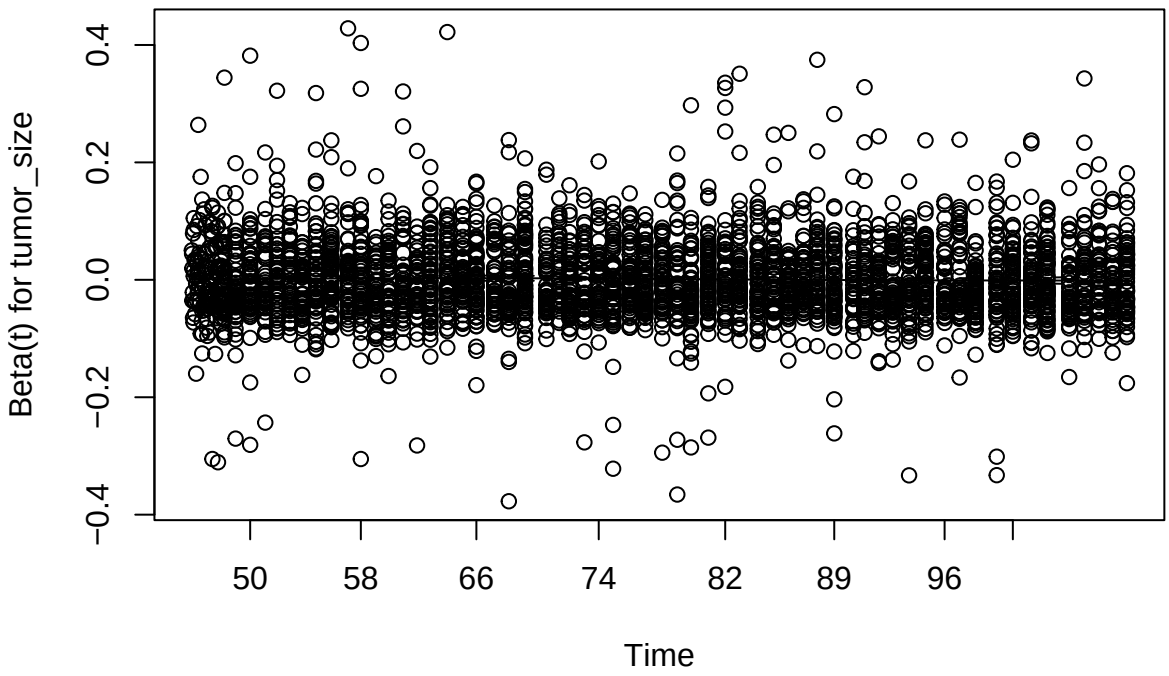

Beta(t) for t_stage
50
0
−50
−150
−250
50
58
66
74
82
89
96
Time

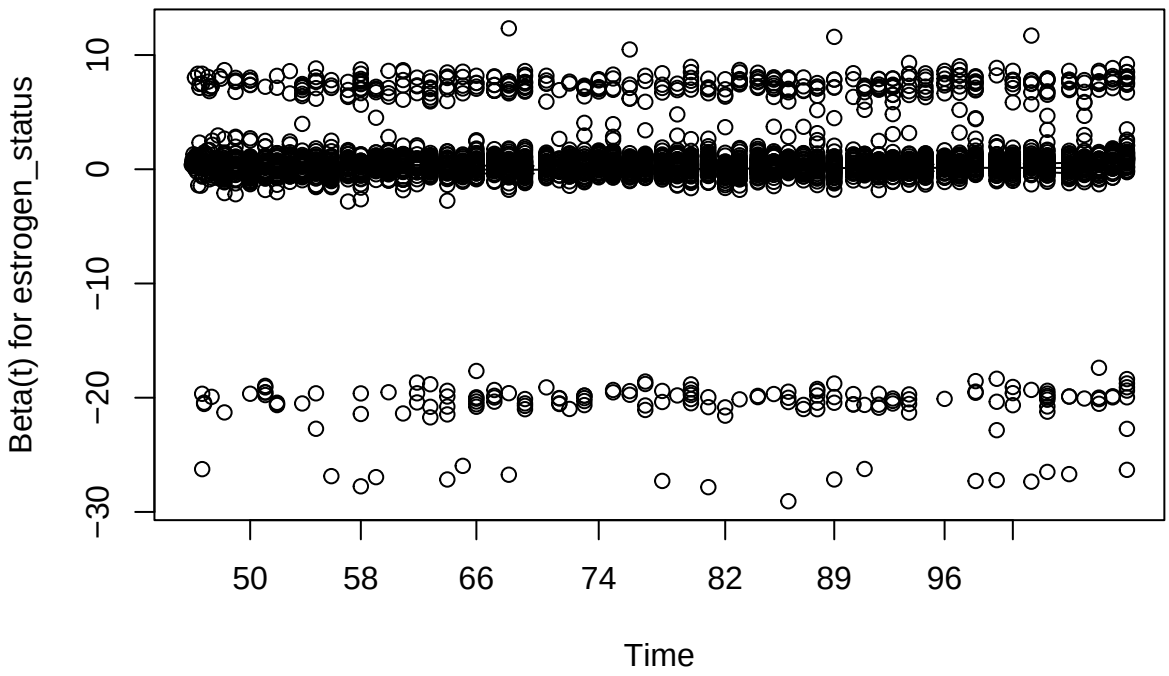

Beta(t) for n_stage
100
50
0
−50
−150
50
58
66
74
82
89
96
Time

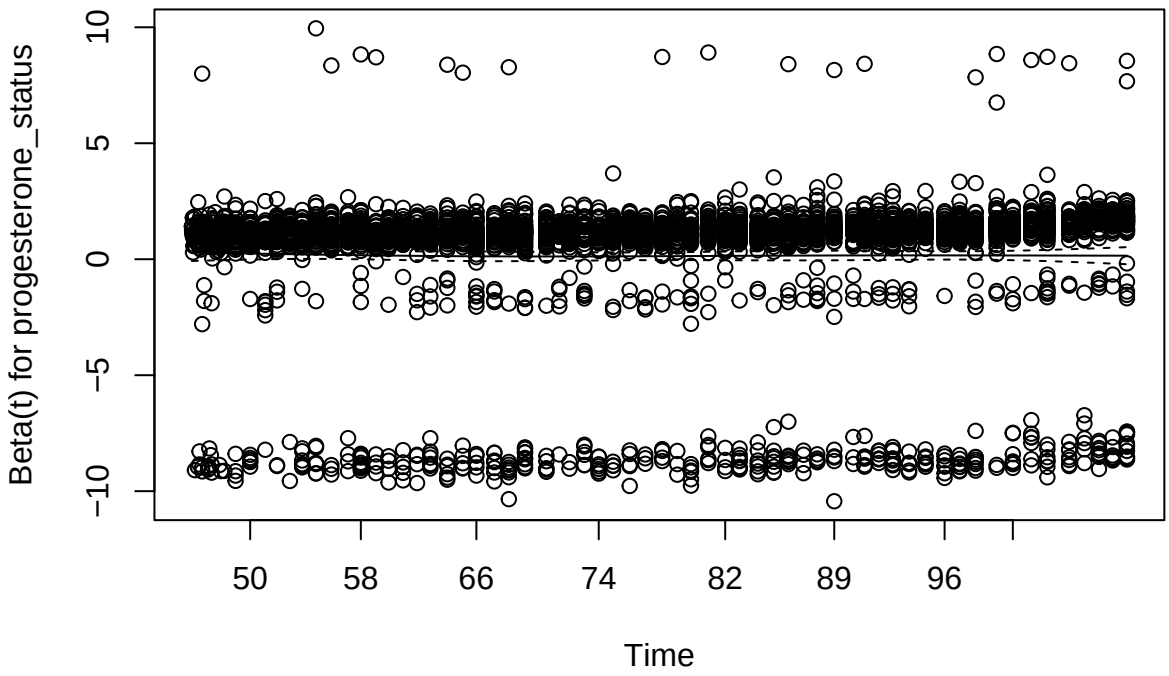

Beta(t) for x6th_stage
100
50
0
−50
−150
50
58
66
74
82
89
96
Time

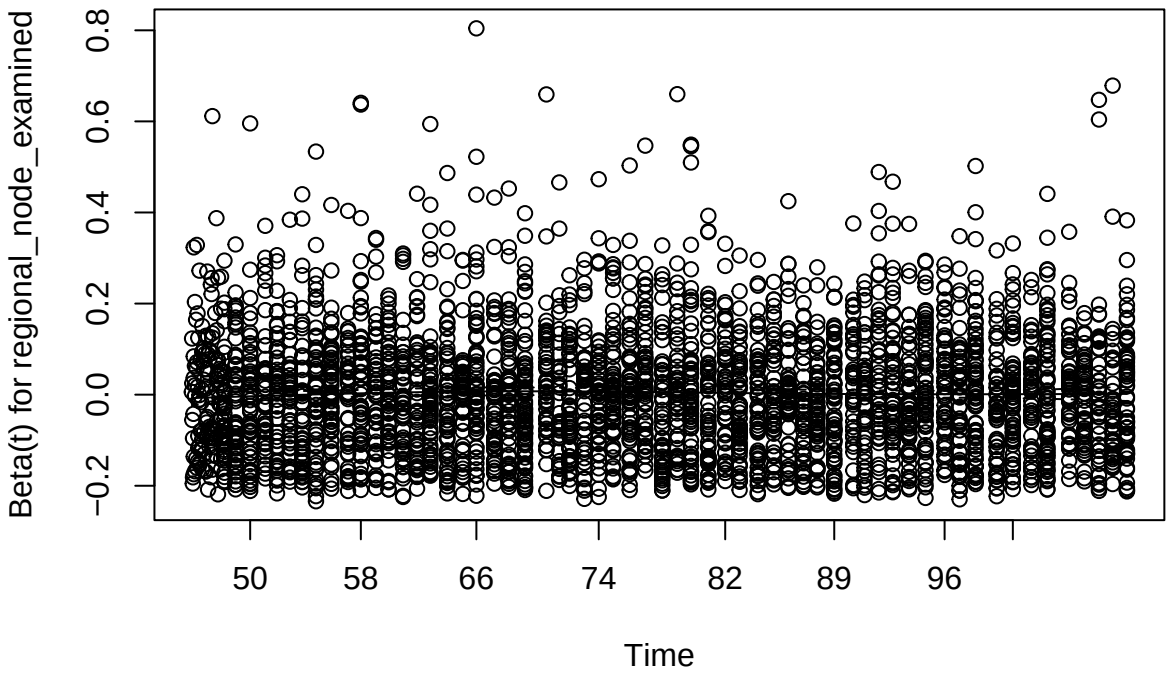

Beta(t) for differentiate
50
0
−50
−150
−250
50
58
66
74
82
89
96
Time

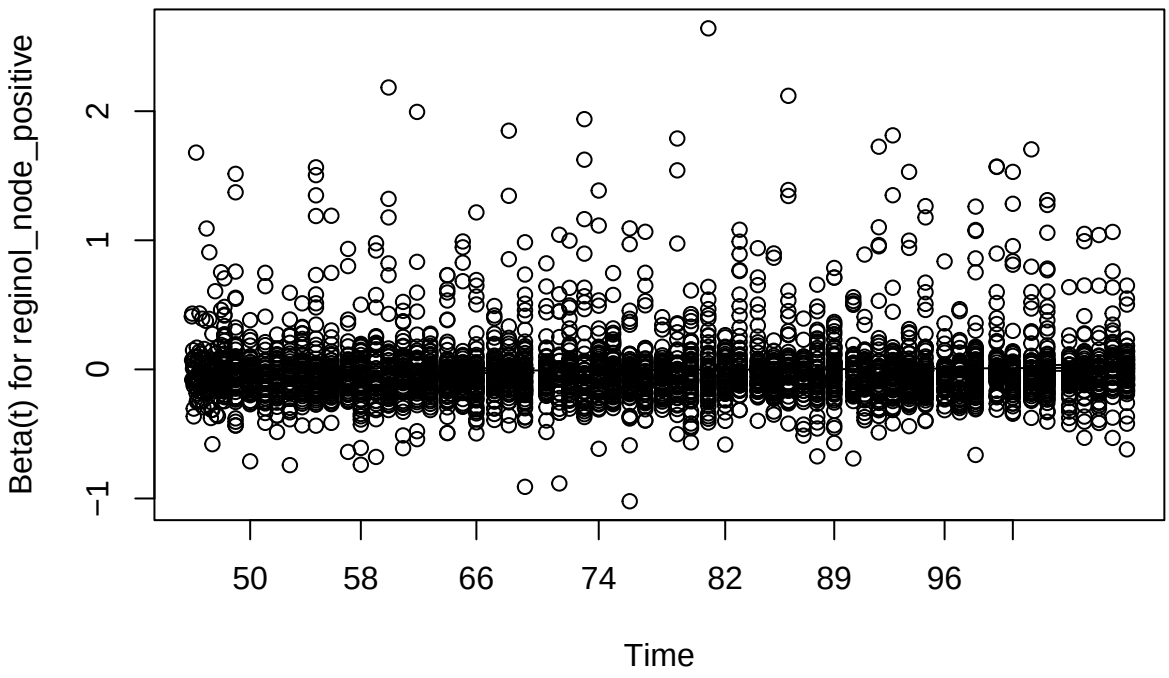

Beta(t) for a_stage
20
0
−20
−40
−60
50
58
66
74
82
89
96
Time


Beta(t) for tumor_size
0.4
0.2
0.0
−0.2
−0.4
50
58
66
74
82
89
96
Time


Beta(t) for estrogen_status
10
0
−10
−20
−30
50
58
66
74
82
89
96
Time


Beta(t) for progesterone_status
10
5
0
−5
−10
50
58
66
74
82
89
96
Time

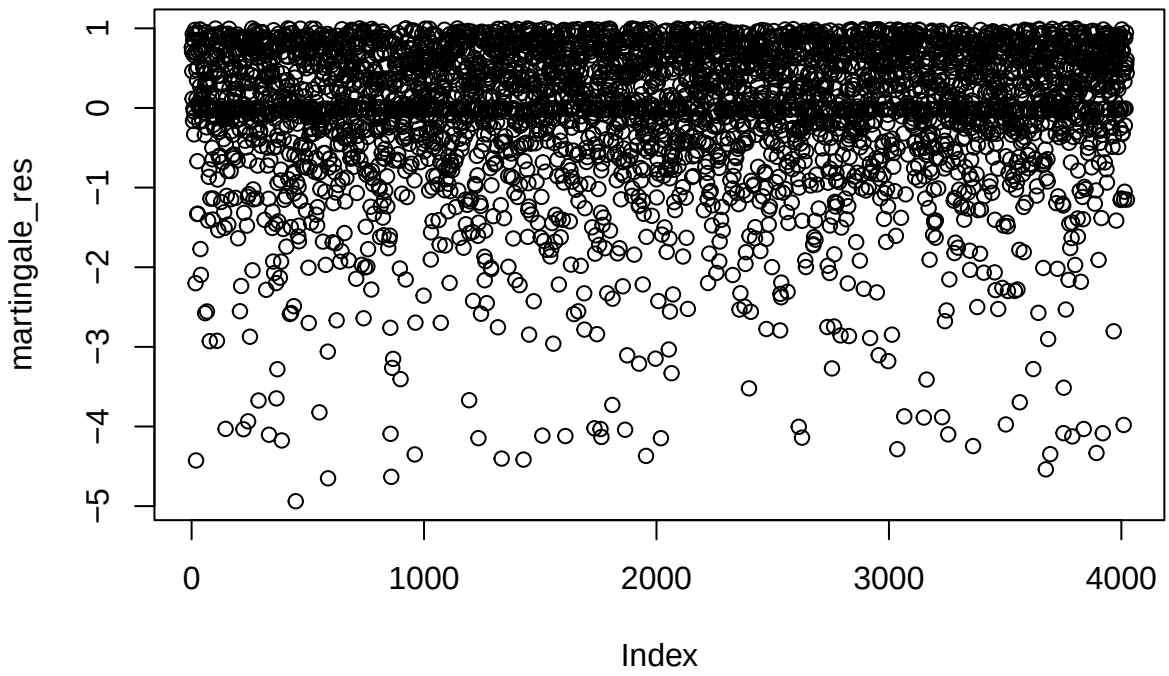

Beta(t) for regional_node_examined
−0.2
0.0
0.2
0.4
0.6
0.8
50
58
66
74
82
89
96
Time



A non-random pattern or a significant global test (p-value) can indicate violations of the assumption.

Identify Influential Observations

```
martingale_res <- residuals(cox_model, type = "martingale")
plot(martingale_res)
```



It seems there are few observations with large negative Martingale residuals, which could be potential outliers or influential observations.