# Week 7 Assignment

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# Blayney Questions 1-4

1) Compare the two treatment groups (treatment 1 versus treatment 2). Plot the respective survival curves, indicating censored subjects. You can distinguish between the two groups using different colours or different line formats or both. Label both x- and y-axes. Add a suitable title. Also, add a legend indicating which line corresponds to which line format. Finally compare the two survival curves (log-rank) and add a p-value to the bottom-right of the plot.

#### library(survival)

## Warning: package 'survival' was built under R version 3.1.3

data(ovarian)

knitr::kable(ovarian)

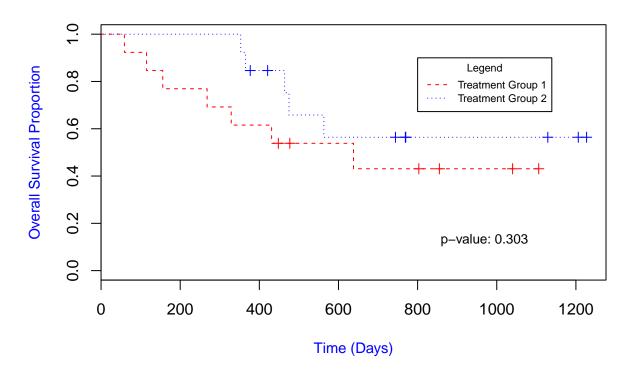
time	fustat	age	resid.ds	rx	ecog.ps
59	1	72.3315	2	1	1
115	1	74.4932	2	1	1
156	1	66.4658	2	1	2
421	0	53.3644	2	2	1
431	1	50.3397	2	1	1
448	0	56.4301	1	1	2
464	1	56.9370	2	2	2
475	1	59.8548	2	2	2
477	0	64.1753	2	1	1
563	1	55.1781	1	2	2
638	1	56.7562	1	1	2
744	0	50.1096	1	2	1
769	0	59.6301	2	2	2
770	0	57.0521	2	2	1
803	0	39.2712	1	1	1
855	0	43.1233	1	1	2
1040	0	38.8932	2	1	2
1106	0	44.6000	1	1	1
1129	0	53.9068	1	2	1

futime	fustat	age	resid.ds	rx	ecog.ps	
1206	0	44.2055	2	2	1	
1227	0	59.5890	1	2	2	
268	1	74.5041	2	1	2	
329	1	43.1370	2	1	1	
353	1	63.2192	1	2	2	
365	1	64.4247	2	2	1	
377	0	58.3096	1	2	1	

Data loaded and now create the plots.

```
my.KMest4 <- survfit(Surv(futime, fustat) ~ rx, data = ovarian)</pre>
plot(my.KMest4, main = "OVARIAN CANCER - OVERALL SURVIVAL", col.main = "black",
    xlab = "Time (Days)", ylab = "Overall Survival Proportion", col.lab = "blue",
    cex.lab = 0.9, col = c("red", "blue"), mark.time = TRUE, lty = 2:3)
legend(800, 0.9, title = "Legend", c("Treatment Group 1", "Treatment Group 2"),
    lty = 2:3, col = c("red", "blue"), cex = 0.7)
survdiff(Surv(futime, fustat) ~ rx, data = ovarian)
## Call:
## survdiff(formula = Surv(futime, fustat) ~ rx, data = ovarian)
         N Observed Expected (0-E)^2/E (0-E)^2/V
## rx=1 13
                  7
                        5.23
                                 0.596
                                             1.06
## rx=2 13
                  5
                        6.77
                                 0.461
                                             1.06
##
## Chisq= 1.1 on 1 degrees of freedom, p= 0.303
legend(800, 0.2, c("p-value: 0.303"), cex = 0.8, box.col = "white")
```

### **OVARIAN CANCER - OVERALL SURVIVAL**



2) Load in the Leukaemia-free survival/transplant data-set:

```
library(KMsurv)
data(alloauto)
knitr::kable(head(alloauto))
```

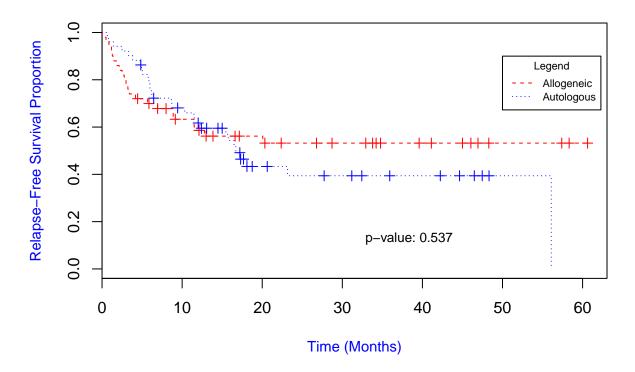
$_{ m time}$	type	delta
0.030	1	1
0.493	1	1
0.855	1	1
1.184	1	1
1.283	1	1
1.480	1	1

Compare the two transplant types (allogeneic vs autologous). Plot the respective relapse-free survival curves, indicating censored subjects. You can distinguish between the two groups using different colours or different line formats or both. Label both x- and y-axes. Add a suitable title. Also, add a legend indicating which line corresponds to which line format. Finally compare the two survival curves (log-rank) and add a p-value to the bottom-right of the plot.

```
my.KMest4 <- survfit(Surv(time, delta) ~ type, data = alloauto, conf.type = "none")
plot(my.KMest4, main = "Leukemia - Free Survival", col.main = "black", xlab = "Time (Months)",</pre>
```

```
ylab = "Relapse-Free Survival Proportion", col.lab = "blue", cex.lab = 0.9,
    col = c("red", "blue"), mark.time = TRUE, lty = 2:3)
survdiff(Surv(time, delta) ~ type, data = alloauto)
## survdiff(formula = Surv(time, delta) ~ type, data = alloauto)
##
##
           N Observed Expected (0-E)^2/E (0-E)^2/V
## type=1 50
                   22
                          24.2
                                   0.195
                                              0.382
                   28
                          25.8
                                   0.182
                                             0.382
## type=2 51
##
   Chisq= 0.4 on 1 degrees of freedom, p= 0.537
legend(50, 0.9, title = "Legend", c("Allogeneic", "Autologous"), lty = 2:3,
    col = c("red", "blue"), cex = 0.7)
legend(30, 0.2, c("p-value: 0.537"), cex = 0.8, box.col = "white")
```

## Leukemia - Free Survival



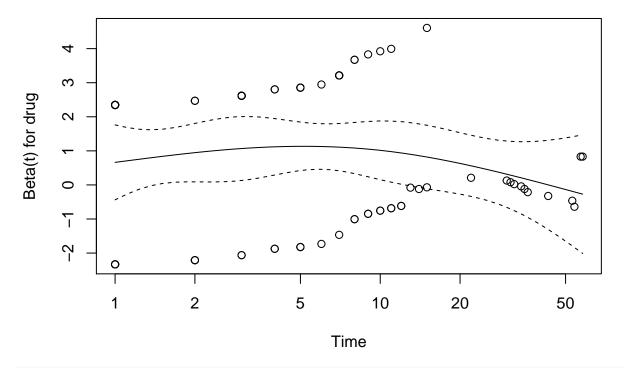
3) Recode the age variables (see below) and repeat the univariate and multivariate analyses.

```
hmohiv <- read.table("http://www.ats.ucla.edu/stat/R/examples/asa/hmohiv.csv",
    sep = ",", header = TRUE)

hmohiv$time <- as.numeric(as.Date(hmohiv[, 7], "%m/%d/%Y") - as.Date(hmohiv[,
    6], "%m/%d/%Y"))
hmohiv$time <- round(hmohiv$time/30.5)</pre>
```

```
s_obj <- Surv(hmohiv$time, hmohiv$censor)
# WORK THROUGH EXAMPLE 2.1-2.

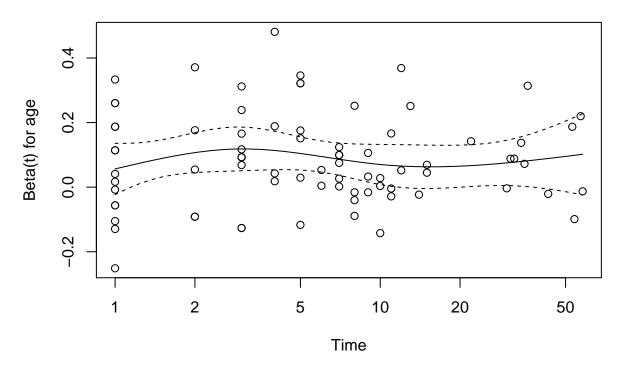
drug.coxph <- coxph(Surv(time, censor) ~ drug, method = "efron", data = hmohiv)
drug_ph <- cox.zph(drug.coxph, transform = "log")
plot(drug_ph[1, ])</pre>
```



```
{\tt drug\_ph}
```

```
## rho chisq p
## drug -0.0746 0.417 0.518

age.coxph <- coxph(Surv(time, censor) ~ age, method = "efron", data = hmohiv)
age_ph <- cox.zph(age.coxph, transform = "log")
plot(age_ph[1, ])</pre>
```



age\_ph

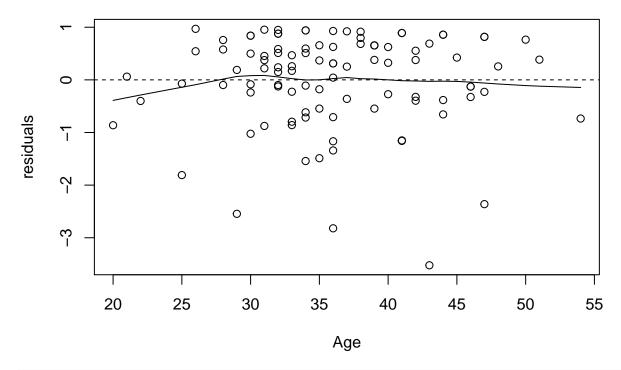
```
## rho chisq p
## age 0.0164 0.0179 0.894
```

```
res <- residuals(age.coxph, type = "martingale")
X <- as.matrix(hmohiv[, "age"]) # matrix of covariates
plot(X[, 1], res, xlab = c("Age")[1], ylab = "residuals")
abline(h = 0, lty = 2) + lines(lowess(X[, 1], res, iter = 0))</pre>
```

## numeric(0)

```
library(car)
```

## Warning: package 'car' was built under R version 3.1.3



agecat <- recode(hmohiv\$age, "20:29='A'; 30:34='B'; 35:39='C';40:54='D'", as.factor = T)
agecat.coxph <- coxph(Surv(hmohiv\$time, hmohiv\$censor) ~ agecat, method = "efron")
summary(agecat.coxph)</pre>

```
## Call:
## coxph(formula = Surv(hmohiv$time, hmohiv$censor) ~ agecat, method = "efron")
##
    n= 100, number of events= 80
##
##
                                         z Pr(>|z|)
            coef exp(coef) se(coef)
##
## agecatB 1.2030
                     3.3301
                              0.4503 2.672 0.00755 **
## agecatC 1.3337
                     3.7951
                              0.4580 2.912 0.00359 **
## agecatD 1.9144
                     6.7831
                              0.4679 4.091 4.29e-05 ***
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
##
##
           exp(coef) exp(-coef) lower .95 upper .95
               3.330
                         0.3003
                                    1.378
                                              8.049
## agecatB
                                    1.547
## agecatC
               3.795
                         0.2635
                                              9.313
               6.783
                         0.1474
                                    2.711
                                             16.971
## agecatD
##
## Concordance= 0.642 (se = 0.04)
## Rsquare= 0.189
                    (max possible= 0.997)
## Likelihood ratio test= 20.92 on 3 df,
                                            p=0.0001091
## Wald test
                        = 17.85 on 3 df,
                                            p=0.0004724
## Score (logrank) test = 19.83 on 3 df,
                                            p=0.0001843
agecat <- recode(hmohiv$age, "20:29='D'; 30:34='B'; 35:39='C';40:54='A'", as.factor = T)
```

```
age <- coxph(formula = Surv(hmohiv$time, hmohiv$censor) ~ agecat, method = "efron")
summary(age)
## Call:
## coxph(formula = Surv(hmohiv$time, hmohiv$censor) ~ agecat, method = "efron")
##
    n= 100, number of events= 80
##
##
             coef exp(coef) se(coef)
                                          z Pr(>|z|)
                     0.4909
                              0.2870 - 2.479
## agecatB -0.7114
                                              0.0132 *
## agecatC -0.5807
                     0.5595
                              0.3122 - 1.860
                                              0.0629 .
## agecatD -1.9144
                     0.1474
                              0.4679 -4.091 4.29e-05 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
##
##
          exp(coef) exp(-coef) lower .95 upper .95
## agecatB
             0.4909
                         2.037
                                  0.27971
                                            0.8617
## agecatC
             0.5595
                          1.787
                                  0.30344
                                            1.0316
## agecatD
             0.1474
                          6.783
                                 0.05892
                                            0.3689
##
## Concordance= 0.642 (se = 0.04)
## Rsquare= 0.189 (max possible= 0.997)
## Likelihood ratio test= 20.92 on 3 df, p=0.0001091
                                           p=0.0004724
## Wald test
                       = 17.85 on 3 df,
                                           p=0.0001843
## Score (logrank) test = 19.83 on 3 df,
multi <- coxph(formula = Surv(hmohiv$time, hmohiv$censor) ~ agecat + hmohiv$drug,</pre>
   method = "efron")
summary(multi)
## coxph(formula = Surv(hmohiv$time, hmohiv$censor) ~ agecat + hmohiv$drug,
##
      method = "efron")
##
    n= 100, number of events= 80
##
##
                                              z Pr(>|z|)
##
                 coef exp(coef) se(coef)
## agecatB
                         0.4685
                                  0.2899 -2.615 0.00891 **
              -0.7582
## agecatC
              -0.6958
                         0.4987
                                  0.3151 -2.208 0.02722 *
              -2.0152
                                0.4804 -4.195 2.73e-05 ***
## agecatD
                         0.1333
## hmohiv$drug 0.8926
                         2.4415
                                  0.2530 3.527 0.00042 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
##
##
               exp(coef) exp(-coef) lower .95 upper .95
## agecatB
                 0.4685
                            2.1345
                                    0.26541
                                                0.8269
                                     0.26892
                 0.4987
                            2.0053
                                                0.9247
## agecatC
## agecatD
                 0.1333
                            7.5019 0.05199
                                                0.3418
## hmohiv$drug
                 2.4415
                            0.4096
                                     1.48685
                                                4.0092
##
```

Does using a larger reference group for the age help in any way? What do you notice about the hazard ratios and confidence intervals? Are the p-values or the concordance index affected?

It appears that the pvalues in the univariate and multivariate increase and the larger reference group for age harms. The harzard ratios and confidence intervals really decrease. Concordance values seem to decrease.

4) For this example, we'll look at data involving drug treatment programs.

First, read in the table:

```
uis <- read.table("http://www.ats.ucla.edu/stat/R/examples/asa/uis.csv", sep = ",",
    header = TRUE)
attach(uis)

## The following object is masked _by_ .GlobalEnv:
##
## age</pre>
```

knitr::kable(head(uis))

_											
id	age	becktota	hercoc	ivhx	ndrugtx	race	treat	site	los	time	censor
1	39	9.00	4	3	1	0	1	0	123	188	1
2	33	34.00	4	2	8	0	1	0	25	26	1
3	33	10.00	2	3	3	0	1	0	7	207	1
4	32	20.00	4	3	1	0	0	0	66	144	1
5	24	5.00	2	1	5	1	1	0	173	551	0
6	30	32.55	3	3	1	0	1	0	16	32	1

For simplicity, we'll only work with the variables mentioned above:

```
uis_small <- uis[, c(1, 2, 4, 6, 8, 9, 11, 12)]
```

For further simplicity, we'll remove the patients with missing values:

```
tiny_uis <- uis_small[apply(uis_small, 1, function(x) !any(is.na(x))), ]</pre>
```

We'll assume that the two different sites are different centres, so we'll want to stratify by this variable. You can do this via:

```
age.coxph <- coxph(Surv(time, censor) ~ age + strata(site), method = "efron",
    data = tiny_uis)</pre>
```

Now, repeat the univariate analyses for the variables: treat, age, ndrugtx and hercoc. Make a note of the concordance index for each. Create a multivariate model using all four variables. What is the concordance index?

```
# univariante
treat <- coxph(Surv(time, censor) ~ treat, method = "efron", data = tiny_uis)</pre>
summary(treat)
## Call:
## coxph(formula = Surv(time, censor) ~ treat, data = tiny_uis,
      method = "efron")
##
##
##
    n= 593, number of events= 481
##
##
            coef exp(coef) se(coef)
                                     z Pr(>|z|)
## treat -0.23023   0.79435   0.09143 -2.518   0.0118 *
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
##
##
         exp(coef) exp(-coef) lower .95 upper .95
## treat
           0.7943
                       1.259
                                 0.664
##
## Concordance= 0.537 (se = 0.012)
## Rsquare= 0.011
                   (max possible= 1 )
## Likelihood ratio test= 6.34 on 1 df,
                                          p=0.01177
                       = 6.34 on 1 df,
## Wald test
                                          p=0.0118
## Score (logrank) test = 6.37 on 1 df,
                                          p=0.01161
age <- coxph(Surv(time, censor) ~ age, method = "efron", data = tiny_uis)
summary(age)
## Call:
## coxph(formula = Surv(time, censor) ~ age, data = tiny_uis, method = "efron")
##
##
    n= 593, number of events= 481
##
##
            coef exp(coef) se(coef)
                                       z Pr(>|z|)
## age -0.014273 0.985829 0.007343 -1.944 0.0519 .
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
##
       exp(coef) exp(-coef) lower .95 upper .95
##
## age
         0.9858
                     1.014
                              0.9717
##
## Concordance= 0.526 (se = 0.014)
## Rsquare= 0.006
                   (max possible= 1 )
## Likelihood ratio test= 3.83 on 1 df,
                                          p=0.05039
## Wald test
                       = 3.78 on 1 df,
                                          p=0.05192
## Score (logrank) test = 3.78 on 1 df,
                                          p=0.05185
```

```
ndrugtx <- coxph(Surv(time, censor) ~ ndrugtx, method = "efron", data = tiny_uis)</pre>
summary(ndrugtx)
## Call:
## coxph(formula = Surv(time, censor) ~ ndrugtx, data = tiny_uis,
      method = "efron")
##
##
   n= 593, number of events= 481
##
##
##
              coef exp(coef) se(coef)
                                          z Pr(>|z|)
## ndrugtx 0.030712 1.031188 0.007543 4.071 4.67e-05 ***
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
##
##
          exp(coef) exp(-coef) lower .95 upper .95
## ndrugtx
              1.031
                        0.9698
                                  1.016
##
## Concordance= 0.545 (se = 0.014)
## Rsquare= 0.024 (max possible= 1)
                                         p=0.0001533
## Likelihood ratio test= 14.33 on 1 df,
                       = 16.58 on 1 df, p=4.675e-05
## Wald test
## Score (logrank) test = 16.71 on 1 df, p=4.358e-05
hercoc <- coxph(Surv(time, censor) ~ hercoc, method = "efron", data = tiny_uis)
summary(hercoc)
## Call:
## coxph(formula = Surv(time, censor) ~ hercoc, data = tiny_uis,
      method = "efron")
##
    n= 593, number of events= 481
##
##
             coef exp(coef) se(coef)
                                          z Pr(>|z|)
## hercoc -0.07720 0.92570 0.04164 -1.854 0.0637 .
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
##
##
         exp(coef) exp(-coef) lower .95 upper .95
## hercoc
            0.9257
                        1.08
                                 0.8532
                                            1.004
## Concordance= 0.525 (se = 0.014)
## Rsquare= 0.006 (max possible= 1)
## Likelihood ratio test= 3.4 on 1 df,
                                        p=0.06523
## Wald test
                       = 3.44 on 1 df, p=0.06372
## Score (logrank) test = 3.44 on 1 df,
                                         p=0.06351
Concordances
treat = .537
age = 0.526
ndrugtx = .545
hercoc = .525
```

```
# multivariant
fit_four_cox_model <- coxph(Surv(time, censor) ~ hercoc + treat + age + ndrugtx,
   method = "efron", data = tiny_uis)
summary(fit_four_cox_model)
## Call:
## coxph(formula = Surv(time, censor) ~ hercoc + treat + age + ndrugtx,
      data = tiny_uis, method = "efron")
##
    n= 593, number of events= 481
##
##
##
               coef exp(coef) se(coef)
                                             z Pr(>|z|)
## hercoc -0.063348 0.938617 0.043388 -1.460 0.14428
         -0.232669 0.792416 0.091776 -2.535 0.01124 *
## treat
          -0.024750 0.975554 0.007688 -3.219 0.00129 **
## ndrugtx 0.035494 1.036131 0.007827 4.535 5.76e-06 ***
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
##
          exp(coef) exp(-coef) lower .95 upper .95
##
## hercoc
             0.9386
                        1.0654
                                  0.8621
                        1.2620
                                   0.6620
## treat
             0.7924
                                            0.9486
## age
             0.9756
                        1.0251
                                   0.9610
                                            0.9904
## ndrugtx
             1.0361
                        0.9651
                                   1.0204
                                            1.0521
## Concordance= 0.575 (se = 0.014)
## Rsquare= 0.053
                  (max possible= 1 )
                                           p=1.611e-06
## Likelihood ratio test= 32.37 on 4 df,
## Wald test
                       = 34.9 \text{ on } 4 \text{ df},
                                           p=4.878e-07
## Score (logrank) test = 35 on 4 df, p=4.645e-07
multi concordance = 0.575
Now run the following (AIC) to determine what variables should be retained:
library(MASS)
## Warning: package 'MASS' was built under R version 3.1.3
stepAIC(fit_four_cox_model)
## Start: AIC=5521.79
## Surv(time, censor) ~ hercoc + treat + age + ndrugtx
##
##
            Df
                   AIC
               5521.8
## <none>
## - hercoc 1 5521.9
## - treat
             1 5526.2
## - age
             1 5530.3
```

## - ndrugtx 1 5537.3

```
## Call:
## coxph(formula = Surv(time, censor) ~ hercoc + treat + age + ndrugtx,
      data = tiny_uis, method = "efron")
##
##
              coef exp(coef) se(coef)
##
                     0.93862 0.04339 -1.46 0.1443
## hercoc -0.06335
                     0.79242 0.09178 -2.54 0.0112
## treat
          -0.23267
## age
          -0.02475
                     0.97555 0.00769 -3.22 0.0013
## ndrugtx 0.03549
                     1.03613 0.00783 4.54 5.8e-06
## Likelihood ratio test=32.4 on 4 df, p=1.61e-06
## n= 593, number of events= 481
```

What variables are retained? What is the concordance index of the final model?

Variables retained are: Ndugtx, Age, Treat

```
## Call:
## coxph(formula = Surv(time, censor) ~ +treat + age + ndrugtx,
       data = tiny_uis, method = "efron")
##
##
    n= 593, number of events= 481
##
##
##
               coef exp(coef) se(coef)
                                              z Pr(>|z|)
          -0.243286   0.784047   0.091483   -2.659   0.00783 **
## treat
## age
          -0.022886 0.977374 0.007580 -3.019 0.00253 **
## ndrugtx 0.037147 1.037845 0.007668 4.844 1.27e-06 ***
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
##
          exp(coef) exp(-coef) lower .95 upper .95
##
## treat
             0.7840
                        1.2754
                                   0.6553
                                              0.938
                                              0.992
             0.9774
                         1.0232
                                   0.9630
## age
## ndrugtx
             1.0378
                         0.9635
                                   1.0224
                                              1.054
##
## Concordance= 0.577 (se = 0.014)
## Rsquare= 0.05
                 (max possible= 1 )
## Likelihood ratio test= 30.25 on 3 df,
                                           p=1.224e-06
## Wald test
                       = 33.13 on 3 df,
                                           p=3.023e-07
## Score (logrank) test = 33.25 on 3 df,
                                           p=2.849e-07
```

Ndugtx, Age, Treat: Concordance = 0.577