tranSurv

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This vignette provides a short tutorial on the usage of the package's main function, `trSurvfit`.

Illustration

Example function in `?trSurvfit`

```
> datgen <- function(n) {
+     a <- -0.3
+     X <- rweibull(n, 2, 4) ## failure times
+     U <- rweibull(n, 2, 1) ## latent truncation time
+     T <- (1 + a) * U - a * X ## apply transformation
+     C <- 10 ## censoring
+     dat <- data.frame(trun = T, obs = pmin(X, C), delta = 1 * (X <= C))
+     return(subset(dat, trun <= obs))
+ }
```

Set a random seed and see data structure.

```
> set.seed(1)
> dat <- datgen(100)
> head(dat)
```

```
       trun      obs delta
1 1.8374416 4.606270     1
2 1.9072099 3.976991     1
3 1.6963782 2.985634     1
4 0.4323355 1.241174     1
5 1.9913542 5.061325     1
6 1.2630309 1.309359     1
```

The `trun` is the truncation time, `obs` is the observed survival time, and `delta` is the censoring indicator. Fitting this with `trSurvfit`:

```
> with(dat, trSurvfit(trun, obs, delta))
```

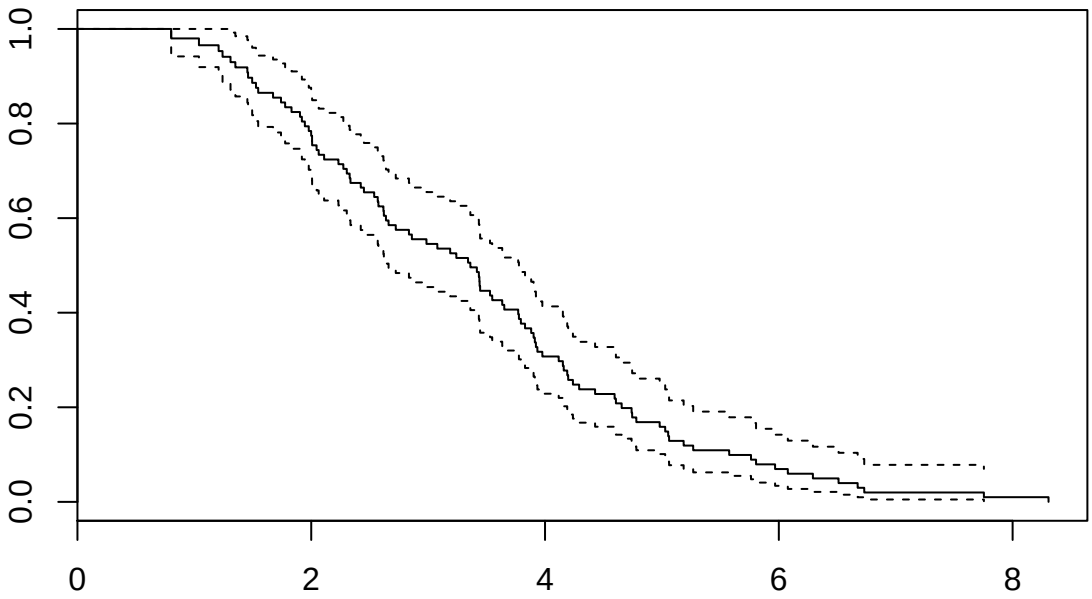
```
Fitting structural transformation model

Call: trSurvfit(trun = trun, obs = obs, delta = delta)

Conditional Kendall's tau = 0.5312 , p-value = 0
Restricted inverse probability weighted Kendall's tau = 0.5312 , p-value = 0
Transformation parameter by minimizing absolute value of Kendall's tau: -0.3011
Transformation parameter by maximizing p-value of the test: -0.3011
```

The function `trSurvfit` gives some important information. The conditional Kendall's tau for the observed data (before transformation) is 0.5312 with a p-value < 0.001. The restricted IPW Kendall's tau (Austin and Betensky, 2014) gives the same result. The transformation parameter, a, turns out to be -0.3011. The estimated survival curve (based on a) can be plotted with `survfit`:

```
> library(survival)
> foo <- with(dat, trSurvfit(trun, obs, delta))
> plot(survfit(Surv(ta, obs, delta) ~ 1, data = foo$qind))
```



Simulation

Make a function to call the transformation parameter α.

```
> do <- function(n){
+   foo <- with(datgen(n), trSurvfit(trun, obs, delta))
+   c(foo$byTau$par[1], foo$byP$par[1])
+ }
```

Try $n = 100$ with 100 replicates:

```
> set.seed(1)
> result <- replicate(100, do(100))
```

This returns a 2 by 100 matrix. The first row gives $\hat{\alpha}$ by maximizing the conditional Kendall's tau and the second row gives $\hat{\alpha}$ by minimizing the p-value from the conditional Kendall's tau test.

```
> summary(t(result))
```

```
       V1                 V2          
 Min.   :-0.3504   Min.   :-0.3504  
 1st Qu.:-0.3175   1st Qu.:-0.3174  
 Median :-0.2999   Median :-0.2999  
 Mean   :-0.3010   Mean   :-0.3010  
 3rd Qu.:-0.2863   3rd Qu.:-0.2862  
 Max.   :-0.2495   Max.   :-0.2495  
```