DTDA: An Updated and Expanded R Package for the Statistical Analysis of Doubly Truncated Data

Jacobo de Uña-Álvarez

(joint work with Carla Moreira and Rosa M. Crujeiras)

Universidade de Vigo

jacobo@uvigo.es

VIII Xornada de Usuarios de R en Galicia

Santiago de C., Oct 14, 2021

Double truncation: definition

- Target variable X observed only when $U \leq X \leq V$
- In that case truncation couple (U, V) observed too
- Prominent example: interval sampling of time-to-event data:

  Subjects with event within $[d_0, d_1]$ recruited

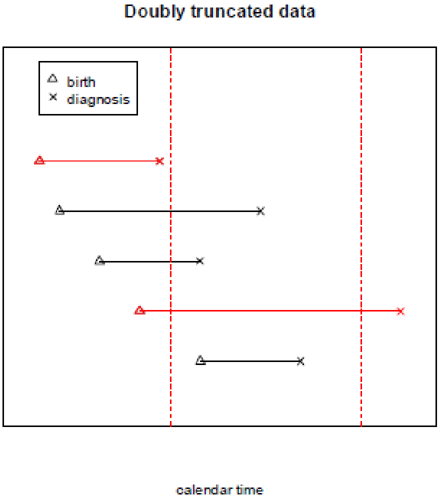
  X: time-to-event

  $\tau = d_1 - d_0$: interval width

  V: time from birth to d_1

  $U = V - \tau$
- Sample: iid triplets (X_i, U_i, V_i), $1 \leq i \leq n$
- (X_1, U_1, V_1) follows the cond cdf of (X, U, V) given $U \leq X \leq V$

Doubly truncated data: interval sampling



Red segments are not observed

Doubly truncated data: fields of application

- **Astronomy**: quasar luminosities
- **Epidemiology**: AIDS, cancer, Parkinson's Disease, Acute Coronary Syndrome, *autopsy-confirmed* neurodegenerative diseases
- **Engineering**: time to failure after installation of a device
- **Social Sciences**/**Finance**: marriage lengths, age at insolvency for companies
- (...)

Doubly truncated data: sampling bias

- Sampling probability for X:

$$G(x) = P(U \leq X \leq V | X = x) = P(U \leq x \leq V)$$

(last equality requires $(U, V) \perp X$)

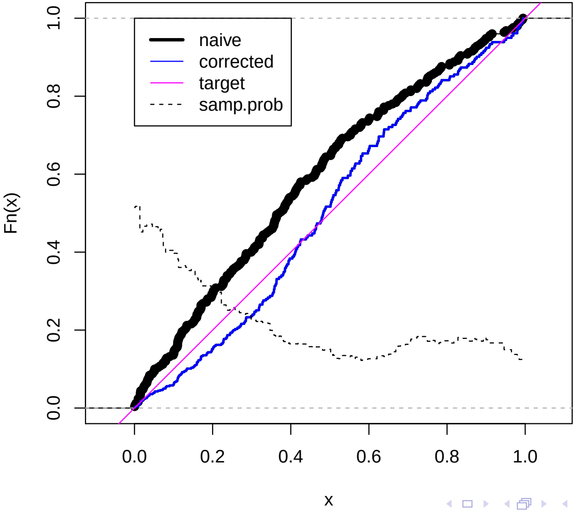
- $G(x)$ may be constant, or may be not
- NPMLE $G_n(x)$ can be computed from the (X_i, U_i, V_i)'s
- NPMLE $F_n(x)$ of the target cdf $F(x) = P(X \leq x)$ is an IPWE:

$F_n(x) = \sum_{i=1}^{n} I(X_i \leq x) G_n(X_i)^{-1} / \sum_{j=1}^{n} G_n(X_j)^{-1}$

Weight attached to X_i: $W_i = G_n(X_i)^{-1} / \sum_{j=1}^{n} G_n(X_j)^{-1}$

- Iterative methods to compute G_n (and F_n) needed (`DTDA`)

Doubly truncated data: simulated example



DTDA package v3.0

- Maintainer: Carla Moreira
- Launched on April 11, 2021
- Update and expansion of the original DTDA (September 21, 2009)
- Main improvements:

- Computational savings through parallel computing (bootstrapping!)
- Smoothing methods to estimate density and hazard functions
- New real datasets
- Simulation of doubly truncated data (interval sampling)

- 46K downloads, 593 last month:

  https://cranlogs.r-pkg.org/badges/grand-total/DTDA

  https://cranlogs.r-pkg.org/badges/DTDA

DTDA package v3.0: available functions

- Three iterative algorithms to compute F_n:

```
efron.petrosian(X, U = NA, V = NA, wt = NA, error = NA,
nmaxit = NA, boot = TRUE, B = NA, alpha = NA, display.F
= FALSE, display.S = FALSE)
```

```
lynden(X, U = NA, V = NA, error = NA, nmaxit = NA, boot
= TRUE, B = NA, alpha = NA, display.F = FALSE,
display.S = FALSE)
```

```
shen(X, U = NA, V = NA, wt = NA, error = NA, nmaxit =
NA, boot = TRUE, boot.type = "simple", B = NA, alpha =
NA, display.FS = FALSE, display.UV = FALSE, plot.joint
= FALSE, plot.type = NULL)
```

- Function `shen()` computes and returns G_n too

DTDA package v3.0: available functions (cont.)

- Smoothing methods for density and hazard functions:

```
densityDT(X, U, V, bw = "DPI2", from, to, n, wg = NA)
```

```
hazardDT(X, U, V, bw = "LSCV", from, to, n, wg = NA)
```

- Alternatively, use

```
density(X, bw = "nrd0", weights = W)
```

with

```
W <- shen(...)$biasf^-1
W <- W / sum(W)
```

but if so take care with bandwidth selection!

DTDA package v3.0: available functions (cont.)

- Random generation of doubly truncated data (interval sampling):

  ```
  rsim.DT(n, tau, model = NULL)
  ```

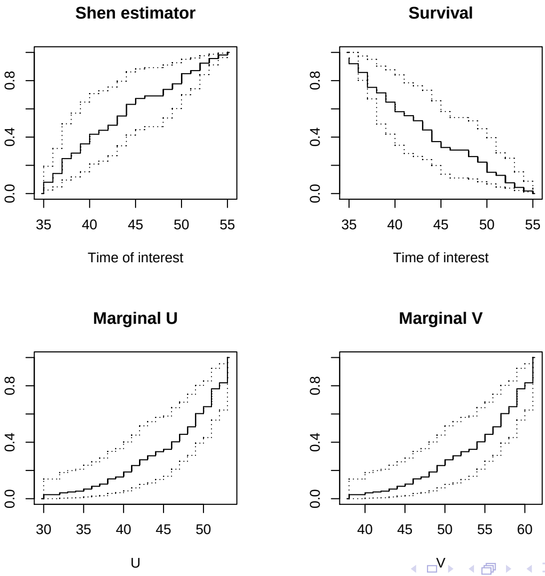
- ...and many real datasets:

  `Quasars`
  `AIDS`
  `ChildCancer`
  `AIDS.DT`
  `EquipSRounded`
  `PDearly`, `PDlate`
  `ACS`, `ACSred`

DTDA in practice: Parkinson's Disease (Clark et al. 2011)

```
> library(DTDA)
> head(PDearly)   #two cases with missing info for V
     X  U  V SNP_A10398G SNP_PGC1a
     1 37 30 38           A         G
     2 46 39 47           A        AG
     3 36 34 42           A         G
     4 54 49 57           A        AG
> PDearly <- na.omit(PDearly)
> attach(PDearly)
> shen(X, U, V, display.FS=TRUE, display.UV=TRUE) -> res
     n.iterations 56
     S0 9.716169e-07
     events 97
     B 500
     alpha 0.05
     Boot simple
```

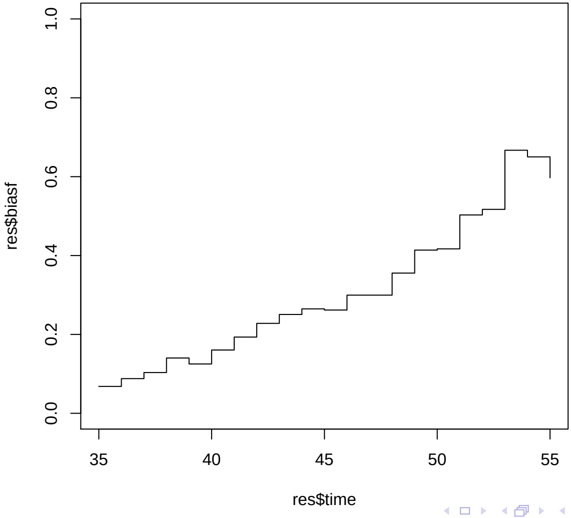
DTDA in practice: Parkinson's Disease (Clark et al. 2011)



DTDA in practice: Parkinson's Disease (Clark et al. 2011)

```
> #sampling probability:
> plot(res$time, res$biasf, type = "s", ylim = c(0,1))

> #save the weights
> #useful to construct consistent estimators later:
> W <- res$biasf^-1
> W <- W / sum(W)

> #estimation of the mean:
> mean(X)  #naive
[1] 46.97938
> sum(W * res$time)  #correct
[1] 43.20277
```

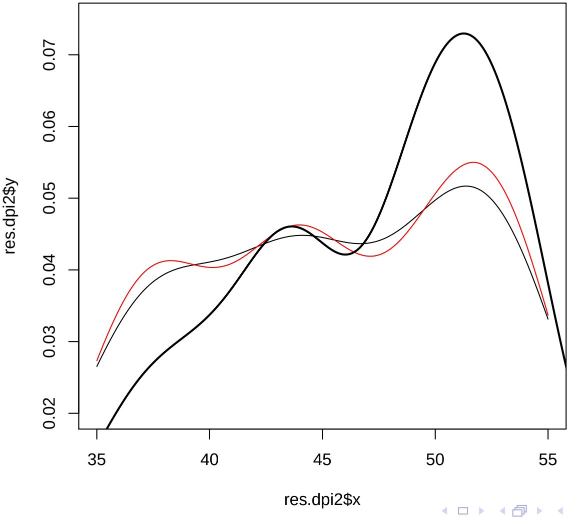
DTDA in practice: Parkinson's Disease (Clark et al. 2011)



DTDA in practice: Parkinson's Disease (Clark et al. 2011)

```
> densityDT(X, U, V, from = min(X), to = max(X),
+ n = 500) -> res.dpi2   #bw default is DPI2
> plot(res.dpi2, type = "l", ylim = c(.02, .075))

> densityDT(X, U, V, bw = "DPI1", from = min(X), to = max(X),
+ n = 500) -> res2.dpi1
> lines(res2.dpi1$x, res2.dpi1$y, col = 2)

> res.dpi2$bw; res2.dpi1$bw
[1] 2.855729
[1] 2.470739

> density(X) -> resn.d    #naive approach
> lines(resn.d$x, resn.d$y, lwd = 2)
> resn.d$bw   #ordinary rule-of-thumb undersmooths
[1] 2.046491
```

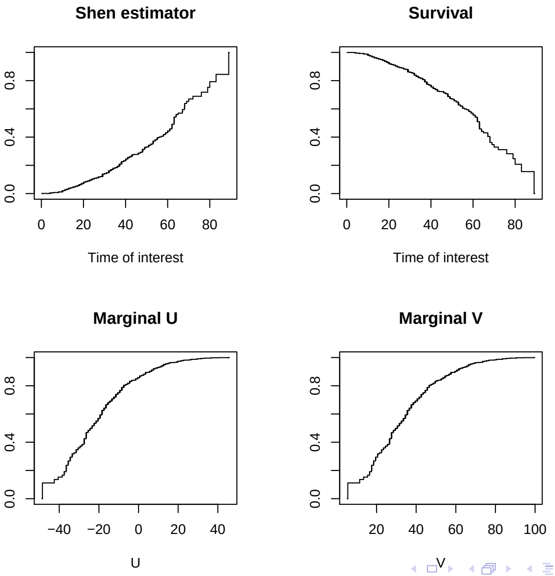
DTDA in practice: Parkinson's Disease (Clark et al. 2011)



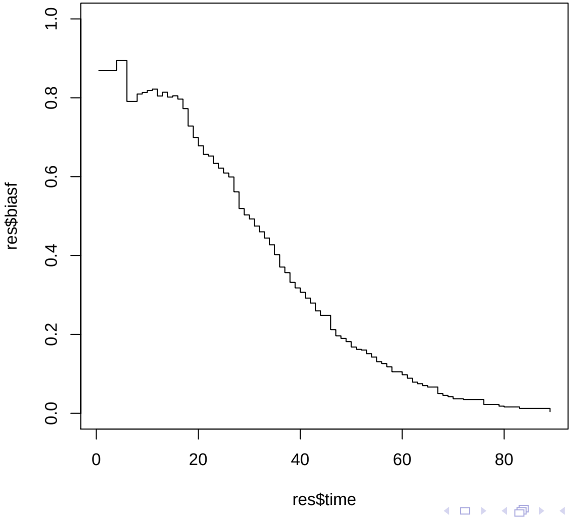
DTDA in practice: AIDS (Kalbfleisch and Lawless 1989)

```
> head(AIDS.DT)
X     U    V AGE
1 0.5 -17.5 36.5  63
2 4.0 -18.5 35.5   1
3 4.0 -18.5 35.5  29
4 4.0 -33.5 20.5  46

> attach(AIDS.DT)
> res <- shen(X, U, V, boot = F, display.F = T,
+ display.UV = T)
n.iterations 23
S0 6.280252e-07
events 295

> plot(res$time, res$biasf, type = "s", ylim = c(0, 1))
```

DTDA in practice



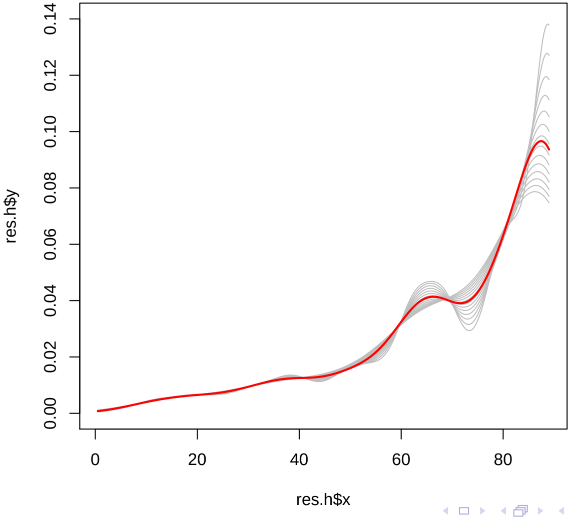
DTDA in practice: AIDS (Kalbfleisch and Lawless 1989)



DTDA in practice: AIDS (Kalbfleisch and Lawless 1989)

```
> #hazard function:
> res.h <- hazardDT(X, U, V, bw = 5, from = min(X),
+ to = max(X), n = 500)
> plot(res.h$x, res.h$y, type = "l", ylim = c(0, .14))

> b <- seq(3, 7, length = 14)
> for (i in 1:k){
+ res.hb <- hazardDT(X, U, V, bw = b[i], from = min(X),
+ to = max(X), n = 500)
+ lines(res.hb$x, res.hb$y, col = "gray")
+ }
> lines(res.h$x, res.h$y, col = 2, lwd = 2)
```

DTDA in practice: AIDS (Kalbfleisch and Lawless 1989)



DTDA in practice: simulating double truncation

- Simulating interval sampling:

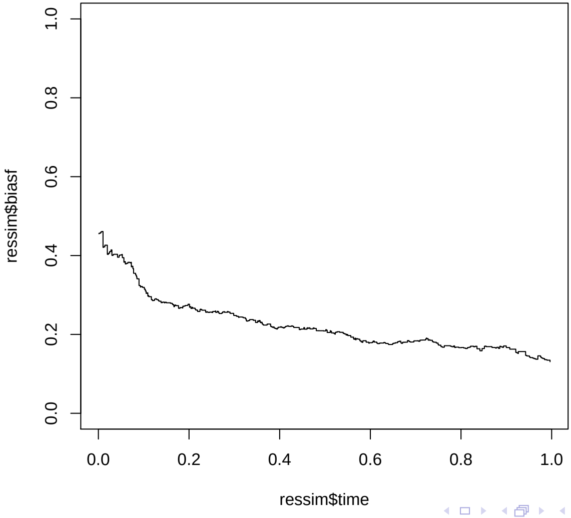
  $X \sim U(0,1)$

  $U \sim U(-\tau,1)$, $V = U + \tau$ in model 1 (no sampling bias)

  $U \sim$ uniform squared (Beta) in model 2 (sampling bias)

```
> set.seed(1234)
> rsim.DT(500, tau = 1/3, model = 2) -> mysim
> str(mysim)
’data.frame’:   500 obs. of  3 variables:
$ X: num  0.11 0.622 0.145 0.443 0.58 ...
$ U: num  -0.1687 0.5222 -0.0967 0.3343 0.5005 ...
$ V: num  0.165 0.856 0.237 0.668 0.834 ...
> ressim <- shen(mysim$X, mysim$U, mysim$V, boot = F)
> plot(ressim$time, ressim$biasf, type = "s", ylim = c(0, 1))
```

DTDA in practice: simulating double truncation



Further use of the sampling probabilities W

- Linear (multiple, polynomial) regression:

  ```
  lm(formula, data, subset, weights = W, na.action, ...)
  ```

- Nonparametric regression (local linear smoothers):

  ```
  sm.regression(x, y, h, design.mat = NA, model = "none",
  weights = W, group = NA, ...)
  ```

- Proportional hazards (Cox) regression: add `+offset(-log(W))` as an extra covariate in formula:

  ```
  coxph(formula, data=, weights, subset, na.action, ...)
  ```

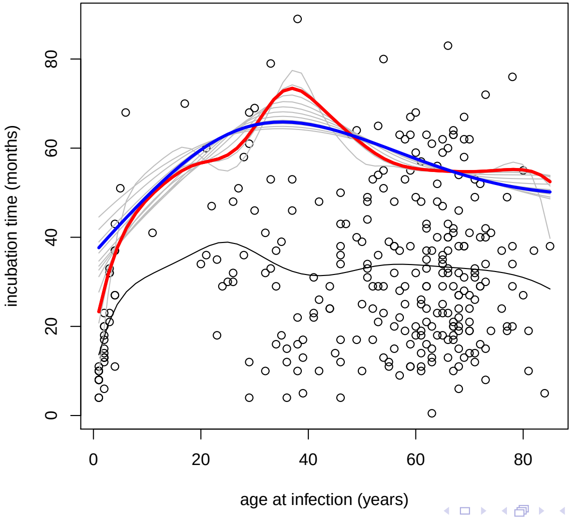
- **Remark:** standard errors must be updated (use e.g. bootstrapping)

Further use of the sampling probabilities `W` (cont.)

- Local linear smoothing:

```
> attach(AIDS.DT)
> W <- res$biasf^-1
> W <- W / sum(W)

> library(sm)
> res.LL <- sm.regression(AGE, X, h = 20, weights = W)
> res.LL2 <- sm.regression(AGE, X, h = 7.59, weights = W)

#naive estimator:
> res.LL2n <- sm.regression(AGE, X, h = 7.59)
```

Further use of the sampling probabilities `W` (cont.)



Further use of the sampling probabilities W (cont.)

- Proportional hazards (Cox) regression:

```
> library(survival)
> coxph(Surv(X) ~ AGE + I(AGE^2) + offset(-log(W)),
+ data = AIDS.DT) -> rescox
> coef(rescox)
          AGE      I(AGE^2)
-0.0290770914  0.0002863366
```

- Same for proportional cause-specific hazards model (competing risks)
- Linear regression:

```
> lm(X ~ AGE + I(AGE^2), data = AIDS.DT,
+ weights = W) -> reslm
> coef(reslm)
(Intercept)         AGE    I(AGE^2)
36.11955323  1.48368927 -0.01785602
```

DTDA package v3.0: discussion

- Three iterative algorithms implemented: `efron.petrosian()`, `lynden()`, `shen()`

- Other packages:

  `double.truncation` by Takeshi Emura

  `SurvTrunc` by Lior Rennert

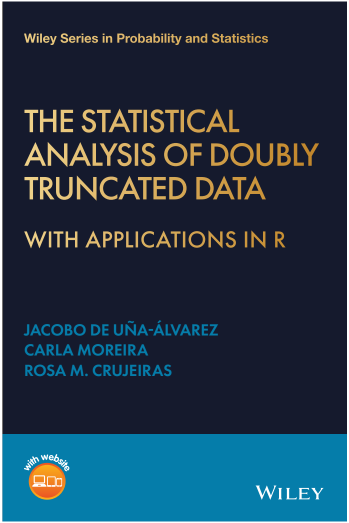
  `DTDA.cif`, `DTDA.ni` by José Carlos Soage

- Advantages of `DTDA`:

- Sampling probabilities $G_n(X_i)$ returned (`shen()`)
- Simple and obvious bootstrap available
- Confidence intervals for the truncation cdf, automatic plots
- Faster computational times
- Smoothing methods

Thanks for your attention!

Forthcoming (January 2022):



Wiley Series in Probability and Statistics

THE STATISTICAL ANALYSIS OF DOUBLY TRUNCATED DATA

WITH APPLICATIONS IN R

JACOBO DE UÑA-ÁLVAREZ
CARLA MOREIRA
ROSA M. CRUJEIRAS

with website

WILEY

Contact: jacobo@uvigo.es

`jacobo.webs.uvigo.es`