SMART analyses

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6/4/2020

##Import Data Set

```
library(haven)
DataFile <- read_sav("R:/DataFile.sav")
View(DataFile)
```

##Use SMARTR package to analyse Adaptive Intervention Strategies

```
library(SMARTAR)
```

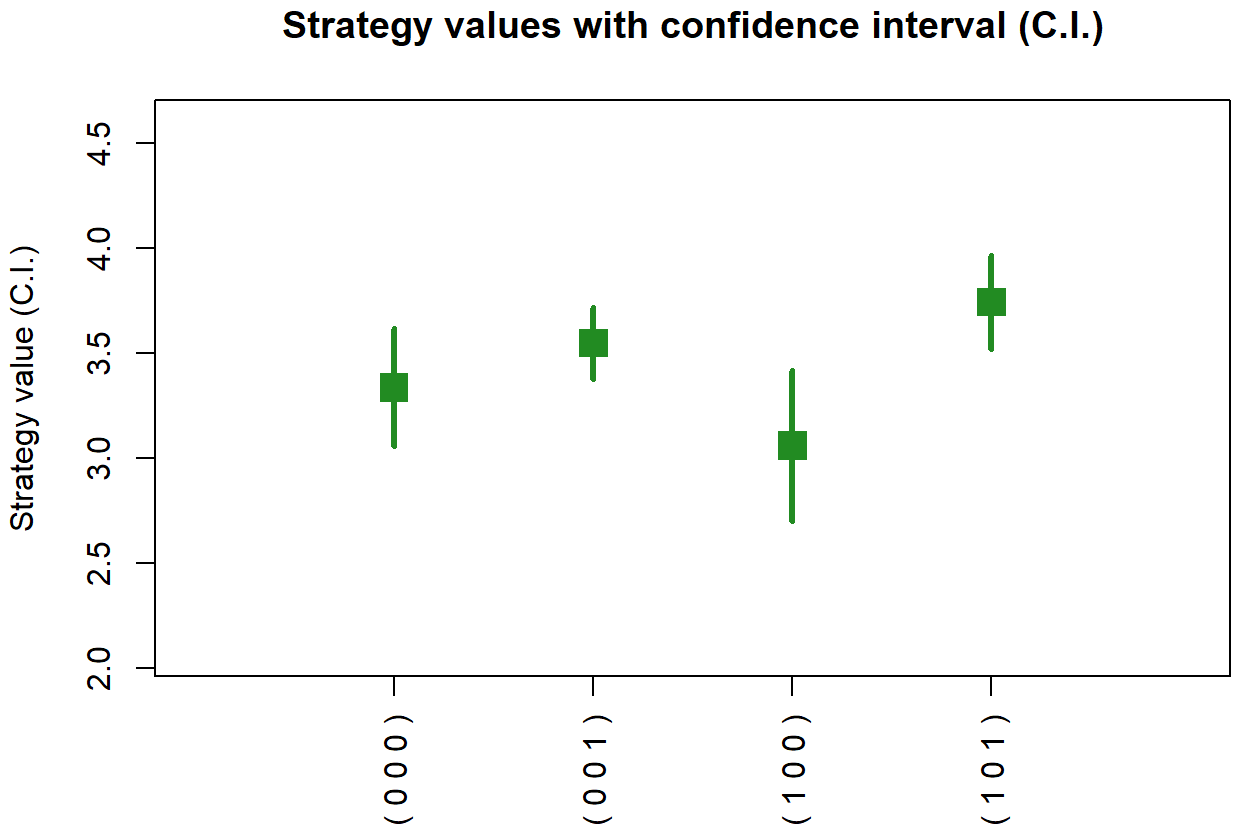
```
## Warning: package 'SMARTAR' was built under R version 3.6.2
```

```
atsmeans(data=DataFile,family="normal",method="Gest",common=FALSE,conf=TRUE,alpha=0.05,plot=T
RUE)
```

```
## $value: estimated strategy values (with confidence intervals)
## $vmat: variance-covariance matrix of estimated strategy values
```

```
## A strategy is defined as a vector of decision makings (d0;d00,d01) for 2 stages
##
## d0 is the stage-1 decision making for A1
## d00 is the stage-2 decision making for A2, conditioning on A1=d0 and O2=0
## d01 is the stage-2 decision making for A2, conditioning on A1=d0 and O2=0
```

```
##
```

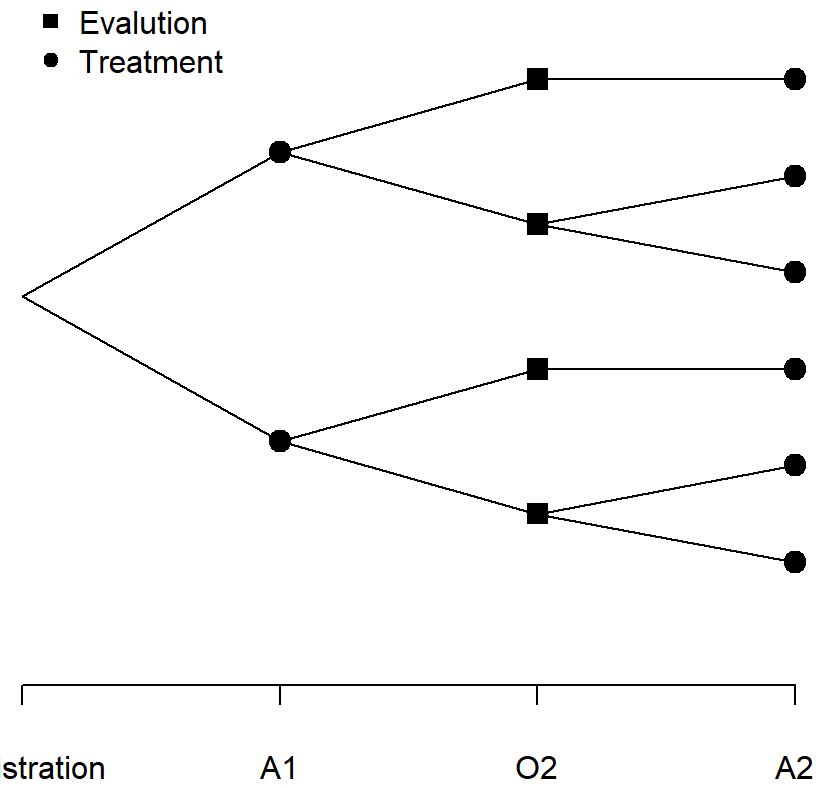



```
## $value
##   ATS d0 d00 d01  N value   se lower upper
## 1   1  0   0   0 53  3.34 0.14  3.06  3.62
## 2   2  0   0   1 55  3.55 0.09  3.38  3.72
## 3   3  1   0   0 51  3.06 0.18  2.70  3.42
## 4   4  1   0   1 58  3.75 0.11  3.52  3.97
##
## $vmat
##        [,1]   [,2]   [,3]   [,4]
## [1,] 0.0205 0.0023 0.0000 0.0000
## [2,] 0.0023 0.0074 0.0000 0.0000
## [3,] 0.0000 0.0000 0.0341 0.0079
## [4,] 0.0000 0.0000 0.0079 0.0128
```

```
seqmeans(data=DataFile,family="normal", plot = "d")
```

```
## Each subject followed one of the below treatment sequences during the trial.
```

```
## A treatment sequence is defined as a vector of values (A1,O2,A2).
```




```
##   SEQ A1 O2 A2  N MEAN  VAR
## 1   1  0  0  0 30 3.53 0.46
## 2   2  0  1  0 23 3.22 1.09
## 3   3  0  1  1 25 3.56 0.34
## 4   4  1  0  0 37 4.00 0.61
## 5   5  1  1  0 14 2.07 0.99
## 6   6  1  1  1 21 3.48 0.66
```

```
smartest(data=DataFile,family="normal",method="Gest",common=FALSE,alpha=0.05,adjust="Bon")
```

```
## $Strategy provides the details of decision makings under strategy labels (ATS)
## $Global.test assesses the null hypothesis of no difference across all the strategy values
## $Pairwise.test compares all the pairs of strategies, of which the labels are shown in $Str
ategy
```

```
## The P values should compare to the critical value adjusted for the Bonferroni correction
```

```
## $Strategy
##      ATS d0 d00 d10  N
## [1,]   1  0   0   0 53
## [2,]   2  0   0   1 55
## [3,]   3  1   0   0 51
## [4,]   4  1   0   1 58
##
## $Global.test
##   size nATS df chisq Pvalue
## 1  150    4  3  17.9  5e-04
##
## $Pairwise.comparisons
##      label  diff lower.CI upper.CI     Z Pvalue
## 1  1 vs. 2 -0.21    -0.61     0.19 -1.38 0.1681
## 2  1 vs. 3  0.28    -0.34     0.89  1.18 0.2366
## 3  1 vs. 4 -0.41    -0.89     0.07 -2.23 0.0258
## 4  2 vs. 1  0.21    -0.19     0.61  1.38 0.1681
## 5  2 vs. 3  0.49    -0.05     1.03  2.39 0.0168
## 6  2 vs. 4 -0.20    -0.57     0.18 -1.38 0.1687
## 7  3 vs. 1 -0.28    -0.89     0.34 -1.18 0.2366
## 8  3 vs. 2 -0.49    -1.03     0.05 -2.39 0.0168
## 9  3 vs. 4 -0.68    -1.15    -0.22 -3.87 0.0001
## 10 4 vs. 1  0.41    -0.07     0.89  2.23 0.0258
## 11 4 vs. 2  0.20    -0.18     0.57  1.38 0.1687
## 12 4 vs. 3  0.68     0.22     1.15  3.87 0.0001
```

##Use Generalized Linear Modeling with Wieghts (Generalized Weighted Least Squares) ##Now that we have our weights we can compare the sequential SMART groups

```
DataFile$AISGroup<-as.factor(DataFile$AISGroup)

# Conduct 6 Group analysis of variance ANOVA
ANOVA.mod <- aov(Y~AISGroup, data = DataFile, weights=SMARTWeights)
ANOVA.mod <- aov(Y~AISGroup, data = DataFile, weights=SMARTWght)

# Conduct Pairwise Comparisons using Tukey's Honest Significant Differences
TukeyHSD(ANOVA.mod,weights=SMARTWeights)
```

```
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = Y ~ AISGroup, data = DataFile, weights = SMARTWght)
##
## $AISGroup
##            diff        lwr        upr     p adj
## 2-1 -0.31594203 -0.9617223  0.3298383 0.7190329
## 3-1  0.02666667 -0.6043228  0.6576561 0.9999961
## 4-1  0.46666667 -0.1057962  1.0391295 0.1795558
## 5-1 -1.46190476 -2.2160814 -0.7077281 0.0000016
## 6-1 -0.05714286 -0.7201012  0.6058154 0.9998674
## 3-2  0.34260870 -0.3306130  1.0158304 0.6838697
## 4-2  0.78260870  0.1639057  1.4013117 0.0047784
## 5-2 -1.14596273 -1.9358122 -0.3561133 0.0006772
## 6-2  0.25879917 -0.4444742  0.9620725 0.8951700
## 4-3  0.44000000 -0.1632487  1.0432487 0.2896667
## 5-3 -1.48857143 -2.2663745 -0.7107683 0.0000022
## 6-3 -0.08380952 -0.7735261  0.6059071 0.9992867
## 5-4 -1.92857143 -2.6596964 -1.1974465 0.0000000
## 6-4 -0.52380952 -1.1604216  0.1128026 0.1714592
## 6-5  1.40476190  0.6008069  2.2087169 0.0000195
```

```
# Install multcomp package
# Use glht() function to conduct multiple pairwise-comparisons for a one-way ANOVA:
library(multcomp)
```

```
## Loading required package: mvtnorm
```

```
## Loading required package: survival
```

```
## Loading required package: TH.data
```

```
## Loading required package: MASS
```

```
##
## Attaching package: 'TH.data'
```

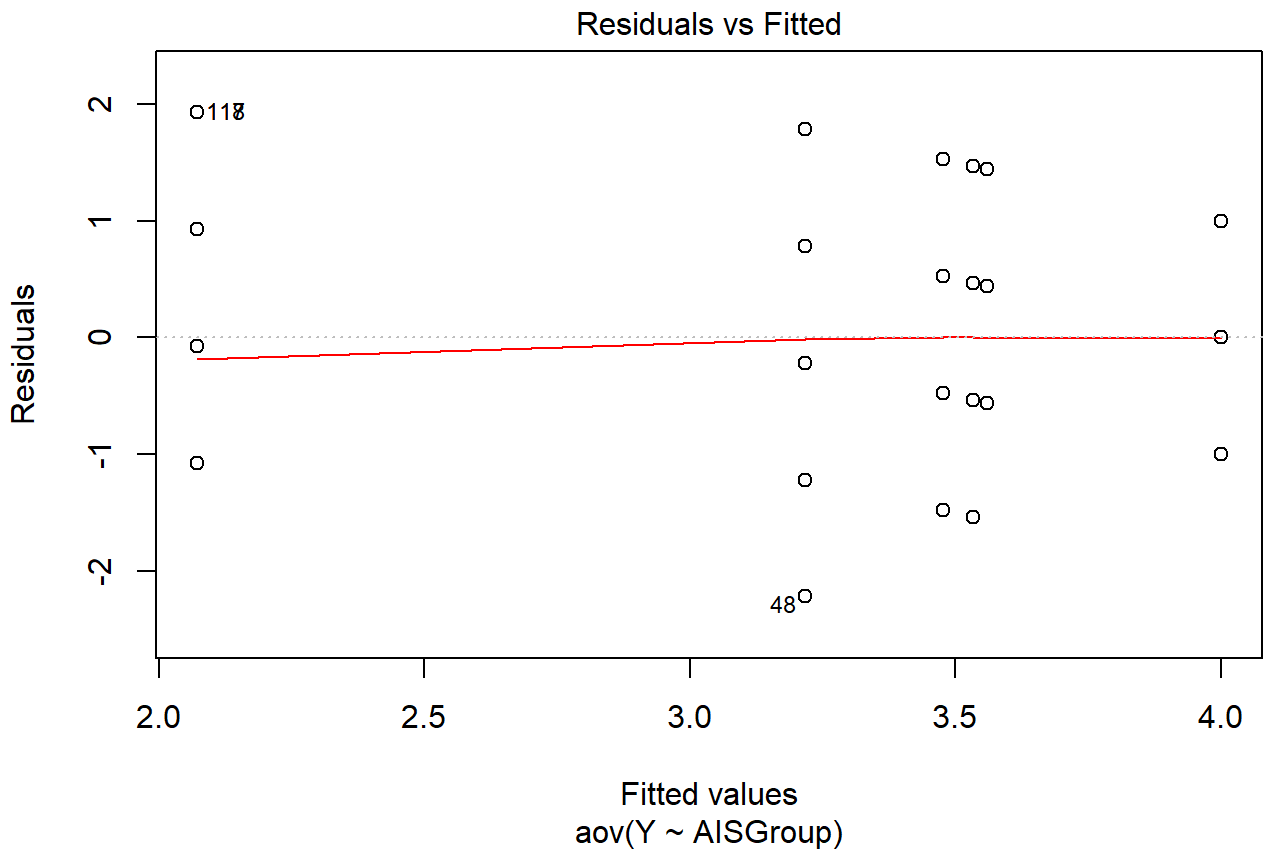
```
## The following object is masked from 'package:MASS':
##
##     geyser
```

```
summary(glht(ANOVA.mod, linfct = mcp(AISGroup = "Tukey")))
```

```
##
##   Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: aov(formula = Y ~ AISGroup, data = DataFile, weights = SMARTWght)
##
## Linear Hypotheses:
##            Estimate Std. Error t value Pr(>|t|)
## 2 - 1 == 0 -0.31594    0.24106  -1.311  0.77734
## 3 - 1 == 0  0.02667    0.23723   0.112  1.00000
## 4 - 1 == 0  0.46667    0.25237   1.849  0.43600
## 5 - 1 == 0 -1.46190    0.26992  -5.416  < 0.001 ***
## 6 - 1 == 0 -0.05714    0.24555  -0.233  0.99990
## 3 - 2 == 0  0.34261    0.20986   1.633  0.57650
## 4 - 2 == 0  0.78261    0.22684   3.450  0.00936 **
## 5 - 2 == 0 -1.14596    0.24622  -4.654  < 0.001 ***
## 6 - 2 == 0  0.25880    0.21923   1.180  0.84444
## 4 - 3 == 0  0.44000    0.22276   1.975  0.35975
## 5 - 3 == 0 -1.48857    0.24246  -6.139  < 0.001 ***
## 6 - 3 == 0 -0.08381    0.21500  -0.390  0.99880
## 5 - 4 == 0 -1.92857    0.25730  -7.495  < 0.001 ***
## 6 - 4 == 0 -0.52381    0.23161  -2.262  0.21527
## 6 - 5 == 0  1.40476    0.25062   5.605  < 0.001 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)
```

```
##Finally, we will test model assumptions

# 1. Plot the variances from the ANOVA model, i.e., visualize Homogeneity of variances
plot(ANOVA.mod, 1)
```




```
# 2. Conduct a formal Levene Test on homogeneity of variance
library(car)
```

```
## Loading required package: carData
```

```
leveneTest(Y~AISGroup, data = DataFile)
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##        Df F value Pr(>F)
## group   5  0.3643 0.8723
##       144
```

##The following is a survival SMART analysis ##Package is DTR for Dynamic Treatment Regimens ## X is A1 treatment in DTR ## R is 02 intermediate response ## Z is A2 treatment ## U is time to event ## delta is the event yes or no

```
library(DTR)
```

```
## Warning: package 'DTR' was built under R version 3.6.3
```

```
data("LDTdata")
View(LDTdata)

## Not run:
data("LDTdata")
est <- LDTestimate(data=LDTdata)
```

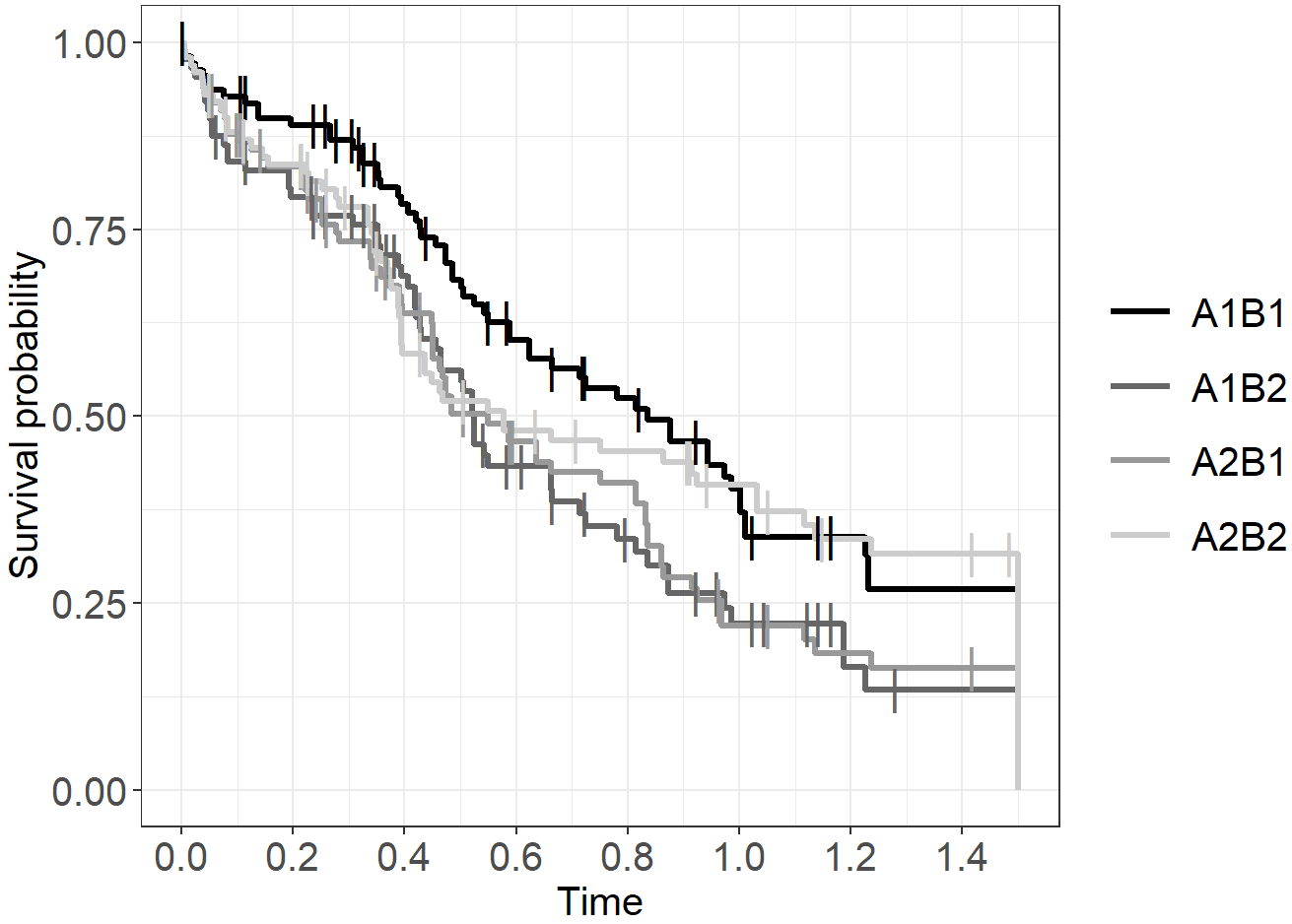
```
## Estimating for A1 arm...
## Estimating for A2 arm...
```

```
est
```

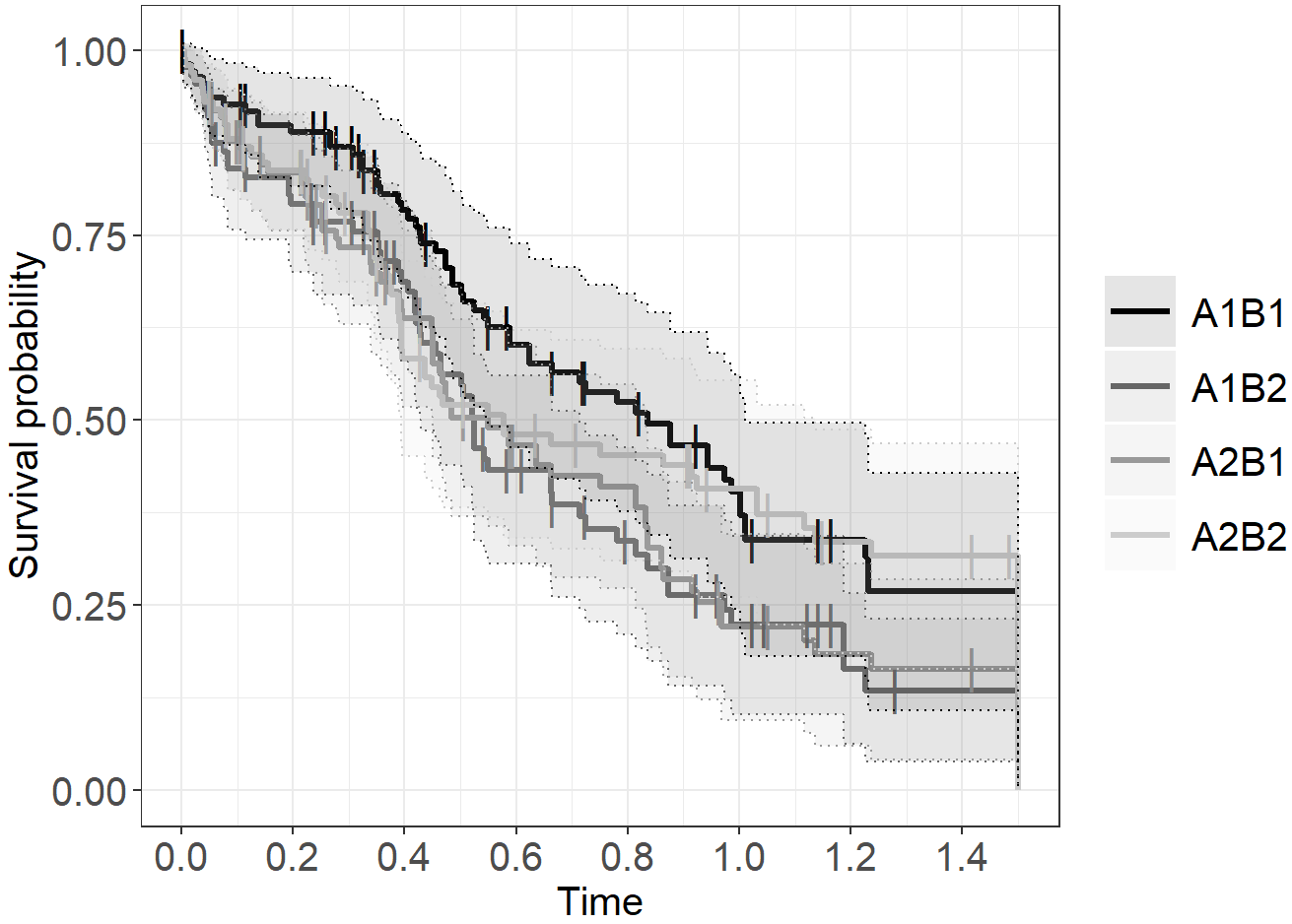
```
## Call: LDTestimate(data = LDTdata)
##
##   DTR records events    median     LCL95     UCL95
##  A1B1      75     54 0.8363004 0.5499846 1.0112419
##  A1B2      75     51 0.5245500 0.4290100 0.7144589
##  A2B1      77     58 0.5495142 0.4500212 0.8327760
##  A2B2      75     55 0.5773552 0.3939629 1.1364390
```

```
## End(Not run)

plot(est, censored=TRUE)
```




```
plot(est, confidence.interval=TRUE, censored=TRUE)
```


1.00
0.75
0.50
0.25
0.00
Survival probability
0.0
0.2
0.4
0.6
0.8
1.0
1.2
1.4
Time
A1B1
A1B2
A2B1
A2B2