```
comment.
comment    First  MPR run with SPSS_R.
comment.
comment use the subset of lung cancer data set.
comment .
comment        <<<<<<<< SPSS preamble >>>>>>>>.
comment.
comment.
comment   Pick up the lung cancer data file.
comment   And look inside .
comment.
GET  FILE='C:\data\spssdata\york\lung_cancer_york.sav'.
file label  Subset of the original lung cancer data set.
DATASET NAME DataSet1 WINDOW=FRONT.
set seed=987654321.
comment.
freq vars=all/format=notable/statistics=none.
```

Frequencies

[DataSet1] C:\data\spssdata\york\lung_cancer_york.sav

Statistics

		surtim	cen	age	agegrp	sex	treat
N	Valid	855	855	855	855	855	855
	Missing	0	0	0	0	0	0

```
freq vars=surtim age//format=notable/histogram.
```

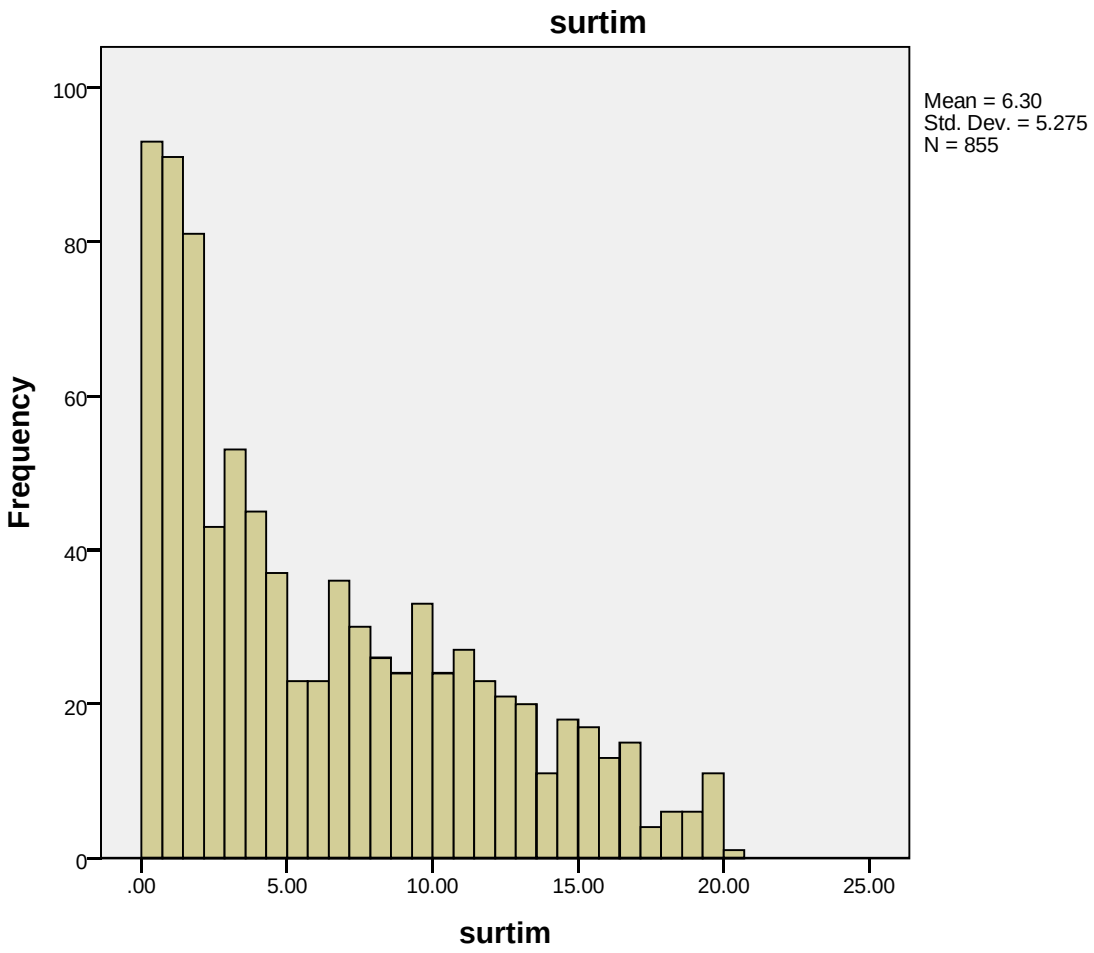
Frequencies

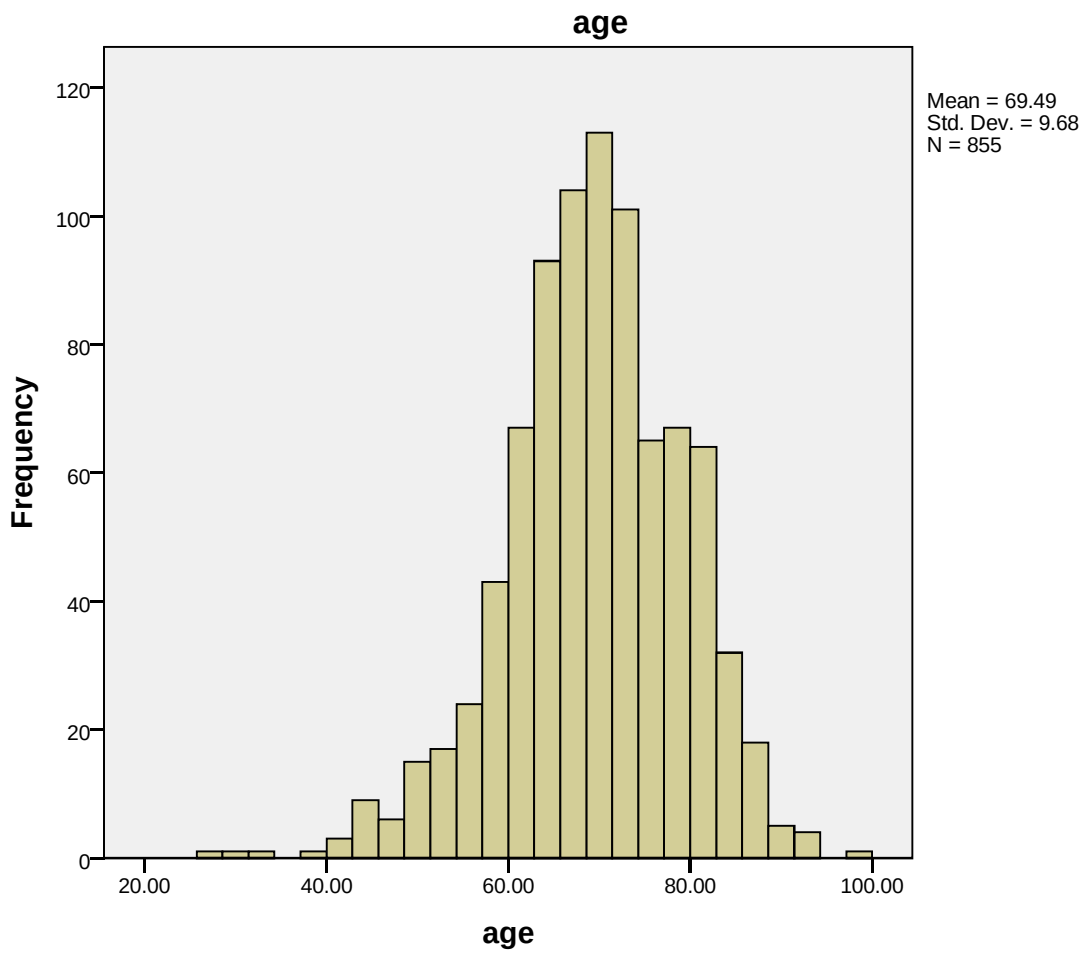
[DataSet1] C:\data\spssdata\york\lung_cancer_york.sav

Statistics

		surtim	age
N	Valid	855	855
	Missing	0	0

Histogram


surtim
Mean = 6.30
Std. Dev. = 5.275
N = 855
Frequency
100
80
60
40
20
0
.00
5.00
10.00
15.00
20.00
25.00
surtim




```
freq vars=cen sex treat.
```

Frequencies

```
[DataSet1] C:\data\spssdata\york\lung_cancer_york.sav
```

Statistics

		cen	sex	treat
N	Valid	855	855	855
	Missing	0	0	0

Frequency Table

cen

		Frequency	Percent	Valid Percent	Cumulative Percent
Valid	.00	182	21.3	21.3	21.3
	1.00	673	78.7	78.7	100.0
	Total	855	100.0	100.0	

sex

		Frequency	Percent	Valid Percent	Cumulative Percent
Valid	.00	291	34.0	34.0	34.0
	1.00	564	66.0	66.0	100.0
	Total	855	100.0	100.0	

treat

		Frequency	Percent	Valid Percent	Cumulative Percent
Valid	1.00	441	51.6	51.6	51.6
	2.00	79	9.2	9.2	60.8
	3.00	45	5.3	5.3	66.1
	4.00	256	29.9	29.9	96.0
	5.00	34	4.0	4.0	100.0
	Total	855	100.0	100.0	

```
KM surtim
  /STATUS=cen(1)
  /PRINT MEAN
  /PLOT SURVIVAL hazard loghazard.
```

Kaplan-Meier

```
[DataSet1] C:\data\spssdata\york\lung_cancer_york.sav
```

Case Processing Summary

Total N	N of Events	Censored	
		N	Percent
855	673	182	21.3%

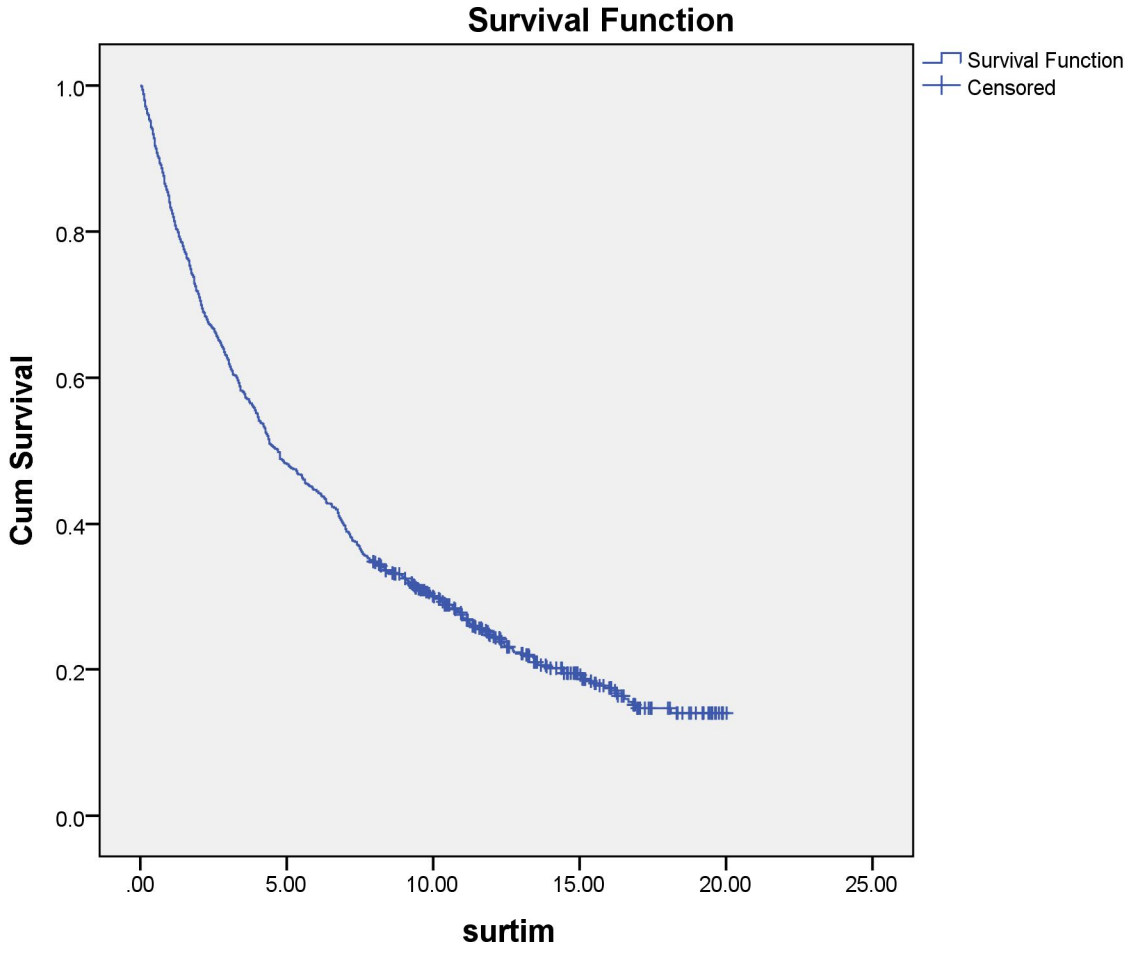
Means and Medians for Survival Time

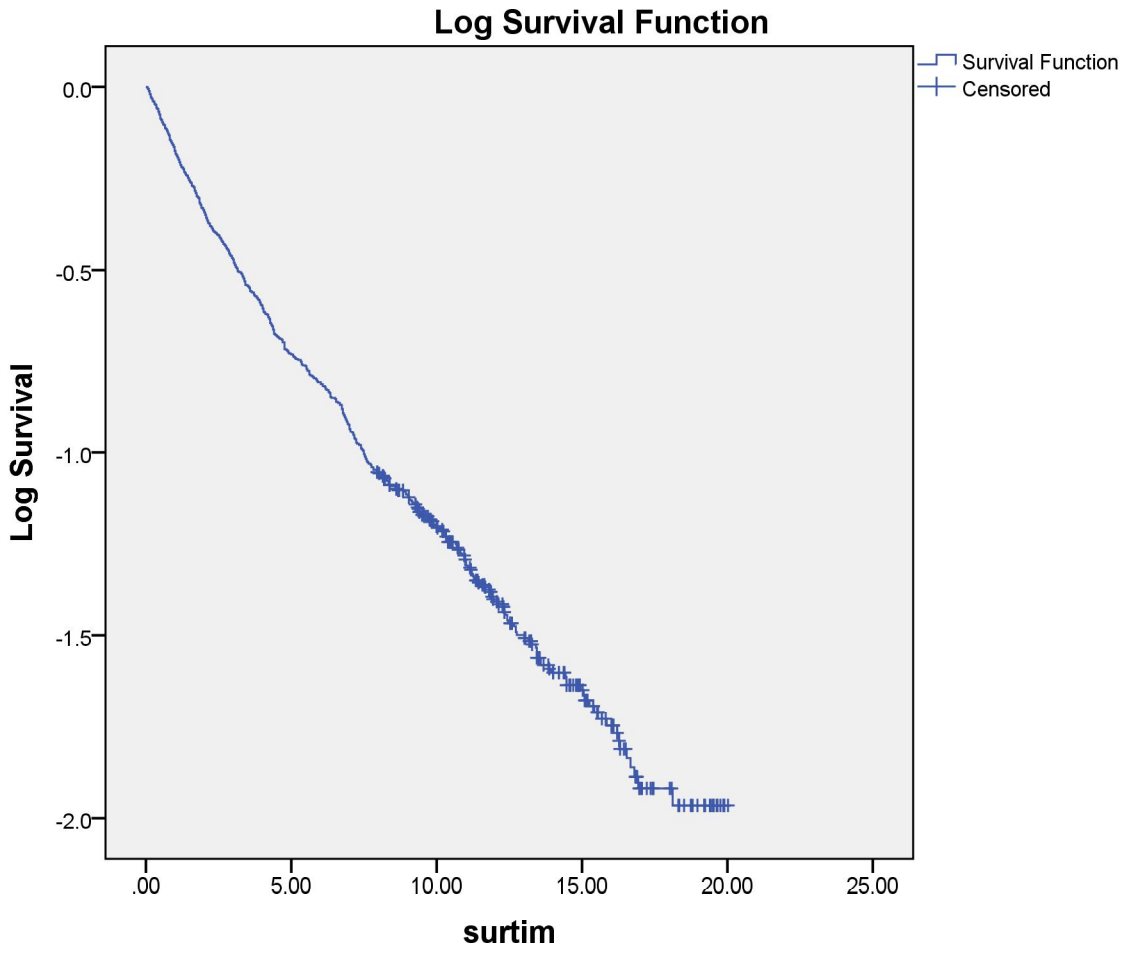
Mean[a]				Median		
		95% Confidence Interval				95% ...
Estimate	Std. Error	Lower Bound	Upper Bound	Estimate	Std. Error	Lower Bound
7.331	.238	6.865	7.797	4.701	.317	4.080

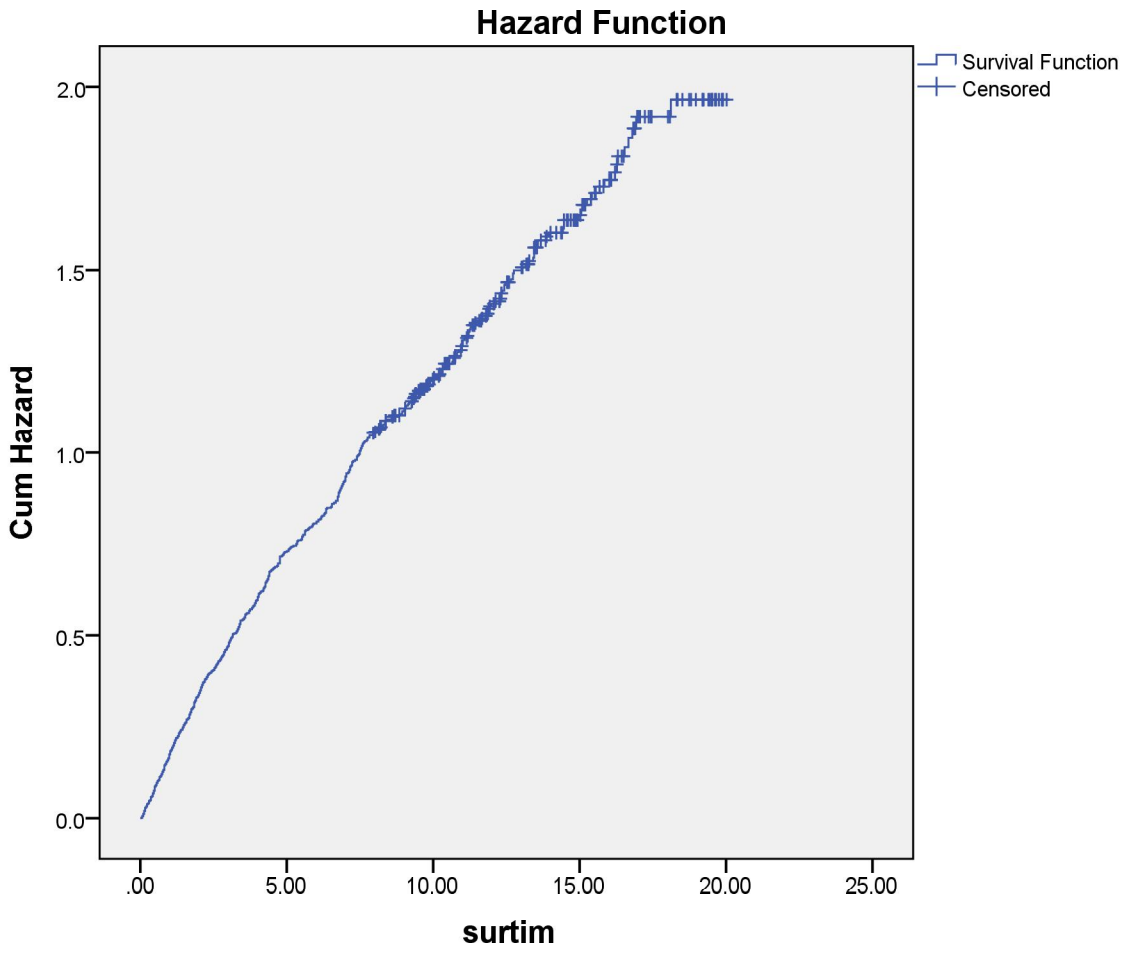
Means and Medians for Survival Time

Median	
95% ...	
Upper Bound	
5.322	

a. Estimation is limited to the largest survival time if it is censored.




Log Survival Function
Survival Function
Censored
Log Survival
0.0
-0.5
-1.0
-1.5
-2.0
.00
5.00
10.00
15.00
20.00
25.00
surtim




```
comment Introduce R .
comment <<<<<<<< 1st  R Block - Generalities  >>>>>>>>.

BEGIN PROGRAM R.
library(survival)           # opens standard R survival library
library(graphics)         # graphical objs not returnable to SPSS
library(mpr)                 # mpr library
library(foreign)            # allows access to file imports
#
# fetch the spss data into the  R  as a dataframe  called cancer
cancer<-spssdata.GetDataFromSPSS()
#attach(cancer)            # attach the dataframe (makes col names availabl
as vars  -we  don't use this)
print(colnames(cancer))
subset<-cancer[1:10,1:6]  #  make a subset of 10 rows and 6 cols to look at
ata: subset is in the top frame now
```

```
print(subset)
print(mean(cancer$surtim))      #surtim is a var in data frame cancer - the v
ars are not in the top frame
print(var(cancer$surtim))
std<-sqrt(var(cancer$surtim) ) # std is now in the top frame
cat("Standard Deviation=", std,"\n")
spsspivottable.Display(subset, title="Data Check ", format=formatSpec.General
Stat)
END PROGRAM.
```

R

```
[DataSet1] C:\data\spssdata\york\lung_cancer_york.sav
```

Data Check

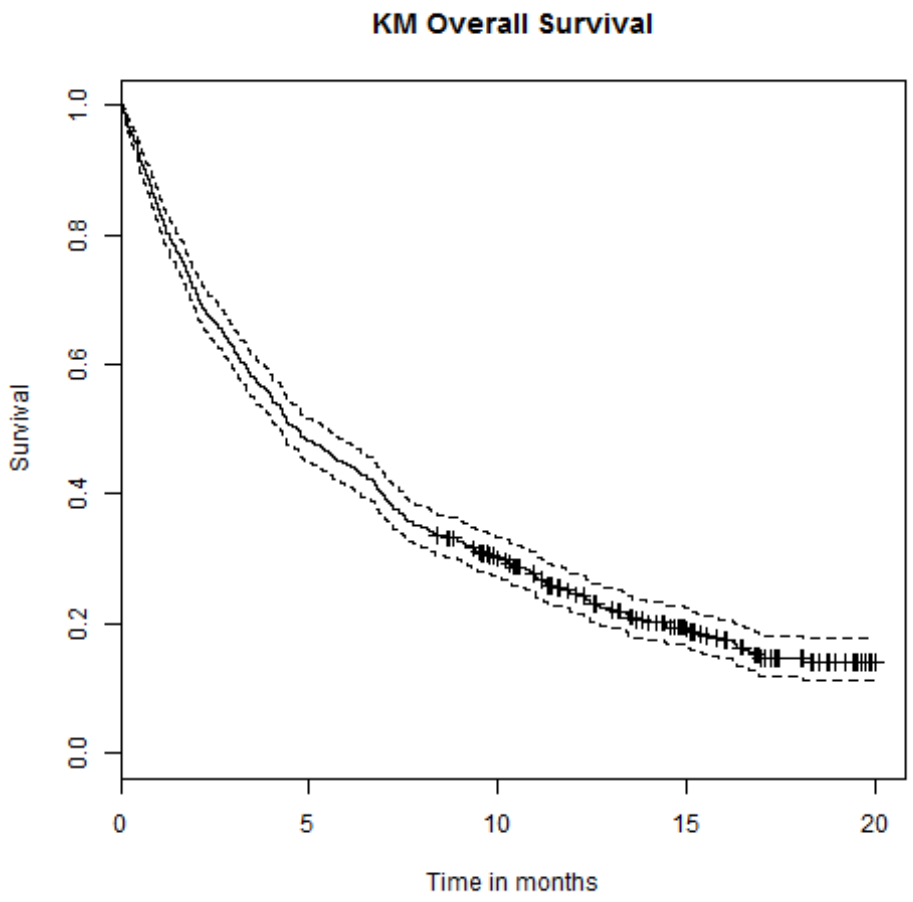
	surtim	cen	age	agegrp	sex	treat
1	.033	1.000	75.567	5.000	1.000	1.000
2	.066	1.000	72.501	5.000	1.000	1.000
3	.066	1.000	78.811	5.000	.000	1.000
4	.066	1.000	84.153	6.000	1.000	1.000
5	.066	1.000	84.153	6.000	1.000	1.000
6	.099	1.000	73.348	5.000	1.000	1.000
7	.099	1.000	68.677	4.000	1.000	1.000
8	.099	1.000	74.904	5.000	1.000	1.000
9	.099	1.000	82.025	6.000	.000	1.000
10	.099	1.000	73.589	5.000	1.000	4.000

```
Loading required package: splines
[1] "surtim" "cen"    "age"    "agegrp" "sex"    "treat"
       surtim cen      age agegrp sex treat
1  0.03287671   1 75.56712      5   1     1
2  0.06575342   1 72.50137      5   1     1
3  0.06575342   1 78.81096      5   0     1
4  0.06575342   1 84.15342      6   1     1
5  0.06575342   1 84.15342      6   1     1
6  0.09863014   1 73.34795      5   1     1
7  0.09863014   1 68.67671      4   1     1
8  0.09863014   1 74.90411      5   1     1
9  0.09863014   1 82.02466      6   0     1
10 0.09863014   1 73.58904      5   1     4
[1] 6.304254
[1] 27.82981
Standard Deviation= 5.275397
```

```
comment <<<<<<<<  Look at the data - remember objects persist from the last R
 block  >>>>>>>> .
BEGIN PROGRAM R.
#
# Make agegrp a factor and also treat (sex is binary - so no need)
#
cancer$agegrp<-factor(cancer$agegrp) # make agegrp a factor
summary(cancer$agegrp)               # check agegrp out
cancer$treat<-factor(cancer$treat)   # make agegrp a factor
summary(cancer$treat)                # check agegrp out
#
# 1 = Palliative, 2 = Surgery, 3 = Chemotherapy, 4 = Radiotherapy, 5 = C+R
#  Black               Red         Green             Blue           Light Blue
#
ls.str(cancer)                       # look at summary of data structure
END PROGRAM.
  2   3   4   5   6
 32  89 311 299 124
  1   2   3   4   5
441  79  45 256  34
age :  num [1:855] 75.6 72.5 78.8 84.2 84.2 ...
agegrp :  Factor w/ 5 levels "2","3","4","5",..: 4 4 4 5 5 4 3 4 5 4 ...
cen :  num [1:855] 1 1 1 1 1 1 1 1 1 1 ...
sex :  num [1:855] 1 1 0 1 1 1 1 1 0 1 ...
surtim :  num [1:855] 0.0329 0.0658 0.0658 0.0658 0.0658 ...
treat :  Factor w/ 5 levels "1","2","3","4",..: 1 1 1 1 1 1 1 1 1 4 ...
BEGIN PROGRAM R.
#
# Begin non-parametric KM
#
KM1 <- survfit(Surv(surtim, cen) ~ 1, data=cancer)
   # uses survival package
plot(KM1, col=1, main='KM Overall Survival',xlab='Time in months', ylab='Surv
ival')
KM2 <- survfit(Surv(surtim, cen) ~ treat, data=cancer)
plot(KM2, col=1:5, main='KM Survival by Treatment',xlab='Time in months', yla
b='Survival')
END PROGRAM.
```

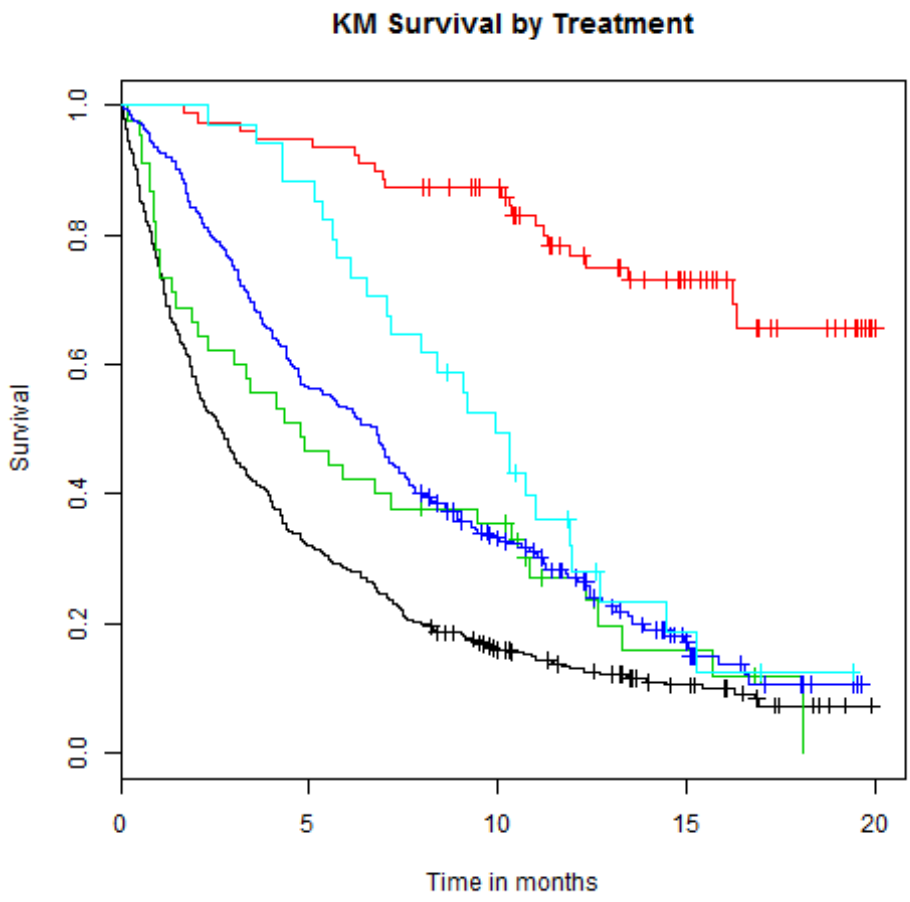
RGraph

```
[DataSet1] C:\data\spssdata\york\lung_cancer_york.sav
```



RGraph

```
[DataSet1] C:\data\spssdata\york\lung_cancer_york.sav
```

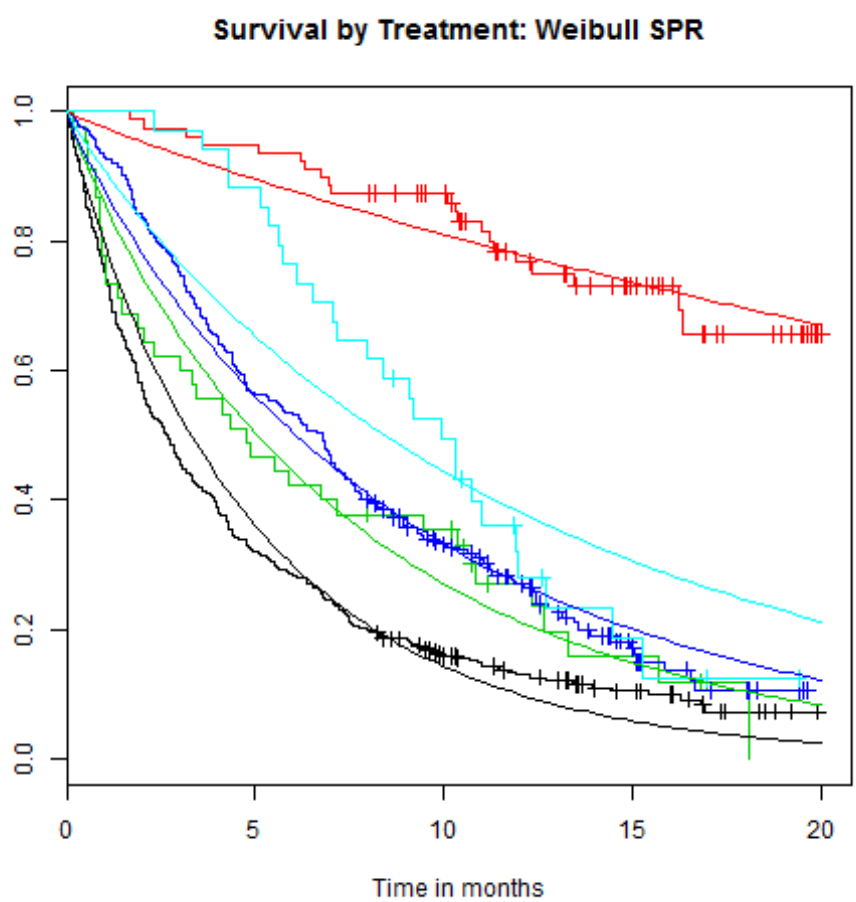



```
BEGIN PROGRAM R.
#
# SPR model with the MPR package
# Parametric Single Linear Predictor Scale - Weibull (default family) [shape
is a constant ~1]
#
mod1 <- mpr(Surv(surtim, cen) ~ list(~ treat, ~ 1), data=cancer)
summary(mod1)
mod2 <- mpr(Surv(surtim, cen) ~ list(~ age, ~ 1), data=cancer)
summary(mod2)
mod3 <- mpr(Surv(surtim, cen) ~ list(~ sex, ~ 1), data=cancer)
summary(mod3)
#
# Construct the model-based  survival tracks for the Weibull for Treatment (m
od1)
#
KM3 <- survfit(Surv(surtim, cen) ~ treat, data=cancer)
```

```
plot(KM3, col=1:5, main='Survival by Treatment: Weibull SPR',xlab='Time in mo
nths')
tvec <- seq(0, max(cancer$surtim), length=100)
Stpred <- predict(mod1, newdata=data.frame(treat=c(1,2,3,4,5)), type="survivo
r",
                   tvec=tvec)
lines(tvec, Stpred[1,], col=1)
lines(tvec, Stpred[2,], col=2)
lines(tvec, Stpred[3,], col=3)
lines(tvec, Stpred[4,], col=4)
lines(tvec, Stpred[5,], col=5)
END PROGRAM.
```

RGraph

```
[DataSet1] C:\data\spssdata\york\lung_cancer_york.sav
```




```
Call:
```

```
mpr(formula = Surv(surtim, cen) ~ list(~treat, ~1), data = cancer)

Model:
  family npar   loglike      aic      bic code
 Weibull    6 -1960.754 3933.508 3962.014    1

Coefficients:
                     Est        SE        Z    Pvalue
(Intercept).b -1.478347  0.075755 -19.5149 < 2.2e-16 ***
treat2.b      -2.225000  0.225024  -9.8878 < 2.2e-16 ***
treat3.b      -0.396785  0.172237  -2.3037   0.02124 *
treat4.b      -0.567393  0.087251  -6.5030 7.873e-11 ***
treat5.b      -0.872426  0.202943  -4.2989 1.717e-05 ***
(Intercept).a -0.072879  0.031695  -2.2994   0.02148 *
---
Overall:
           Chisq Df    Pvalue
treat2.b 97.7692  1 < 2.2e-16 ***
treat3.b  5.3071  1   0.02124 *
treat4.b 42.2892  1 7.873e-11 ***
treat5.b 18.4803  1 1.717e-05 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
Call:
mpr(formula = Surv(surtim, cen) ~ list(~age, ~1), data = cancer)

Model:
  family npar   loglike      aic      bic code
 Weibull    3 -2051.898 4109.796 4124.049    1

Coefficients:
                      Est         SE        Z    Pvalue
(Intercept).b -2.9938064  0.2938605 -10.1878 < 2.2e-16 ***
age.b          0.0174544  0.0040204   4.3415 1.415e-05 ***
(Intercept).a -0.1461868  0.0323803  -4.5147 6.341e-06 ***
---
Overall:
       Chisq Df    Pvalue
age.b 18.849  1 1.415e-05 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
Call:
```

```
mpr(formula = Surv(surtim, cen) ~ list(~sex, ~1), data = cancer)

Model:
  family npar   loglike      aic      bic code
 Weibull    3 -2061.348 4128.695 4142.948    1

Coefficients:
                     Est        SE        Z    Pvalue
(Intercept).b -1.794302  0.089386 -20.0735 < 2.2e-16 ***
sex.b          0.031796  0.081444   0.3904    0.6962
(Intercept).a -0.152864  0.032533  -4.6988 2.617e-06 ***
---
Overall:
        Chisq Df Pvalue
sex.b 0.15241  1 0.6962
BEGIN PROGRAM R.
#
# Now lets look at MPR models - where we model the shape too
#
mod4 <- mpr(Surv(surtim, cen) ~ list(~ treat+age+sex, ~ treat+age+sex), data=
cancer) # multi-factor model
summary(mod4)
END PROGRAM.
Call:
mpr(formula = Surv(surtim, cen) ~ list(~treat + age + sex, ~treat +
    age + sex), data = cancer)

Model:
  family npar  loglike     aic      bic code
 Weibull   14 -1937.57 3903.14 3969.656    1

Coefficients:
                      Est         SE       Z    Pvalue
(Intercept).b -1.0421057  0.5242825 -1.9877  0.046847 *
treat2.b      -3.9620260  0.8468658 -4.6785 2.890e-06 ***
treat3.b      -0.5222322  0.3230655 -1.6165  0.105988
treat4.b      -1.2724620  0.1911968 -6.6552 2.828e-11 ***
treat5.b      -4.5034777  1.0026347 -4.4916 7.068e-06 ***
age.b         -0.0026932  0.0068501 -0.3932  0.694201
sex.b         -0.0590750  0.1388299 -0.4255  0.670457
(Intercept).a -0.3777362  0.1943796 -1.9433  0.051981 .
treat2.a       0.6200657  0.2065035  3.0027  0.002676 **
```

```
treat3.a       0.0937646  0.1447785  0.6476  0.517217
treat4.a       0.3516002  0.0731233  4.8083 1.522e-06 ***
treat5.a       1.0768549  0.1826698  5.8951 3.745e-09 ***
age.a          0.0022618  0.0023778  0.9512  0.341498
sex.a          0.0235548  0.0545359  0.4319  0.665804
---
Overall:
             Chisq Df    Pvalue
treat2.ba 46.24535  2 9.077e-11 ***
treat3.ba  4.28247  2    0.1175
treat4.ba 46.97435  2 6.304e-11 ***
treat5.ba 50.03358  2 1.366e-11 ***
age.ba     1.21978  2    0.5434
sex.ba     0.20375  2    0.9031
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

BEGIN PROGRAM R.
#
# Do backwards selection
#
stepmpr(mod4, scope = list(lower = ~ 1, upper = ~ treat+age+sex))
END PROGRAM.
-----------------------------------------------------------------
Step(0)

Components:
1 ~treat + age + sex
2 ~treat + age + sex
-----------------------------------------------------------------
Step(1)

   comp move  term  family npar loglike    aic    bic code
1   1&2    -   sex Weibull   12 -1937.7 3899.3 3956.4    1
2   1&2    -   age Weibull   12 -1938.1 3900.2 3957.2    1
3     1    -   age Weibull   13 -1937.6 3901.3 3963.0    1
4     1    -   sex Weibull   13 -1937.7 3901.3 3963.1    1
5     2    -   sex Weibull   13 -1937.7 3901.3 3963.1    1
6     2    -   age Weibull   13 -1937.9 3901.9 3963.6    1
7     *    *     * Weibull   14 -1937.6 3903.1 3969.7    1
8     2    - treat Weibull   10 -1957.1 3934.1 3981.7    1
9     1    - treat Weibull   10 -1989.2 3998.5 4046.0    1
```

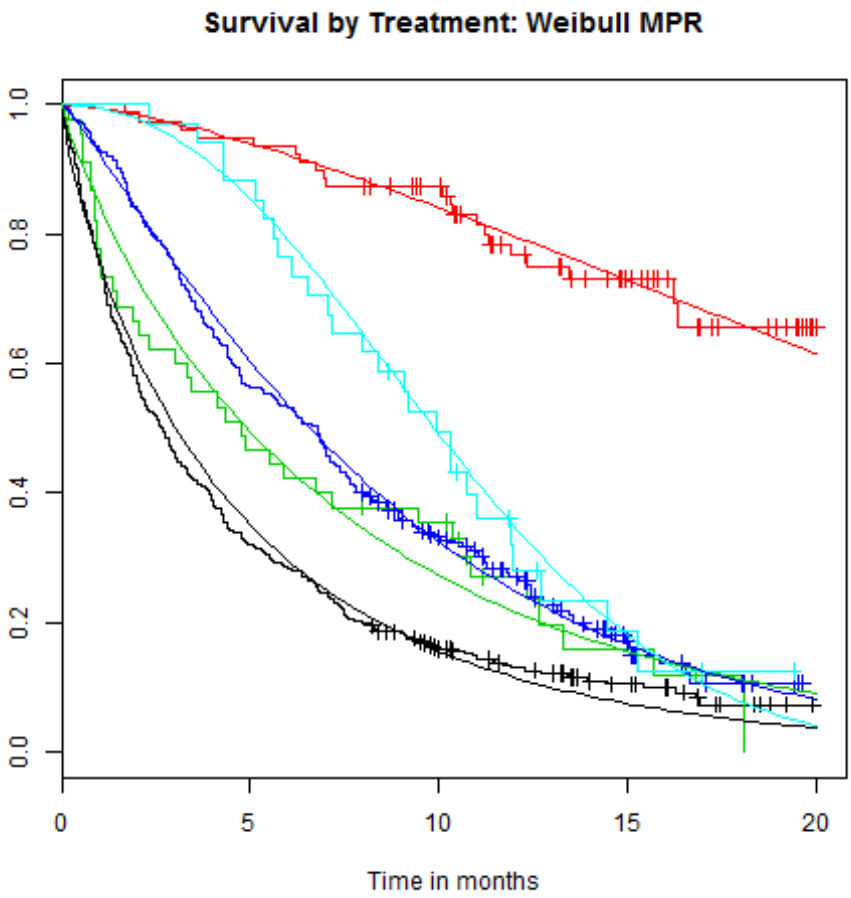
```
10  1&2    - treat Weibull    6 -2049.7 4111.5 4140.0    1

Components:
1 ~treat + age
2 ~treat + age
-----------------------------------------------------------------
Step(2)

   comp move  term  family npar loglike    aic    bic code
1   1&2    -   age Weibull   10 -1938.1 3896.2 3943.8    1
2     1    -   age Weibull   11 -1937.7 3897.4 3949.7    1
3     2    -   age Weibull   11 -1938.0 3898.0 3950.2    1
4     *    *     * Weibull   12 -1937.7 3899.3 3956.4    1
5     2    +   sex Weibull   13 -1937.7 3901.3 3963.1    1
6     1    +   sex Weibull   13 -1937.7 3901.3 3963.1    1
7   1&2    +   sex Weibull   14 -1937.6 3903.1 3969.7    1
8     2    - treat Weibull    8 -1957.1 3930.3 3968.3    1
9     1    - treat Weibull    8 -1989.4 3994.8 4032.8    1
10  1&2    - treat Weibull    4 -2049.8 4107.5 4126.5    1

Components:
1 ~treat
2 ~treat
-----------------------------------------------------------------
Step(3)

   comp move  term  family npar loglike    aic    bic code
1     *    *     * Weibull   10 -1938.1 3896.2 3943.8    1
2     2    +   age Weibull   11 -1937.7 3897.4 3949.7    1
3     1    +   age Weibull   11 -1938.0 3898.0 3950.2    1
4     1    +   sex Weibull   11 -1938.1 3898.2 3950.5    1
5     2    +   sex Weibull   11 -1938.1 3898.2 3950.5    1
6   1&2    +   age Weibull   12 -1937.7 3899.3 3956.4    1
7   1&2    +   sex Weibull   12 -1938.1 3900.2 3957.2    1
8     2    - treat Weibull    6 -1960.8 3933.5 3962.0    1
9     1    - treat Weibull    6 -1998.1 4008.2 4036.7    1
10  1&2    - treat Weibull    2 -2061.4 4126.8 4136.4    1

Components:
1 ~treat
2 ~treat
-----------------------------------------------------------------
```

```
Call:
mpr(formula = Surv(surtim, cen) ~ list(~treat, ~treat), data = cancer,
    hessian = TRUE)

Model:
  family npar  loglike     aic      bic code
 Weibull   10 -1938.12 3896.24 3943.751    1

Coefficients:
Beta:
(Intercept).b      treat2.b      treat3.b      treat4.b      treat5.b
   -1.2804028    -3.9094993    -0.4991512    -1.2612904    -4.0581416
Alpha:
(Intercept).a      treat2.a      treat3.a      treat4.a      treat5.a
  -0.19379109    0.59276445    0.07233967    0.33698062    0.96813221
BEGIN PROGRAM R.
#
# skip the intermediate steps using trace=-1
stepmpr(mod4, scope = list(lower = ~ 1, upper = ~ treat+age+sex), trace=-1)
#
# Fit the final model separately - always safer
#
mod5<-mpr(Surv(surtim, cen) ~ list(~ treat, ~ treat), data=cancer)
summary(mod5)
#
# Make the model-based survival plot
#
KM4 <- survfit(Surv(surtim, cen) ~ treat, data=cancer)
plot(KM4, col=1:5, main='Survival by Treatment: Weibull MPR',xlab='Time in mo
nths')
tvec <- seq(0, max(cancer$surtim), length=100)
Stpred <- predict(mod5, newdata=data.frame(treat=c(1,2,3,4,5)), type="survivo
r",
                  tvec=tvec)
#
# Recall that mod5 is Weibull MPR treatment model
# mod5 <- mpr(Surv(surtim, cen) ~ list(~ treat, ~ treat), data=cancer,family=
"Weibull")
#
lines(tvec, Stpred[1,], col=1)
lines(tvec, Stpred[2,], col=2)
```

```
lines(tvec, Stpred[3,], col=3)
lines(tvec, Stpred[4,], col=4)
lines(tvec, Stpred[5,], col=5)
END PROGRAM.
```

RGraph

```
[DataSet1] C:\data\spssdata\york\lung_cancer_york.sav
```




```
BEGIN PROGRAM R.
#
# remove treat from first component - then add it back
#
update(mod5, list(~. - treat, ~ .))
update(mod5, list(~. + treat, ~ .))
summary(mod5)                        #just checking whats in mod5
#
```

```
# Change the family of the full model mod4 to the log-logistic and save as mo
d6
#
mod6<-update(mod4, ~ ., family="Loglogistic")
summary(mod6)
#
# do backwards elimination on mod6
#
stepmpr(mod6, scope = list(lower = ~ 1, upper = ~ treat+age+sex), trace=-1)
#
# Fit the final model
#
mod7<- mpr(Surv(surtim, cen) ~ list(~ treat, ~ treat), data=cancer,family="Lo
glogistic")
summary(mod7)
END PROGRAM.
Call:
mpr(formula = Surv(surtim, cen) ~ list(~1, ~treat), data = cancer)

Model:
  family npar  loglike     aic      bic code
 Weibull    6 -1998.09 4008.18 4036.687    1

Coefficients:
Beta:
(Intercept).b
    -1.757191
Alpha:
(Intercept).a      treat2.a      treat3.a      treat4.a      treat5.a
  -0.01658634   -0.90322796   -0.11329664   -0.12131875   -0.18065231
Call:
mpr(formula = Surv(surtim, cen) ~ list(~treat, ~treat), data = cancer)

Model:
  family npar  loglike     aic      bic code
 Weibull   10 -1938.12 3896.24 3943.751    1

Coefficients:
Beta:
(Intercept).b      treat2.b      treat3.b      treat4.b      treat5.b
   -1.2804028    -3.9094993    -0.4991512    -1.2612904    -4.0581416
Alpha:
```

```
(Intercept).a      treat2.a      treat3.a      treat4.a      treat5.a
  -0.19379109    0.59276445    0.07233967    0.33698062    0.96813221
Call:
mpr(formula = Surv(surtim, cen) ~ list(~treat, ~treat), data = cancer)

Model:
  family npar  loglike     aic      bic code
 Weibull   10 -1938.12 3896.24 3943.751    1

Coefficients:
                    Est        SE        Z    Pvalue
(Intercept).b -1.280403  0.080004 -16.0042 < 2.2e-16 ***
treat2.b      -3.909499  0.833389  -4.6911 2.718e-06 ***
treat3.b      -0.499151  0.319463  -1.5625  0.118178
treat4.b      -1.261290  0.187567  -6.7245 1.762e-11 ***
treat5.b      -4.058142  0.883128  -4.5952 4.324e-06 ***
(Intercept).a -0.193791  0.041023  -4.7240 2.313e-06 ***
treat2.a       0.592764  0.204724   2.8954  0.003786 **
treat3.a       0.072340  0.143155   0.5053  0.613332
treat4.a       0.336981  0.072246   4.6644 3.096e-06 ***
treat5.a       0.968132  0.164040   5.9018 3.595e-09 ***
---
Overall:
            Chisq Df    Pvalue
treat2.ba 51.1215  2 7.927e-12 ***
treat3.ba  4.6784  2   0.09641 .
treat4.ba 50.4259  2 1.122e-11 ***
treat5.ba 48.2204  2 3.381e-11 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
Call:
mpr(formula = Surv(surtim, cen) ~ list(~treat + age + sex, ~treat +
    age + sex), data = cancer, family = "Loglogistic")

Model:
      family npar   loglike      aic      bic code
 Loglogistic   14 -1926.546 3881.093 3947.608    1

Coefficients:
                     Est         SE       Z    Pvalue
(Intercept).b -1.5985489  0.6870161 -2.3268 0.0199759 *
treat2.b      -4.2138442  0.8850672 -4.7610 1.926e-06 ***
```

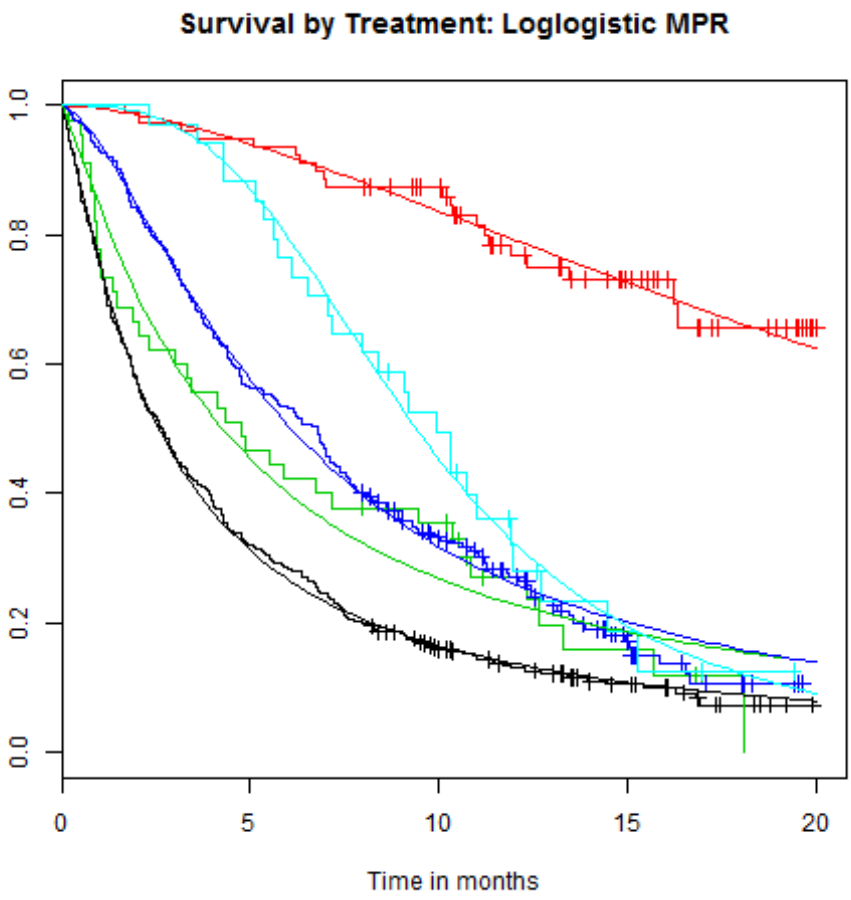
```
treat3.b      -0.5295746  0.3609838 -1.4670 0.1423675
treat4.b      -1.5877500  0.2222457 -7.1441 9.057e-13 ***
treat5.b      -5.9257008  1.2339634 -4.8022 1.570e-06 ***
age.b          0.0062657  0.0090645  0.6912 0.4894194
sex.b          0.0068044  0.1722965  0.0395 0.9684980
(Intercept).a  0.0542118  0.2184913  0.2481 0.8040425
treat2.a       0.3207622  0.2033608  1.5773 0.1147252
treat3.a      -0.0041162  0.1413257 -0.0291 0.9767641
treat4.a       0.2587257  0.0750831  3.4459 0.0005692 ***
treat5.a       0.9916346  0.1837430  5.3969 6.782e-08 ***
age.a          0.0016020  0.0028013  0.5719 0.5673961
sex.a          0.0131480  0.0566618  0.2320 0.8165043
---
Overall:
             Chisq Df    Pvalue
treat2.ba 94.71724  2 < 2.2e-16 ***
treat3.ba  3.63330  2    0.1626
treat4.ba 56.92772  2 4.348e-13 ***
treat5.ba 29.79812  2 3.384e-07 ***
age.ba     2.31023  2    0.3150
sex.ba     0.12098  2    0.9413
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
Call:
mpr(formula = Surv(surtim, cen) ~ list(~treat, ~treat), data = cancer,
    family = "Loglogistic", hessian = TRUE)

Model:
      family npar   loglike      aic      bic code
 Loglogistic   10 -1927.737 3875.474 3922.985    1

Coefficients:
Beta:
(Intercept).b      treat2.b      treat3.b      treat4.b      treat5.b
   -1.1409457    -4.2551510    -0.5599687    -1.6303519    -5.6450921
Alpha:
(Intercept).a      treat2.a      treat3.a      treat4.a      treat5.a
    0.1806975     0.3087209    -0.0212777     0.2466284     0.9270128
Call:
mpr(formula = Surv(surtim, cen) ~ list(~treat, ~treat), data = cancer,
    family = "Loglogistic")
```

```
Model:
      family npar   loglike      aic      bic code
 Loglogistic   10 -1927.737 3875.474 3922.985    1

Coefficients:
                     Est        SE        Z    Pvalue
(Intercept).b -1.140946  0.095464 -11.9516 < 2.2e-16 ***
treat2.b      -4.255151  0.873496  -4.8714 1.108e-06 ***
treat3.b      -0.559969  0.357740  -1.5653 0.1175138
treat4.b      -1.630352  0.215581  -7.5626 3.951e-14 ***
treat5.b      -5.645092  1.134331  -4.9766 6.472e-07 ***
(Intercept).a  0.180698  0.042095   4.2927 1.765e-05 ***
treat2.a       0.308721  0.201363   1.5332 0.1252375
treat3.a      -0.021278  0.140010  -0.1520 0.8792084
treat4.a       0.246628  0.072654   3.3945 0.0006874 ***
treat5.a       0.927013  0.168576   5.4991 3.818e-08 ***
---
Overall:
              Chisq Df    Pvalue
treat2.ba 105.1787  2 < 2.2e-16 ***
treat3.ba   4.5688  2    0.1018
treat4.ba  66.9202  2 2.941e-15 ***
treat5.ba  30.5607  2 2.311e-07 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
BEGIN PROGRAM R.
#
# Now get the model-based loglogistic survival tracks  for the treat, treat M
PR model
#
KM5 <- survfit(Surv(surtim, cen) ~ treat, data=cancer)
plot(KM5, col=1:5, main='Survival by Treatment: Loglogistic MPR',xlab='Time i
n months')
tvec <- seq(0, max(cancer$surtim), length=100)
Stpred <- predict(mod7, newdata=data.frame(treat=c(1,2,3,4,5)), type="survivo
r",
                  tvec=tvec)
lines(tvec, Stpred[1,], col=1)
lines(tvec, Stpred[2,], col=2)
lines(tvec, Stpred[3,], col=3)
lines(tvec, Stpred[4,], col=4)
lines(tvec, Stpred[5,], col=5)
```

```
END PROGRAM.
```

RGraph

```
[DataSet1] C:\data\spssdata\york\lung_cancer_york.sav
```

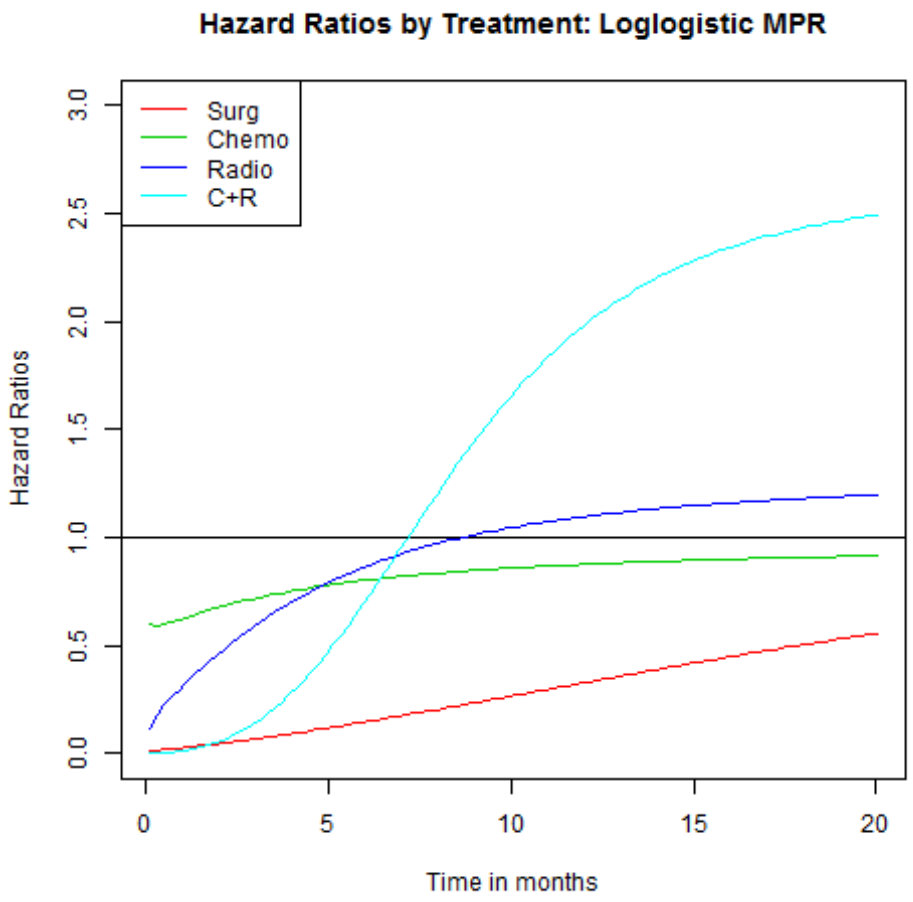



```
BEGIN PROGRAM R.
#
# Predict  hazards and compute hazard ratios
#
tvec <- seq(0.1, max(cancer$surtim), length=100)  # don'tstart at zero
Stpred <- predict(mod7, newdata=data.frame(treat=c(1,2,3,4,5)), type="hazard"
, tvec=tvec)
hrat2<-Stpred[2,]/Stpred[1,] # surgery/palliative
hrat3<-Stpred[3,]/Stpred[1,] # chemotherapy/pallitive
hrat4<-Stpred[4,]/Stpred[1,] # radiotherapy/pallitive
hrat5<-Stpred[5,]/Stpred[1,] #(C+R)/pallitive
#
```

```
# Get max hazard ratio
#
maxhr<-max(hrat2, hrat3,hrat4,hrat5)
maxhr
END PROGRAM.
[1] 2.491932
BEGIN PROGRAM R.
#
# Plot the Hazard ratios
#
plot( hrat2~tvec,  col=2, main='Hazard Ratios by Treatment: Loglogistic MPR',
xlab='Time in months',
      ylab='Hazard Ratios', type="l", ylim=c(0, 3))
#
abline(h=1) # put a reference line at hrat
lines(tvec, hrat2, col=2)  # put surgery on
lines(tvec, hrat3, col=3)  # put chemo on
lines(tvec, hrat4, col=4)  # put radio on
lines(tvec, hrat5, col=5)  # put C+R on
legend("topleft", c(paste( c("Surg", "Chemo", "Radio", "C+R"))), lty = 1, col
 = 2:5)
#
# End of script
END PROGRAM.
```

RGraph

```
[DataSet1] C:\data\spssdata\york\lung_cancer_york.sav
```


Hazard Ratios by Treatment: Loglogistic MPR
Surg
Chemo
Radio
C+R
Hazard Ratios
0.0
0.5
1.0
1.5
2.0
2.5
3.0
0
5
10
15
20
Time in months