Nonparametric Estimation of a distribution function from doubly truncated data under dependence

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Abstract

The NPMLE of a distribution function from doubly truncated data was introduced in the seminal paper of Efron and Petrosian (1999). The consistency of the Efron-Petrosian estimator depends however on the assumption of independent truncation. In this work we introduce an extension of the Efron-Petrosian NPMLE when the lifetime and the truncation times may be dependent. The proposed estimator is constructed on the basis of a copula function which represents the dependence structure between the lifetime and the truncation times. Two different iterative algorithms to compute the estimator in practice are introduced, and their performance is explored through an intensive Monte Carlo simulation study. We illustrate the use of the estimators on a real data example.

Introduction

Let $X^*$ be the random variable of ultimate interest or 'lifetime', with distribution function (df) $F$, and assume that it is doubly truncated by the random pair $(U^*, V^*)$ with joint df $K$, where $U^*$ and $V^* (U^* \leq V^*)$ are the left and right truncation variables respectively. This means that the triplet $(U^*, X^*, V^*)$ is observed if and only if $U^* \leq X^* \leq V^*$, while no information is available when $X^* < U^*$ or $X^* > V^*$. We assume that the truncation comes from the existence of an observational window of length $\phi$, and therefore $V^* = U^* + \phi \ (\phi > 0)$. This model is suitable when the sample reduces to
individuals with event dates between two fixed calendar times (e.g. Moreira and de Uña-Álvarez (2010)). Austin and Betensky (2014) termed this type of truncation as ‘complete truncation dependence’, while Zhu and Wang (2012, 2014) referred this problem as ‘interval sampling’. Besides, we assume that \( U^\ast \) depends on the lifetime, and that the dependence structure of \( (X^\ast, U^\ast) \) is given by a copula function such that (cfr. Nelsen (2006))

\[
P(X^\ast \leq x, U^\ast \leq u) = C_\theta (F(x), G(u)),
\]

where \( G(u) = K(u, \infty) \) is the marginal df of \( U^\ast \) and \( C_\theta \) a parametric family of copula’s, with \( \theta \) belonging to a certain euclidean parametric space \( \Theta \). Dependent truncation may appear in practice when, for example, the birth date of the process \( (U^\ast) \) has influence on the subsequent lifetime of interest \( (X^\ast) \); Austin and Betensky (2014) introduced a test for independence based on a Kendall’s Tau in this setting. For example, in the study of transfusion-related AIDS in Section 3, the incubation time \( X^\ast \) is doubly truncated by the time from HIV infection to January 1, 1982 (\( U^\ast \)) and the lapse time from HIV infection to the end of study (July 1, 1986) (\( V^\ast \)). Hereby we note that several persons in this study were infected a long time ago with the HIV virus without developing AIDS. Considering that the knowledge about AIDS was not well in the early days of the epidemic, this suggests that there is a positive dependence between \( X^\ast \) and \( U^\ast \), and several persons with a HIV infection mated go unnoticed.

To assess the degree of dependence between lifetime and truncation variables Chaieb et al. (2006) propose a semiparametric estimation for a copula model describing dependent truncation data. Emura et al. (2011) and Emura and Wang (2012) considered estimators based on conditional likelihood and nonparametric likelihood, respectively. The referred author Emura (2015) revisits the estimation presented in Chaieb et al. (2006) and proposes a different algorithm of solving their estimation function. For the best of our knowledge, these contributions on the dependence between lifetime and truncation time only referred to the case of one-sided truncation. This paper presents new statistical methods for modeling a possible dependency between \( X^\ast \) and \( (U^\ast, U^\ast + \phi) \) when only triplets such that \( U^\ast \leq X^\ast \leq U^\ast + \phi \) are observed.

Let \((U_i, X_i, V_i), i = 1, ..., n\) denote the sampling information, these are iid data with the distribution of \((U^\ast, X^\ast, V^\ast)\) conditionally on \( U^\ast \leq X^\ast \leq V^\ast \).

Under the given model, the full likelihood of the \((U_i, X_i, V_i)\)’s is given by (see the Appendix)

\[
L(\theta, f, k) = \prod_{i=1}^{n} \frac{W_{ii} f_i k_i}{\sum_{j=1}^{n} \sum_{m=1}^{n} W_{jm} f_j k_m J_{mj}}, \quad (1)
\]

where \( f = (f_1, f_2, ..., f_n) \) and \( k = (k_1, k_2, ..., k_n) \) are distributions putting probability \( f_i \) on \( X_i \) and \( k_i \) on \( (U_i, V_i) \) and where \( J_{ij} = I_{[U_i \leq X_j \leq U_i + \phi]} \) and

\[
W_{ij} = C_\theta^{(1,1)} (F_i, K_j), \quad \text{with} \quad F_i = \sum_{m=1}^{n} f_m I_{[X_m \leq X_i]} \quad \text{and} \quad K_i = \sum_{m=1}^{n} k_m I_{[U_m \leq U_i]}. \quad \text{Here,}
\]

\( C_\theta^{(1,1)} \) denotes the density of the copula family.
For independent truncation, we have $C_{\theta}^{(1,1)} = 1$ and the likelihood (1) reduces to that in Efron and Petrosian (1999). When $X^*$ and $U^*$ are dependent, the weights $W_{ij}$ introduce a suitable correction of the Efron-Petrosian NPMLE. The goal is the estimation of the $r + 2n$ parameters $\theta, f_i$ and $k_i$, $i = 1, \ldots, n$, where $r$ denotes the dimension of $\Theta$. Then, the NPMLE’s of $F(x)$ and $G(u)$ under truncation are simply obtained as $\hat{F}(x) = \sum_{i=1}^{n} f_i I_{[X_i \leq x]}$ and $\hat{G}(u) = \sum_{i=1}^{n} \hat{k}_i I_{[U_i \leq u]}$.

This paper is organized as follows. In Section 1 two different algorithms to estimate the parameter $\theta$ and the distributions $F$ and $G$ are introduced. The finite sample behaviour of the estimators is investigated through simulations in Section 2. An application to the analysis of AIDS incubation times is provided in Section 3, while the conclusions are deferred to Section 4. Technical details are provided in the Appendix.

1 The estimators

First, we introduce a simple algorithm to estimate the parameters. Here we assume for the moment that the weights $W_{ij}$ are free of $f$ and $k$. Then, by differentiating the loglikelihood with respect to the $f_m$’s and $k_m$’s we obtain the following simple score equations:

$$\frac{\partial \log L}{\partial f_m} = 0 \iff f_m = \left[ \sum_{i=1}^{n} \frac{1}{K^w_i} \right]^{-1} \frac{1}{K^w_m}, \quad m = 1, \ldots, n$$

with $K^w_i = \sum_{j=1}^{m} W_{ij} k_j J_{ji}$, and

$$\frac{\partial \log L}{\partial k_m} = 0 \iff k_m = \left[ \sum_{i=1}^{n} \frac{1}{F^w_i} \right]^{-1} \frac{1}{F^w_m}, \quad m = 1, \ldots, n$$

with $F^w_i = \sum_{j=1}^{m} W_{ij} f_j J_{ij}$. Equations (2) and (3) can be used to introduce the following iterative simple algorithm.

Step 0 Take the Efron-Petrosian NPMLE for independent truncation $f^{(0)} = (f_1^{EP}, \ldots, f_n^{EP}), k^{(0)} = (k_1^{EP}, \ldots, k_n^{EP})$ as initial solution for $f$ and $k$, and compute

$$\theta^{(0)} = \arg\max_{\theta} L^{(0)}(\theta),$$

where,

$$L^{(0)}(\theta) = \prod_{i=1}^{n} \frac{C_{\theta}^{(1,1)} \left( F_i^{(0)}, K_i^{(0)} \right) f_i^{(0)} k_i^{(0)}}{\sum_{m=1}^{n} \sum_{m=1}^{n} C_{\theta}^{(1,1)} \left( F_j^{(0)}, K_j^{(0)} \right) f_j^{(0)} k_m^{(0)} J_{mj}},$$

and where $F_i^{(0)} = \sum_{m=1}^{n} f_m^{(0)} I_{[X_m \leq X_i]}$ and $K_i^{(0)} = \sum_{m=1}^{n} k_m^{(0)} I_{[U_m \leq U_i]}$. 


Step 1 Use (3) to improve \(k^{(0)}\):
\[
k_m^{(1)} = \left[ \sum_{i=1}^{n} \frac{1}{F_{i}^{u_{0},0}} \right]^{-1} \frac{1}{F_{m}^{u_{0},0}}, \quad m = 1, \ldots, n
\]
where \(w_0 = \{W_{ij}^{(0)} : 1 \leq i, j \leq n\}\), \(W_{ij}^{(0)} = c_{\theta^{(0)}}^{(1,1)}(F_{i}^{(0)}, K_{j}^{(0)})\) and \(F_{i}^{u_{0},0} = \sum_{j=1}^{n} W_{ij}^{(0)} f_{j}^{(0)} J_{ij}\)

Step 2 Use (2) to improve \(f^{(0)}\):
\[
f_m^{(1)} = \left[ \sum_{i=1}^{n} \frac{1}{K_{i}^{u_{0},1}} \right]^{-1} \frac{1}{K_{m}^{u_{0},1}}, \quad m = 1, \ldots, n
\]
where \(K_{i}^{u_{0},1} = \sum_{j=1}^{n} W_{ij}^{(0)} k_{j}^{(1)} J_{ji}\)

Step 3 Improve \(\theta^{(0)}\) by taking
\[
\theta^{(1)} = \arg\max_{\theta} L^{(1)}(\theta),
\]
where
\[
L^{(1)}(\theta) = \prod_{i=1}^{n} \left( \sum_{j=1}^{n} \sum_{m=1}^{1} c_{\theta}^{(1,1)}(F_{i}^{(1)}, K_{i}^{(1)}) f_{j}^{(1)} k_{j}^{(1)} J_{mij} \right)^{n},
\]
and where \(F_{i}^{(1)} = \sum_{m=1}^{n} f_{m}^{(1)} I_{[X_{m} \leq X_{i}]}, \quad K_{i}^{(1)} = \sum_{m=1}^{n} k_{m}^{(1)} I_{[U_{m} \leq U_{i}]}
\]

Step 4 Repeat steps (1) – (3) until convergence.

That is, algorithm Step 0-Step 4 fits the copula function by starting with the Efron-Petrosian NPMLE estimator under independent truncation. Then, it improves first \(k\) and then \(f\) by using the simple score equations (3) and (2); and, finally, it updates \(\theta\) by maximizing the loglikelihood (based on the improved \(k\) and \(f\)) with respect to the copula parameter. This procedure is repeated until a stable solution is reached. As convergence criterion, we have used \(\max_{1 \leq i \leq n} |f_{i}^{q-1} - f_{i}^{q}| \leq 1e - 06\) and \(\max_{1 \leq j \leq n} |k_{j}^{q-1} - k_{j}^{q}| \leq 1e - 06\) and \(\max_{1 \leq q \leq n} |\theta_{q}^{q-1} - \theta_{q}^{q}| \leq 1e - 06\). Then, the NPMLE’s \(\hat{F}(x)\) and \(\hat{G}(u)\) are constructed from the q-th solution \(f_{i}^{q}, k_{j}^{q}\) and \(\theta^{q}\).

A second algorithm to estimate the different parameters is called the full algorithm and is obtained if one differentiates the loglikelihood with respect to \(f\) and \(k\) by taking the dependence of the \(W_{ij}\)’s on these parameters into account. Then, the substitutes for equations (3) and (2) are (see the Appendix for details):
\[
\frac{\partial \log L}{\partial f_m} = 0 \iff f_m = \left[ \sum_{i=1}^{n} \frac{1}{nA_i + nK_i^w - \alpha B_i} \right]^{-1} \frac{1}{nA_m + nK_m^w - \alpha B_m}, \quad m = 1, \ldots, n \quad (4)
\]

with \( A_m = \sum_{i=1}^{n} \sum_{j=1}^{n} W_{ij}^{(2)} f_i k_j J_i I_{[X_m \leq X_i]}, \) \( B_m = \sum_{i=1}^{n} \frac{W_{ii}^{(2,1)} I_{[X_m \leq X_i]}}{W_{ii}^{(1,1)}} \) and \( \alpha = \sum_{j=1}^{n} \sum_{m=1}^{n} W_{jm}^{(1,1)} f_j k_m J_{m j}, \) and

\[
\frac{\partial \log L}{\partial k_m} = 0 \iff k_m = \left[ \sum_{i=1}^{n} \frac{1}{nC_i + nF_i^w - \alpha D_i} \right]^{-1} \frac{1}{nC_m + nF_m^w - \alpha D_m}, \quad m = 1, \ldots, n \quad (5)
\]

with \( C_m = \sum_{i=1}^{n} \sum_{j=1}^{n} W_{ij}^{(1,2)} f_i k_j J_i I_{[U_m \leq U_i]} \) and \( D_m = \sum_{i=1}^{n} \frac{W_{ii}^{(1,2)} I_{[U_m \leq U_i]}}{W_{ii}^{(1,1)}} \).

In (4) and (5) we use the notation \( W_{ij}^{(l,m)} \), \( 1 \leq l, m \leq 2 \), for \( C_{\theta}^{(l,m)}(F_i, K_j) \), where \( C_{\theta}^{(l,m)}(u, v) = \frac{\partial^{l+m}}{\partial u^l \partial v^m} C_{\theta}(u, v) \). Note that \( W_{ij} = W_{ij}^{(n,v)} \) with this notation.

The 'full' algorithm we propose is defined following Steps 0-4 above, but using these two equations (4) and (5) in the place of (3) and (2). Note that moving from the simple EM algorithm to this full algorithm implies changing the way in which \( k \) and \( f \) are improved, while the updating of \( \theta \) (Step 0) remains the same.

In Section 2 we investigate through simulations the performance of these two algorithms for several copula functions and marginal models. Interestingly, it is seen that the simple algorithm is accurate enough for practical purposes, while giving a more efficient solution in terms of computational speed. For the final implementation we multiply \( A_m, B_m, C_m \) and \( D_m \) by \( n/n + 1 \); this is equivalent to replace each \( W_{ij} = \frac{C_{\theta}^{(1,1)}(F_i, K_j)}{W_{ij}^{(n,v)}} \) by \( W_{ij}^* = C_{\theta}^{(1,1)} \left( \frac{n}{n + 1} F_i, \frac{n}{n + 1} K_j \right) \), which avoids problems at the upper-right corner of the copulas function.

Since the truncation interval \((U^*, V^*)\) prevents us from always observing the lifetime of interest \( X^* \), we are not able to fully see the dependence structure between \((X^*, U^*)\) which was expressed using a copula function \( C \). Hence, we note that it is not possible to estimate the association copula function and the marginal distributions without introducing extra assumptions. The copula function \( C \) and the marginal distributions \( F \) and \( K \) are in this case non-identifiable from the observed data. To avoid this non-identifiability while estimating the copula function and marginal distributions in this model by the two estimating algorithms, we do as in Ding (2012) for left-truncated data and assume that all copula functions used in the simulations and real data analysis, satisfy the identifiability condition in Ding (2012) and are strong lower-left tail identifiable. Under this condition, we noted that the estimation of the copula
function and the marginal distributions is identified in this model. In the future, we intend to study in more detail whether this condition is also sufficient for the identifiability under interval truncation.

In practice, it is important to report standard errors to know the accuracy of a given estimator for the triplet \((\theta, F, K)\). To this end, we propose to use a bootstrap algorithm based on the fitted chosen copula. To be specific, let \((T_1, T_2)\) be a pair of \(U(0, 1)\) random variables following the fitted copula \(C_{\theta^*}\). Let \(U^* = \hat{G}^{-1}(T_1)\) and \(X^* = \hat{F}^{-1}(T_2)\) where \(\hat{F}\) and \(\hat{G}(\cdot) = \hat{K}(\cdot, \infty)\) are the estimators based on the simple or the full algorithm, and \(\hat{F}^{-1}\) and \(\hat{G}^{-1}\) are their respective quantile functions. Reject the pair \((U^*, X^*)\) if \(U^* \leq X^* \leq U^* + \phi\) is violated. Form a resample of \(n\) data following this scheme, and repeat up to forming \(B\) resamples. Then, the bootstrap standard error of \(\hat{\theta}\), \(\hat{F}\) or \(\hat{K}\) is defined as the standard deviation of these estimators along the \(B\) resamples. In Section 2 we include some simulation results for this method when the goal is the estimation of the standard error of \(\hat{\theta}\); these results suggest that the copula-based bootstrap performs well.

## 2 Simulations

In this section we investigate the finite sample performance of the algorithms proposed in Section 1 through simulations. We simulate the scenario \(X^* \sim U(0, 1), U^* \sim U(-0.6, 0.4)\) and then we take \(V^* = U^* + \phi\), with \(\phi = 1.5\). Note that, in this way, the df of \(X^*\) is identifiable, because the lower (resp. upper) limit of the support of \(U^*\) (resp. \(V^*\)) is smaller than the lower (resp. upper) limit of the support of \(X^*\). We consider three different copula families: the Farlie-Gumble-Morgentein (FGM) copula (Case 1), the Frank copula (Case 2) and the Clayton copula (Case 3).

In Case 1 the variables \(X^*\) and \(U^*\) follow a FGM copula family with parameter \(\theta\), that is, \(C_\theta(u_1, u_2) = u_1 u_2 + \theta u_1 u_2 (1 - u_1) (1 - u_2), \theta \in [-1, 1]\). The Kendall’s Tau \((\tau_\theta)\) corresponding to this copula is \(\tau_\theta = \frac{2}{9} \theta\). We consider the cases \(\theta = -1, -0.5, 1\) reporting association levels between \(X^*\) and \(U^*\) equal to \(-0.2, -0.1\) and \(0.2\) (Models 1.1-1.3 respectively). Specifically, the simulation algorithm is as follows (cfr. Exercise 3.23 in Nelsen (2006)):

Step 1 Generate two independent uniform \((0, 1)\) variables \(X^*\) and \(T\);

Step 2 Set \(a = 1 + \theta(1 - 2X^*)\) and \(b = \sqrt{(a^2 - 4(a - 1)T)}\);

Step 3 Set \(U^* = 2T/(b - a)\);

Step 4 The desired pair is \((X^*, U^*)\), satisfying the condition \(U^* \leq X^* \leq U^* + \phi\);

Step 5 Update \(U^*\) to be \(U^* - 0.6\) according to its support \((-0.6, 0.4)\)
where $D_1(\alpha) = \frac{1}{\alpha} \int_0^\infty \frac{t-1}{\alpha t} dt$ is a Debye function of the first kind. We consider the cases $\theta = -2.1, -1, 1.86, 5.74, 20.9$ corresponding to association levels of $-0.2, -0.1, 0.2, 0.5$ and $0.9$ respectively (Models 2.1-2.5). The simulation algorithm is as follows (cfr. Exercise 4.17 in Nelsen (2006)):

Step 1 Generate two independent uniform $(0, 1)$ variables $T$ and $U^*$;
Step 2 Set $X^* = -(1/\theta) \log(1 + (T(\exp(-\theta) - 1))/(T + (1 - T) \exp(-\theta \times U^*)))$;
Step 3 The desired pair is $(X^*, U^*)$, satisfying the condition $U^* \leq X^* \leq U^* + \phi$;
Step 4 Update $U^*$ to be $U^* - 0.6$ according to its support $(-0.6, 0.4)$.

In Case 3 the variables $X^*$ and $U^*$ follow a Clayton copula family with generator $\psi_\theta(t) = \theta^{-1}(t^{-\theta} - 1), \theta > 0$, i.e.,

$$C_\theta(u_1, u_2) = \left(u_1^{-\theta} + u_2^{-\theta} - 1\right)^{-1/\theta}, \theta \in (0, \infty).$$

This copula implies a Kendall’s Tau $\tau_\theta = \frac{\theta}{\theta + 2}$. We consider the cases $\theta = 0.5, 2, 18$ corresponding respectively to association levels of $0.2, 0.5$ and $0.9$ (Models 3.1-3.3). The simulation algorithm is as follows (cfr. Exercise 4.17 in Nelsen (2006)):

Step 1 Generate independent random variables $Y_1, Y_2 \sim \text{Exp}(1)$;
Step 2 Independently generate $Z_0 \sim \Gamma(1/\theta, 1)$, and compute $U^* = (1 + Y_2/Z_0)^{(-\theta)}$;
Step 3 Finally compute $X^* = (1 + Y_1/Z_0)^{(-\theta)}$;
Step 4 The desired pair is $(X^*, U^*)$, satisfying the condition $U^* \leq X^* \leq U^* + \phi$;
Step 5 Update $U^*$ to be $U^* - 0.6$ according to its support $(-0.6, 0.4)$.

The values of $\theta$ for the several copulas correspond to the same association levels (Kendall’s Tau). This will be interesting when interpreting the simulation results. The simulated scenarios result in different truncations proportions according to the different copula families and parameter values ($\theta$) considered. For instance, in Case 1, the proportion of truncation ranges from 4% (Model 1.3) to 13% (Model 1.1); in Case 2, from 1% (Model 2.4) to 13% (Model 2.1); and in Case 3, from 1% (Model 3.1) to 8% (Model 3.3).

In Figures 1 to 3 we report the MSE of the proposed estimators ($\hat{F}$ and $\hat{K}$) for each $\theta$ and for the several copulas, computed along 1000 Monte Carlo trials of size $n = 250$ and $n = 500$, at the deciles of the distribution of $X^*$. We performed simulations for lower sample sizes ($n = 50, 100$) too, reporting similar results (not shown). The MSEs decrease when increasing the sample size thus suggesting the consistency of the proposed methods. In Figure 1 (Models 1.1 to 1.3, FGM copula) we report the results of both simple and full algorithms (top from bottom). In these figure we see that, in general, the simple algorithm provides MSE’s slightly larger than those of the full algorithm. Since the full algorithm is computationally heavier see Table 3 we have evaluated the relative increase of the MSE when moving from the full to the simple algorithm.
(\(RMSE = (MSE_{\text{simple}} - MSE_{\text{full}})/MSE_{\text{full}}\)) for the four sample sizes \(n = 50, 100, 250, 500\) and all the simulated scenarios, see Table 1. In this table we see that the median increase is only of 1.19%, 0.65%, or 0% depending on the copula (FGM, Frank and Clayton resp.). Besides, by looking at the first quartile of \(RMSE\) we see that the simple method is doing it better than the full method at least 25% of the times. On the other hand, the third quartiles reveal that 75% of the times the RMSE is below 5%, 3.8% or 2.43% depending again on the copula. Models for which the full algorithm report the best relative performance are those with large negative association, particularly when estimating \(K\).

Overall, the simple algorithm seems to be the best option according to its good relative performance and computational speed. This is why we only display the results corresponding to the simple algorithm for Frank and Clayton copulas.

In Table 2 we display the bias and standard deviation of the estimator \(\hat{\theta}\) obtained from the simple algorithm along the 1,000 trials, for each copula function and sample sizes \(n = 250, 500\). As expected, it is seen that the bias and
Figures 2. MSE's of the proposed estimators $\hat{F}$ and $\hat{K}$, in each decile, for Clayton copula. $N = 250$ (left) $N = 500$ (right). Case2.

Figures 3. MSE's of the proposed estimators $\hat{F}$ and $\hat{K}$, in each decile, for Frank copula. $N = 250$ (left) $N = 500$ (right). Case3.

|          | $Q_1$  | $Q_2$  | $Q_3$  | Mean  |
|----------|--------|--------|--------|-------|
| FGM      | -0.0045| 0.0119 | 0.0500 | 0.0221|
| Frank    | -0.0166| 0.0065 | 0.0280 | 0.0026|
| Clayton  | -0.0248| 0.0000 | 0.0243 | 0.0010|

Table 1. The quartiles and mean of the overall RMSE's, considering the sample sizes $n = 50, 100, 250$ and 500 on each function $F$ and $K$ for different $\theta$'s and copula.

The standard deviation decrease when increasing the sample size. The bias and the standard deviation get larger as the association degree increases, although an exception to this is found for the standard deviation and FGM copula.

We have computed the bias and variance of the NPMLE proposed by Shen (2010) for the functions $F$ and $K$, which ignores the possible dependence between $X^*$ and $U^*$. While the variance of the NPMLE and that of the
Table 2. The bias and the standard deviation of the estimator $\hat{\theta}$ obtained from the simple algorithm along the 1,000 trials, for each copula function and sample sizes $n = 250, 500$.

| Copula | n   | $\theta$ | Bias($\hat{\theta}$) | sd($\hat{\theta}$) |
|--------|-----|----------|----------------------|---------------------|
|        | -1  | 0.0712   | 0.1133               |
|        | 250 | -0.5     | -0.0122              | 0.2307              |
|        | 1   | -0.0851  | 0.1293               |
| FGM    |     |          |                      |
|        | -1  | 0.0505   | 0.0817               |
|        | 500 | -0.5     | -0.0020              | 0.1634              |
|        | 1   | -0.0574  | 0.0915               |
|        | -2.1| -0.0844  | 0.6568               |
|        | -1  | -0.0482  | 0.5358               |
|        | 250 | 1.86     | 0.0086               | 0.4535              |
|        | 5.74| 0.0327   | 0.5453               |
|        | 20.9| -0.1879  | 1.3279               |
|        | -2.1| -0.0125  | 0.4609               |
|        | -1  | -0.0063  | 0.3904               |
|        | 500 | 1.86     | 0.0076               | 0.3353              |
|        | 5.74| 0.0130   | 0.3895               |
|        | 20.9| -0.1145  | 0.9041               |
|        | 0.5 | 0.0564   | 0.0725               |
|        | 250 | 2        | -0.0723              | 0.1338              |
|        | 18  | -0.0852  | 0.2523               |
| Clayton |     |          |                      |
|        | 0.5 | 0.0412   | 0.0548               |
|        | 500 | 2        | 0.0523               | 0.0929              |
|        | 18  | 0.0684   | 0.1786               |

copula-based estimator are of the same order (results not shown), the bias of the NPMLE can be two orders of magnitude larger than that corresponding to the proposed estimator. This can be seen from Figure 4, in which the bias of the NPMLE for the three copulas under several dependence degrees is depicted for $n = 500$ (the case $n = 250$ reported similar results). As expected, this bias becomes more visible as the association level grows. For instance, in Case 1, the bias of the NPMLE of $F$ when $\theta = 1$ is approximately 1.8 times that corresponding to $\theta = -0.5$ (Figure 4 top left panel); similar results hold for $K$ (Figure 4 top right panel). In Case 2, the bias of the NPMLE of $F$ when $\theta = 20.9$ is approximately 2.4 times that corresponding to $\theta = 1.86$.

As mentioned in Section 1, the bootstrap method can be applied to estimate the standard error of both the marginal distributions and the copula parameter. We have evaluated the performance of the copula-based bootstrap method when estimating the standard error of $\hat{\theta}$. To this end, we have computed the ratio between the bootstrap standard error and the true standard deviation of $\hat{\theta}$ along 500 Monte Carlo trials (the true standard error was approximated by the Monte Carlo standard deviation). In Table 3 we report the mean and the standard
Figure 4. Bias of the NMLE proposed by Shen, in each decile, and each functions $F$ (left) and $K$ (right), for FGM, Frank and Clayton copulas (from top to bottom), with sample size $n = 500$ and different $\tau$’s.
deviation of this ratio $Q$ along the simulated runs for the three copula functions with $n = 50$ and $n = 250$. From this table it is seen that the bootstrap performs well, giving a more accurate estimation of the standard error of $\hat{\theta}$ as the sample size increases.

| n   | Copula | mean (Q) | sd(Q) |
|-----|--------|----------|-------|
| 50  | FGM    | 0.8804   | 0.2108|
|     | Clayton| 0.9102   | 0.2019|
|     | Frank  | 1.0828   | 0.1909|
| 250 | FGM    | 1.0047   | 0.1135|
|     | Clayton| 0.9872   | 0.1023|
|     | Frank  | 1.0001   | 0.0900|

Table 3. Mean and standard error of the quotient $Q$.

3 Real data illustration

For illustration purposes, in this section we consider epidemiological data on transfusion-related Acquired Immune Deficiency Syndrome (AIDS). The AIDS Blood Transfusion Data are collected by the Centers for Disease Control (CDC), which is from a registry data base, a common source of medical data (see Bilker and Wang (1996); Kalbfleisch and Lawless (1989)). The variable of interest ($X^*$) is the induction or incubation time, which is defined as the time elapsed from Human Immunodeficiency virus (HIV) infection to the clinical manifestation of full-blown AIDS. The CDC AIDS Blood Transfusion Data can be viewed as being doubly truncated. The data were retrospectively ascertained for all transfusion-associated AIDS cases in which the diagnosis of AIDS occurred prior to the end of the study, thus leading to right-truncation. Besides, because HIV was unknown prior to 1982, any cases of transfusion-related AIDS before this time would not have been properly classified and thus would have been missed. Thus, in addition to right-truncation, the observed data are also truncated from the left. See Bilker and Wang (1996), section 5.2, for further discussions.

The data include 494 cases reported to the CDC prior to January 1, 1987, and diagnosed prior to July 1, 1986. Of the 494 cases, 295 had consistent data, and the infection could be attributed to a single transfusion or short series of transfusions. Our analyses are restricted to this subset, which is entirely reported in Kalbfleisch and Lawless (1989), Table 1. Values of $U^*$ were obtained by measuring the time from HIV infection to January 1, 1982; while $V^*$ was defined as time from HIV infection to the end of study (July 1, 1986). Note that the difference between $V^*$ and its respective $U^*$ is always 4.5 years.

More specifically, our goal is to correct the Efron-Petrosian estimator of $F$ for the possible dependence between AIDS incubation time and the date of HIV infection (left truncation variable). In order to assess this dependence, in Table 4 we report the value of $\hat{\theta}$ (as well as the corresponding Kendall’s Tau $\tau_\theta$) obtained from the two proposed algorithms (full and simple), for the three copula families (FGM, Clayton and Frank). The number of iterations needed for
each convergence for each algorithm and copula function are included. Bootstrap standard errors and 95% confidence intervals based on the bootstrap and the normal approximation are reported too. From this Table 4 it is seen that (a) the three copulas indicate a positive association between $U^*$ and $X^*$, as it was anticipated in , and (b) the full algorithm is more computationally demanding. An exception to conclusion (b) is found for the Clayton copula, for which the full algorithm fails to provide a likely value for $\theta$. A possible explanation for this is that the full algorithm is unable to get away from the initial values of $(\theta, F, K)$ (the ones corresponding to the independent setting) when using this particular Copula. The second and third order derivatives of the Clayton copula are unbounded when $u_1, u_2$ go to zero, so, for small values of $F$ and $K$, we get that the value of the different weights $W$ containing these second order derivatives gets very big and will dominate the likelihood function and also the optimum. The small number of iterations needed to achieve the optimal value for the Clayton copula is much smaller than for the other copula functions. This indicates that possibly a local optimum has been reached instead of the global optimum. For the FGM copula and Frank copula we do not have this problem. For the FGM copula, we also, however, note that the optimal value of theta is reached at the upper limit of the parameter space of possible theta values for this copula. This means that the association is in-fact larger than what can be obtained by this copula function. Hence this copula function is not properly suited to look at the association between the incubation time and the truncation time.

In Figure 5 (simple and full algorithms) the cumulative df for the incubation times (left panels) and the truncation time $U$ (right panels) using the three copulas and the NPMLE under independence are jointly depicted. From this Figure it is seen that the choice of the copula has some influence in the resulting estimator; however, in general, all the copulas are able to somehow correct the negative (resp. positive) bias of the NPMLE of the incubation time (resp. left-truncation time) distribution under independence. In this aspect, we note that only the Frank copula function is able to take the full association between the incubation time and the truncation time into account. The FGM-copula tries to do this but is restricted by its limited parameter space and therefore delivers a result between the result of the Frank copula and the independence setting. As discussed, the results for the full algorithm based on the Clayton copula should not be taken as realistic.

4 Conclusions

In this paper we have introduced an extension of the Efron-Petrosian NPMLE when the lifetime and the truncation times may be dependent. We assume that $U^*$ depends on the lifetime, and that the dependence structure of $(X^*, U^*)$ is given by a copula function, with arguments $\theta$, $F$ and $G$. Two different algorithms to estimate the parameter $\theta$ and the distributions $F$ and $G$ have been introduced, the full and the simple algorithms.

The performance of these two algorithms has been evaluated though simulations for several copula functions and marginal models. Both estimators
| Copula | n. iter | \( \hat{\theta} \) | SEboot | Interval | Kendall’s \( \tau \) |
|--------|---------|----------------|--------|----------|------------------|
| FGM    | 55      | 0.982          | 0.3273 | (0.3404;1.6235) | 0.22             |
| Clayton| 114     | 0.487          | 0.0785 | (0.3330;0.6408) | 0.20             |
| Frank  | 179     | 3.35           | 0.7758 | (1.8294;4.8706) | 0.38             |
| FGM    | 131     | 1              | 0.2425 | (0.5246;1.4754) | 0.22             |
| Clayton| 25      | 0.07           | 0.0584 | (-0.0445;0.1845) | 0.03             |
| Frank  | 186     | 3.46           | 0.6452 | (2.1954;4.7245) | 0.38             |

Table 4. Number of iterations, estimated \( \hat{\theta} \), the correspondent Kendall’s \( \tau \), the standard error and the confidence interval for \( \hat{\theta} \), using both algorithms, simple (top) and full (bottom). AIDS data.

Figure 5. Cumulative distribution function for the incubation times (left) and the truncation time \( U \) (right) using FGM copula (red dashed line), Clayton copula (blue dashed line), Frank copula (green dashed line) and the NPMLE of Efron and Petrosian (black solid line). Simple algorithm (top) and Full algorithm (bottom). AIDS data.

are asymptotically equivalent in the sense of their convergence to the same solution. While the simple algorithm provides MSE’s slightly larger than those of the full algorithm, but the full algorithm has revealed computationally heavier. The evaluations of the RMSE’s allows to concluded that the simple algorithm
is the best option according to its good relative performance and computational speed. The systematic bias of the Efron-Petrosian NPMLE under dependence has been evaluated too, being more evident for a stronger dependence degree.

In order to estimate the standard error of both the marginal distributions and the copula parameter we have introduced a bootstrap procedure. In our simulation studies the bootstrap performs well, giving a more accurate estimation of the standard error of \( \hat{\theta} \) with an increasing sample size.

A real data illustration has been provided. We have applied both algorithms to correct the Efron-Petrosian estimator of \( F \) for the possible dependence between AIDS incubation time and the date of HIV infection, for different copula families (FGM, Clayton and Frank). The three copulas indicated a positive association between \( U^* \) and \( X^* \) when applying both algorithms. An exception was found for the Clayton copula, for which the full algorithm failed to provide a likely value for \( \theta \), a numerical issue probably related to the instability of the third-order derivatives of the Clayton copula around zero.

Appendix

With the notations in Section 1, the joint density of \((X^*, U^*)\) conditionally on \( U^* \leq X^* \leq U^* + \phi \) at point \((x, u)\) is given by

\[
\frac{C_{\theta}^{(1,1)}(F(x), G(u)) f(x) k(u)}{\int_{u \leq x \leq u + \phi} C_{\theta}^{(1,1)}(F(x), G(u)) dF(x) dG(u)}.
\]

This justifies the likelihood (1). In order to get the NPMLE for \( \theta, f \) and \( k \), we maximize the likelihood function (1), under the constraints \( \sum_{i=1}^{n} f_i = 1 \) and \( \sum_{i=1}^{n} k_i = 1 \). The loglikelihood is given by

\[
\log L(\theta, f, k) = \sum_{i=1}^{n} \left[ \log(f_i) + \log(k_i) + \log(W_{ii}^{(1,1)}) - \log \left( \sum_{j=1}^{n} \sum_{m=1}^{n} W_{jm}^{(1,1)} f_j k_m J_{jm} \right) \right],
\]

from which

\[
\frac{\partial \log L(\theta, f, k)}{\partial f_m} =
\]

\[
= \frac{1}{f_m} + \sum_{i=1}^{n} \frac{W_{ii}^{(2,1)}}{W_{ii}^{(1,1)}} I_{[x_m \leq x_i]} - \sum_{j=1}^{n} \sum_{l=1}^{n} \left[ W_{jl}^{(2,1)} I_{[x_m \leq x_j]} f_j k_l J_{lj} + W_{jl}^{(1,1)} I_{[x_m = x_j]} k_l J_{lj} \right] / \sum_{j=1}^{n} \sum_{l=1}^{n} W_{jl}^{(1,1)} f_j k_l J_{lj}.
\]
\[
= \frac{1}{f_m} + \sum_{i=1}^{n} \frac{W_{ii}^{(2,1)}}{W_{ii}^{(1,1)}} I_{[X_m \leq X_i]} - \frac{\sum_{j=1}^{n} \sum_{l=1}^{n} W_{jl}^{(2,1)} f_{j,k_l J_l j} I_{[X_m \leq X_j]} + \sum_{l=1}^{n} W_{ml}^{(1,1)} k_l J_{lm}}{\sum_{j=1}^{n} \sum_{l=1}^{n} W_{jl}^{(1,1)} f_{j,k_l J_l j}},
\]
and similarly
\[
\frac{\partial \log L(\theta, f, k)}{\partial k_m} =
= \frac{1}{k_m} + \sum_{i=1}^{n} \frac{W_{ii}^{(1,2)}}{W_{ii}^{(1,1)}} I_{[U_m \leq U_i]} - \frac{\sum_{j=1}^{n} \sum_{l=1}^{n} W_{jl}^{(1,2)} f_{j,k_l J_l j} I_{[U_m \leq U_j]} + \sum_{j=1}^{n} W_{jm}^{(1,1)} f_{j,J_{mj}}}{\sum_{j=1}^{n} \sum_{l=1}^{n} W_{jl}^{(1,1)} f_{j,k_l J_l j}}.
\]
Solving the equation \( \frac{\partial \log L(\theta, f, k)}{\partial f_m} = 0 \) we get
\[
\frac{1}{f_m} = \frac{\sum_{j=1}^{n} \sum_{l=1}^{n} W_{jl}^{(2,1)} f_{j,k_l J_l j} I_{[X_m \leq X_j]} + \sum_{l=1}^{n} W_{ml}^{(1,1)} k_l J_{lm}}{\sum_{j=1}^{n} \sum_{l=1}^{n} W_{jl}^{(1,1)} f_{j,k_l J_l j}} - \sum_{i=1}^{n} \frac{W_{ii}^{(2,1)} I_{[X_m \leq X_i]}}{W_{ii}^{(1,1)}}
\]
from which
\[
f_m =
= \frac{\sum_{j=1}^{n} \sum_{l=1}^{n} W_{jl}^{(1,1)} f_{j,k_l J_l j}}{n \sum_{j=1}^{n} \sum_{l=1}^{n} W_{jl}^{(2,1)} f_{j,k_l J_l j} I_{[X_m \leq X_j]} + n \sum_{l=1}^{n} W_{ml}^{(1,1)} k_l J_{lm} - \sum_{j=1}^{n} \sum_{l=1}^{n} W_{jl}^{(1,1)} f_{j,k_l J_l j} + \sum_{i=1}^{n} \frac{W_{ii}^{(2,1)} I_{[X_m \leq X_i]}}{W_{ii}^{(1,1)}}}
\]
\[
= \frac{\alpha}{nA_m + nK_m^W - \alpha B_m}.
\]
Since \( \sum_{m=1}^{n} f_m = 1 \), we get that
\[
\alpha \sum_{m=1}^{n} \frac{1}{nA_m + nK_m^W - \alpha B_m} = 1
\]
Then,
\[
\alpha = \left[ \sum_{m=1}^{n} \frac{1}{nA_m + nK_m^W - \alpha B_m} \right]^{-1}.
\]
This proves the score equation (4).

To justify the score equation (5), from \( \frac{\partial \log L(\theta, f, k)}{\partial k_m} = 0 \), we have similarly:

\[
\frac{1}{k_m} = \frac{\sum_{j=1}^{n} \sum_{l=1}^{n} W_{jl}^{(1,2)} f_j k_l J_{lj} I_{[U_m \leq U_k]} + \sum_{j=1}^{n} W_{jm}^{(1,1)} f_j J_{mj}}{\alpha} - \sum_{i=1}^{n} \frac{W_{ii}^{(1,2)} I_{[U_m \leq U_i]}}{W_{ii}^{(1,1)}}.
\]

From this equation and since \( \sum_{m=1}^{n} k_m = 1 \), we get (5).

\[
k_h = \left[ \sum_{m=1}^{n} \frac{1}{n} \sum_{j=1}^{n} \sum_{l=1}^{n} W_{jl}^{(1,2)} f_j k_l J_{lj} I_{[X_m \leq X_i]} + \sum_{l=1}^{n} W_{ml}^{(1,1)} k_l J_{lm} - \alpha \sum_{i=1}^{n} W_{ii}^{(2,1)} I_{[X_m \leq X_i]} W_{ii}^{(1,1)} \right]^{-1}
\times \frac{1}{n} \sum_{j=1}^{n} \sum_{l=1}^{n} W_{jl}^{(1,2)} f_j k_l J_{lj} I_{[U_m \leq U_k]} + \sum_{j=1}^{n} W_{j}^{(1,1)} f_j J_{hj} - \alpha \sum_{i=1}^{n} W_{ii}^{(2,1)} I_{[U_m \leq U_i]} W_{ii}^{(1,1)}
\]

References

Austin, M. D. and R. A. Betensky (2014). Eliminating bias due to censoring in kendall’s tau estimators for quasi-independence of truncation and failure. *Comput. Stat. Data Anal. 73*, 16–26.

Bilker, W. B. and M.-C. Wang (1996). A semiparametric extension of the mann-whitney test for randomly truncated data. *Biometrics 52*, 10–20.

Chaieb, L., L.-P. Rivest, and B. Abdous (2006). Estimating survival under a dependent truncation. *Biometrika 93*, 655–669.

Ding, A. A. (2012, Oct). Copula identifiability conditions for dependent truncated data model. *Lifetime Data Analysis 18*(4), 397–407.

Efron, B. and V. Petrosian (1999). Nonparametric methods for doubly truncated data. *Journal of the American Statistical Association 94*, 824–834. MR1723343.

Emura, T. and Murotani, K. (2015). An algorithm for estimating survival under a copula-based dependent truncation model. *TEST 24*(4), 734–751.

Emura, T. and W. Wang (2012). Nonparametric maximum likelihood estimation for dependent truncation data based on copulas. *Journal of Multivariate Analysis 110*, 171 – 188.

Emura, T., W. Wang, and H.-N. Hung (2011). Semi-parametric inference for copula models for truncated data. *Statistica Sinica 21*(1), 349–367.

Kalbfleisch, J. D. and J. F. Lawless (1989). Inference based on retrospective ascertainment: An analysis of the data on transfusion-related aids. *American Statistical Association 84*, 360–372.
Moreira, C. and J. de Uña-Álvarez (2010). Bootstrapping the npmle for doubly truncated data. *Journal of Nonparametric Statistics* 22, 567–583. MR2682208.

Nelsen, R. B. (2006). *An Introduction to Copulas (Springer Series in Statistics).* Secaucus, NJ, USA: Springer-Verlag New York, Inc.

Shen, P. (2010). Nonparametric analysis of doubly truncated data. *Annals of the Institute of Statistical Mathematics* 62, 835–853.

Woodroofe, M. (1985). Estimating a distribution function with truncated data. *The Annals of Statistics* 13, 163–177. MR0773160.

Zhu, H. and M.-C. Wang (2012). Analysing bivariate survival data with interval sampling and application to cancer epidemiology. *Biometrika* 99(2), 345–361.

Zhu, H. and M.-C. Wang (2014). Nonparametric inference on bivariate survival data with interval sampling: association estimation and testing. *Biometrika* 101(3), 519–533.