Consistency of survival tree and forest models:

splitting bias and correction

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Abstract: Random survival forests and survival trees are popular models in statistics and machine learning. However, there is a lack of general understanding regarding consistency, splitting rules and influence of the censoring mechanism. In this paper, we investigate the statistical properties of existing methods from several interesting perspectives. First, we show that traditional splitting rules with censored outcomes rely on a biased estimation of the within-node failure distribution. To exactly quantify this bias, we develop a concentration bound of the within-node estimation based on non i.i.d. samples and apply it to the entire forest. Second, we analyze the entanglement between the failure and censoring distributions caused by univariate splits, and show that without correcting the bias at an internal node, survival tree and forest models can still enjoy consistency under suitable conditions. In particular, we demonstrate this property under two cases: a finite-dimensional case where the splitting variables and cutting points

are chosen randomly, and a high-dimensional case where the covariates are weakly correlated. Our results also apply to an independent covariate setting, which is commonly used in the random forest literature for high-dimensional sparse models. However, it may be unavoidable that the convergence rate depends on the total number of variables in the failure and censoring distributions. Third, we propose a new splitting rule that compares bias-corrected cumulative hazard functions at each internal node. We show that the rate of consistency of this new model depends only on the number of failure variables. We perform simulation studies to confirm that the proposed bias-correction can substantially benefit the prediction error.

Key words and phrases: Random Forests, Survival Analysis, Consistency, Adaptive Concentration, Bias Correction

1. Introduction

Random forest [9] is among the most popular and powerful machine learning tools. The main advantage of tree-based [11] models is their nonparametric nature. Although there has been a surge of research on understanding random forests, their theoretical properties have not been fully understood, even in regression settings. [26] is one of the early attempts to connect random forests to nearest neighbor predictors. Later on, a series of works including [6, 5, 18] and [28] established theoretical results on simplified tree-building processes or specific aspects of the model. More recently, [43]

established consistency results based on an improved splitting rule criteria; [39, 4] analyzed the confidence intervals induced from a random forest model; [27] established connections with Bayesian variable selection in the high-dimensional setting; [35] showed consistency of the original random forests model on an additive model structure; and [40] studied the variance component of random forests and established corresponding concentration inequalities. For a comprehensive review of related topics, we refer to [7, 4].

In this paper, we focus on the theoretical properties of a particular type of model, in which the outcomes are right-censored [17]. Censored survival data frequently appear in biomedical studies when the actual clinical outcome may not be directly observed due to early dropout or other reasons. Many random forest models have been developed for survival outcomes. This includes [21, 20, 23, 42, 36, 13], and many others. However, there are few established theoretical results despite the popularity of these methods in practice, especially in genetic and clinical studies. For a general review of related topics, including single-tree based survival models, we refer to [8]. To the best of our knowledge, the only consistency result to date is given by [22] who considered the setting where all predictors are categorical. Some other results are established based on augmented outcomes which transform the problem to a fully observed regression model [37].

Our analysis provides insights into the consistency of survival forests and trees in general settings. In particular, we investigate whether existing methodologies enjoy consistency if the splitting rule is searched by comparing the survival distributions of the two potential child nodes. The answer is mixed because a biased selection of the splitting rule may occur if there are marginal dependencies between the failure and censoring variables. We show that this drawback could be overcome in at least two general settings: a finite-dimensional case if the splitting rule is data-independent [5, 25], and a high-dimensional case if the marginal failure distribution signal is sufficiently large. However, the convergence rate may inevitably depend on the total dimension of variables that are involved in both the failure and the censoring models. This phenomenon occurs even when the covariates are uniformly distributed, as long as the failure and censoring times are not marginally independent. Such a result is surprising compared with traditional parametric and semiparametric survival literature. However, it demonstrates the complexity of random forest models due to the marginal splitting nature.

Motivated by above results, we propose a new bias-correction procedure that actively selects the best splitting variable at each internal node without the influence of the censoring distribution. This establishes a con-

nection with existing methodology developments such as [20] and [37] who convert censored observations to fully observed ones through the inverse probability of censoring weighting. However, our proposed splitting rule is much more general in the sense that it compares the distributions of failure time from the two potential child nodes, rather than focusing on the mean differences. We further show that this new approach untangles the failure and censoring distributions, and improves the rate of convergence of tree and forest models so that the rate depends only on the number of important variables that define the failure distribution. Simulation studies are provided in Appendices to confirm that the proposed bias-correction can substantially benefit the prediction error.

2. Survival tree and forest models

The essential element of tree-based survival models is recursive partitioning. A d-dimensional feature space $\mathcal{X}$ is partitioned into terminal nodes. For a single tree model, we denote the collection of these terminal nodes as $\mathscr{A} = \{\mathcal{A}_u\}_{u \in \mathcal{U}}$, where $\mathcal{U}$ is a set of indices, $\mathcal{X} = \bigcup_{u \in \mathcal{U}} \mathcal{A}_u$ and $\mathcal{A}_u \cap \mathcal{A}_l = \emptyset$ for any $u \neq l$. We also call $\mathscr{A}$ a partition of the feature space $\mathcal{X}$. In a traditional tree-building process [11], binary splitting rules are used. Hence all terminal node are hyper-rectangles.

Following standard notations in the survival analysis literature, let $\mathcal{D}_n = \{X_i, Y_i, \delta_i\}_{i=1}^n$ be a set of n i.i.d. copies of the covariates, observed survival time, and censoring indicator, where the observed survival time $Y_i = \min(T_i, C_i)$, and $\delta_i = \mathbb{1}(T_i \leq C_i)$. We assume that each T_i follows a conditional distribution $F_i(t) = \mathrm{pr}(T_i \leq t \mid X_i)$, where the survival function is denoted by $S_i(t) = 1 - F_i(t)$, the cumulative hazard function (CHF) $\Lambda_i(t) = -\log\{S_i(t)\}$, and the hazard function $\lambda_i(t) = \mathrm{d}\Lambda_i(t)/\mathrm{d}t$. The censoring time C_i follows the conditional distribution $G_i(t) = \mathrm{pr}(C_i \leq t \mid X_i)$, where a non-informative censoring mechanism, $T_i \perp C_i \mid X_i$, is assumed.

In tree-based survival models, terminal node estimation is a crucial part. For any node $\mathcal{A}_u$, this can be obtained through the Kaplan-Meier [24] estimator for the survival function or the Nelson-Aalen [31, 1] estimator of the CHF based on the within-node samples. Our focus in this paper is on the following Nelson-Aalen estimator

$$\widehat{\Lambda}_{\mathcal{A}_u,n}(t) = \sum_{s \leq t} \frac{\sum_{i=1}^n \mathbb{1}(\delta_i = 1)\mathbb{1}(Y_i = s)\mathbb{1}(X_i \in \mathcal{A}_u)}{\sum_{i=1}^n \mathbb{1}(Y_i \geq s)\mathbb{1}(X_i \in \mathcal{A}_u)}, \qquad (2.1)$$

and the associated Nelson-Altshuler estimator [2] for the survival function when needed:

$$\widehat{S}_{\mathcal{A}_u,n}(t) = \exp\left\{-\widehat{\Lambda}_{\mathcal{A}_u,n}(t)\right\}.$$

A survival tree model yields a collection of doublets $\{\mathcal{A}_u, \widehat{\Lambda}_{\mathcal{A}_u,n}\}_{u \in \mathcal{U}}$.

In a survival forest model [23, 42], a set of B trees are fitted. Hence, a collection of partitions $\{\{\mathcal{A}_u^b, \widehat{\Lambda}_{\mathcal{A}_u^b, n}\}_{u \in \mathcal{U}_b}\}_{b=1}^B$ is constructed. To facilitate better understanding, we provide a high-level outline (Algorithm 1 in Appendix S1) of a survival forest model.

3. Biasedness of splitting rules

3.1 Within-node estimation

To begin our analysis, we start by investigating the Kaplan-Meier (KM) and the Nelson-Altshuler (NA) estimators of the survival function. The main reason we revisit these classical methods is that these methods are wildly used for terminal node estimation in fitted survival trees. The following lemma bounds their difference through an exact inequality regardless of the underlying data distribution. The proof follows mostly from [15] and is given in the Appendices.

Lemma 1. *Let $\widehat{S}_{KM}(t)$ and $\widehat{S}_{NA}(t)$ be the Kaplan-Meier and the Nelson-Altshuler estimators, respectively, obtained using the same set of samples $\{Y_i, \delta_i\}_{i=1}^n$. Then we have,*

$$|\widehat{S}_{KM}(t) - \widehat{S}_{NA}(t)| < \widehat{S}_{KM}(t) \frac{4}{\sum_{i=1}^n \mathbb{1}(Y_i \geq t)},$$

for any observed failure time point t such that $\widehat{S}_{KM}(t) > 0$.

The above result suggests that calculating the difference between two KM curves is asymptotically the same as using the NA estimator as long as we only calculate the curve up to a time point where the sample size is sufficiently large. For this purpose, Assumption 1 is always used throughout this paper. Note that similar assumptions are commonly used in the survival analysis literature, for examples, $\mathrm{pr}(T \geq \tau) > 0$ in [17], and $\mathrm{pr}(C \geq \tau) > 0$ in [30] for some maximum study follow-up time τ. Then, with large probability, $\widehat{S}_{NA}(t) = \widehat{S}_{KM}(t) + O(1/n)$ across all terminal nodes.

Assumption 1. *There exists a fixed maximum follow-up time $0 < \tau < \infty$ and a constant $M \in (0,1)$, such that*

$$\mathrm{pr}(Y \geq \tau \mid X = x) \geq M,$$

for all $x \in \mathcal{X}$.

3.2   A motivating example

Noticing that the splitting rule selection process is essentially comparing the survival curves computed from two potential child nodes, we take a closer look at this process. Most existing analyses of the KM estimator assume that the observations are i.i.d. [12, 19] or at least one set of the failure times or censoring times are i.i.d. [41]. However, this is almost always not

true for tree-based methods at any internal node because both T_i's and C_i's

typically depend on the covariates. The question is whether this affects

the selection of the splitting variable. We first use a simulation study to

demonstrate this issue.

Consider the split at a particular node. We generate three random

variables: $X^{(1)}$, $X^{(2)}$ and $X^{(3)}$ from a multivariate normal distribution with

mean 0 and covariance matrix Σ, where all diagonal elements of Σ are 1,

and the nonzero off-diagonal elements are $\Sigma_{12} = \Sigma_{21} = 0.8$. The failure dis-

tribution is exponential with mean $\exp(-1.25X^{(1)} - X^{(3)} + 2)$. We consider

two censoring distributions for C: an exponential distribution with mean 2

for all subjects, i.e., independent of T; and the second one is an exponential

distribution with mean equal to $\exp(-3X^{(2)})$. The splitting rule is searched

for by maximizing the log-rank test statistic between the two potential child

nodes $\{X^{(j)} \leq c, X \in \mathcal{A}\}$ and $\{X^{(j)} > c, X \in \mathcal{A}\}$, and the cutting point c

is searched on the range of the variable. In an ideal situation, one would

expect the best splitting rule to be constructed using $X^{(1)}$ with large prob-

ability, since it carries the most signal. This is indeed the case shown in

the first row of Table 1 for the i.i.d. censoring case, but not so much for

the dependent censoring case. The simulation is done with $n = 1000$ and

repeated 1000 times. While this only demonstrates the splitting process on

a single node, the consequence of this on the consistency of the entire tree is much more involved since the entire tree structure can be altered by the censoring distribution. It is difficult to draw a definite conclusion at this point, but the impact of the censoring distribution is clearly demonstrated.

Table 1: Probability of selecting the splitting variable.

Censoring distribution	$X^{(1)}$	$X^{(2)}$	$X^{(3)}$
G_i identical	0.978	0.001	0.021
G_i depends on $X_i^{(2)}$	0.281	0.037	0.682

3.3   Survival estimation based on non i.i.d. observations

It now seems impossible to analyze the consistency without exactly quantifying the within node estimation performance. We look at two different quantities corresponding to the two scenarios used above. The first one is an averaged CHF within any node $\mathcal{A}$:

$$\Lambda_{\mathcal{A}}(t) = \frac{1}{\mu(\mathcal{A})} \int_{x \in \mathcal{A}} \Lambda(t \mid x) \mathrm{d}\mathrm{P}(x), \tag{3.2}$$

where P is the distribution of X, and $\mu(\mathcal{A}) = \int_{x \in \mathcal{A}} \mathrm{d}\mathrm{P}(x)$ is the measure of node $\mathcal{A}$. Clearly, since in the first case, the censoring distribution is not covariate dependent, we are asymptotically comparing $\Lambda_{\mathcal{A}}(t)$ on the two

child nodes, which results in the selection of the first variable. This should also be considered as a rational choice since $X^{(1)}$ contains more signal at the current node.

In the second scenario, i.e., the dependent censoring case, the within-node estimator $\widehat{\Lambda}_{\mathcal{A},n}(t)$ does not converge to the $\Lambda_{\mathcal{A}}(t)$ in general, which can be inferred from the following theorem. As the main result of this section, Theorem 1 is interesting in its own right for understanding tree-based survival models, since it establishes a bound on the survival estimation under independent but non-identically distributed samples, which is a more general result than [41]. It quantifies exactly the estimation performance for each potential child node, hence is also crucial for understanding splitting rules in general.

Theorem 1. *Let $\widehat{\Lambda}_n(t)$ be the Nelson-Aalen estimator of the CHF from a set of n independent samples $\{Y_i, \delta_i\}_{i=1}^n$ subject to right censoring, where the failure and censoring distributions (not necessarily identical) are given by F_i's and G_i's. Under Assumption 1, we have for $\epsilon_1 \leq 2$ and $n > 4/(\epsilon_1^2 M^4)$,*

$$\mathrm{pr}\left(\sup_{t<\tau}\left|\widehat{\Lambda}_n(t) - \Lambda_n^*(t)\right| > \epsilon_1\right) < 16(n+2)\exp\left\{\frac{-nM^4\epsilon_1^2}{1152}\right\}, \qquad (3.3)$$

where

$$\Lambda_n^*(t) = \int_0^t \frac{\sum[1-G_i(s)]\mathrm{d}F_i(s)}{\sum[1-G_i(s)][1-F_i(s)]}. \qquad (3.4)$$

The proof is deferred to Appendix S2. Based on Theorem 1, if we restrict ourselves to any node $\mathcal{A}$, the difference between the within-node estimator $\widehat{\Lambda}_{\mathcal{A},n}(t)$ and

$$\Lambda^*_{\mathcal{A},n}(t) = \int_0^t \frac{\sum_{X_i \in \mathcal{A}}[1 - G_i(s)]\mathrm{d}F_i(s)}{\sum_{X_i \in \mathcal{A}}[1 - G_i(s)][1 - F_i(s)]} \qquad (3.5)$$

is bounded above, where $\Lambda^*_{\mathcal{A},n}(t)$ is some version of the underlying true cumulative hazard contaminated by the censoring distribution. Noting that $\Lambda^*_{\mathcal{A},n}(t)$ also depends on the sampling points X_i's, we further develop Lemma S5 in the Appendix to verify that $\Lambda^*_{\mathcal{A},n}(t)$ and its expected version $\Lambda^*_{\mathcal{A}}(t)$ are close enough, where

$$\Lambda^*_{\mathcal{A}}(t) = \int_0^t \frac{E_{X \in \mathcal{A}}[1 - G(s \mid X)]\mathrm{d}F(s \mid X)}{E_{X \in \mathcal{A}}[1 - G(s \mid X)][1 - F(s \mid X)]}. \qquad (3.6)$$

It is easy to see that the difference between $\Lambda^*_{\mathcal{A},n}(t)$ and $\Lambda_{\mathcal{A}}(t)$ will vanish if the F_i's are identical within a node $\mathcal{A}$ (a sufficient condition). Note that this is what we are hoping for eventually at a terminal node.

$$\Lambda^*_{\mathcal{A},n}(t) = \int_0^t \frac{\sum_{X_i \in \mathcal{A}}[1 - G_i(s)]}{\sum_{X_i \in \mathcal{A}}[1 - G_i(s)]} \frac{\mathrm{d}F(s)}{1 - F(s)}$$

$$(\text{if } F_i \equiv F \text{ for all } X_i \in \mathcal{A})$$

$$= \int_0^t \frac{\mathrm{d}F(s)}{1 - F(s)} = \frac{1}{\mu(\mathcal{A})} \int_{x \in \mathcal{A}} \int_0^t \frac{\mathrm{d}F(s)}{1 - F(s)}\mathrm{d}\mathrm{P}(x) = \Lambda_{\mathcal{A}}(t). \quad (3.7)$$

As we demonstrated in the simulation study above, comparing $\widehat{\Lambda}_{\mathcal{A},n}(t)$ between two child nodes may lead to a systematically different selection

of splitting variables than using $\Lambda_{\mathcal{A}}(t)$ which is not known a priori. The main cause of the differences between these two quantities is that the NA estimator treats each node as a homogeneous group, which is typically not true. Another simple interpretation is that although the conditional independence assumption $T \perp C \mid X$ is satisfied, we have instead $T \not\perp C \mid \mathbb{1}(X^{(j)} < x)$ at an internal node. This tangling between the censoring and failure distributions makes it a very challenging problem because, at each internal node, we may only select one variable to split.

4. Consistency of survival tree and forest

It becomes apparent now that this bias plays an important role in the asymptotic properties of survival tree and forest models. However, an important question we may ask is, whether this affects the consistency of existing methodologies? To answer this question, we provide several analyses of consistency in different settings. Noticing that difficulty arises when the splitting rule is highly data-dependent, we first investigate the consistency under random splitting rules and finite d (Section 4.2) to help our understanding. An analog of this result for regression and classification settings was proposed by [10], and further analyzed by [26, 6, 5, 3] and many others. However, it is significantly more difficult when the splitting rule is

data-dependent, especially when the number of dimensions d is diverging with n. Note that $\widehat{\Lambda}_n(t)$ is a biased estimator of the within node averaged CHF, any marginal comparison splitting rule may falsely select a variable involved in the censoring mechanism. Furthermore, any dependencies in the high-dimensional setting may lead us to further falsely select a noise variable because they will marginally carry signals. Hence, we investigate a high-dimensional setting where the noise variables have weak dependencies with the important variables (to be defined later). Under suitable conditions and some necessary modifications to the tree-build process, we show that a survival tree or forest model can still achieve consistency. However, the rate may be affected by the censoring distribution. To establish these results, we use the variance-bias breakdown, i.e., for any x,

$$\left|\widehat{\Lambda}_n(t \mid x) - \Lambda(t \mid x)\right| \leq \left|\widehat{\Lambda}_n(t \mid x) - \Lambda_n^*(t \mid x)\right| + \left|\Lambda_n^*(t \mid x) - \Lambda(t \mid x)\right|,$$

and start by analyzing the variance component of a survival tree estimator.

4.1   Adaptive concentration bounds of survival trees and forests

We focus on quantifying the survival forest models from a new angle, namely the adaptive concentration [40] of each terminal node estimator to the true within-node expectation. In the sense of the variance-bias breakdown, the goal of this section is to quantify a version of the variance component of

a tree-based model estimator. To be precise, with large probability, our main results bound $\left|\widehat{\Lambda}_{\mathcal{A},n}(t) - \Lambda^*_{\mathcal{A},n}(t)\right|$ across all possible terminal nodes in a fitted tree or forest. The adaptiveness comes from the fact that the target of the concentration is the censoring contaminated version $\Lambda^*_{\mathcal{A},n}(t)$, which is adaptively defined for each node $\mathcal{A}$ with the observed samples, rather than as a fixed universal value. The results in this section have many implications. Since this bound is essentially the variance part of the estimator, we can then focus the bias for showing consistencies. Although this may still pose challenges in specific situations, our later examples of consistency provide a framework that is largely applicable to most existing methods.

We start with some additional definitions and notations. Following our previous assumptions on the underlying data-generating model, we observe a set of n i.i.d. samples $\mathcal{D}_n$. We view each tree as a partition of the feature space, denoted $\mathscr{A} = \{\mathcal{A}_u\}_{u\in\mathcal{U}}$, where the $\mathcal{A}_u$'s are non-overlapping hyper-rectangular terminal nodes. We first define a valid survival tree and forest estimators of the CHF. Roughly speaking, with certain constraints, these are all the possible survival tree or forest estimators resulted from a set of observed data. A tree partition $\mathscr{A}$ is $\{\alpha, k\}$-valid [40] if it satisfies two conditions: 1). For each splitting, the child node contains at least a

fraction $\alpha \in (0, 0.5)$ of the training samples in its parent node; and 2). Each terminal node contains at least k training examples. We denote the set of all $\{\alpha, k\}$-valid tree partitions by $\mathcal{V}_{\alpha,k}(\mathcal{D})$. In addition, we define the collection $\{\mathscr{A}^{(b)}\}_{b=1}^{B}$ as a valid forest partition if each of its tree partitions are valid. We denote the set of all such valid forest partitions as $\mathcal{H}_{\alpha,k}(\mathcal{D})$. A valid survival tree or forest estimator is induced from the corresponding valid set.

Definition 1 (Valid survival tree and forest). Given the observed data $\mathcal{D}_n$, a valid survival tree estimator of the CHF is induced by a valid partition $\mathscr{A} \in \mathcal{V}_{\alpha,k}(\mathcal{D}_n)$ with $\mathscr{A} = \{\mathcal{A}_u\}_{u \in \mathcal{U}}$:

$$\widehat{\Lambda}_{\mathscr{A},n}(t \mid x) = \sum_{u \in \mathcal{U}} \mathbb{1}(x \in \mathcal{A}_u)\widehat{\Lambda}_{\mathcal{A}_u,n}(t), \tag{4.8}$$

where each $\widehat{\Lambda}_{\mathcal{A}_u,n}(t \mid x)$ is defined by Equation (2.1). Furthermore, a valid survival forest $\widehat{\Lambda}_{\{\mathscr{A}_{(b)}\}_1^B,n}$ is defined as the average of B valid survival trees induced by a collection of valid partitions $\{\mathscr{A}_{(b)}\}_1^B \in \mathcal{H}_{\alpha,k}(\mathcal{D}_n)$,

$$\widehat{\Lambda}_{\{\mathscr{A}_{(b)}\}_1^B,n}(t \mid x) = \frac{1}{B}\sum_{b=1}^{B} \widehat{\Lambda}_{\mathscr{A}_{(b)},n}(t \mid x). \tag{4.9}$$

We also define the censoring contaminated survival tree and forest, which are asymptotic versions of the corresponding within-node average estimators of the CHF. Note that by Theorem 1, these averages are censoring contaminated versions $\Lambda^*_{\mathcal{A},n}(t)$, but not the true averages $\Lambda_{\mathcal{A}}(t)$.

4.1 Adaptive concentration bounds of survival trees and forests17

Definition 2 (Censoring contaminated survival tree and forest)**.** Given the observed data $\mathcal{D}_n$ and $\mathscr{A} \in \mathcal{V}_{\alpha,k}(\mathcal{D}_n)$, the corresponding CHF of the censoring contaminated survival tree is defined as

$$\Lambda^*_{\mathscr{A},n}(t \mid x) = \sum_{u \in \mathcal{U}} \mathbb{1}(x \in \mathcal{A}_u) \Lambda^*_{\mathcal{A}_u,n}(t), \qquad (4.10)$$

where each $\Lambda^*_{\mathcal{A}_u,n}(t)$ is defined by Equation (3.5). Furthermore, let $\{\mathscr{A}_{(b)}\}_1^B \in \mathcal{H}_{\alpha,k}(\mathcal{D}_n)$. Then the censoring contaminated survival forest is given by

$$\Lambda^*_{\{\mathscr{A}_{(b)}\}_1^B,n}(t \mid x) = \frac{1}{B} \sum_{b=1}^{B} \Lambda^*_{\mathscr{A}_{(b)},n}(t \mid x). \qquad (4.11)$$

Our adaptive concentration bound result considers the quantity

$$\widehat{\Lambda}_{\mathscr{A},n}(t \mid x) - \Lambda^*_{\mathscr{A},n}(t \mid x)$$

for all valid partitions $\mathscr{A} \in \mathcal{V}_{\alpha,k}(\mathcal{D}_n)$. We first specify several regularity assumptions. The first assumption is a bound on the dependence of the individual features. Note that in the literature, uniform distributions are often assumed [6, 5] on the covariates, which implies independence. To allow dependency among covariates, we assume the following assumption, which have also been considered in [40]. Without loss of generality, we assume that covariates are distributed on $[0,1]^d$.

Assumption 2. *Covariates $X \in [0,1]^d$ are distributed according to a density function $p(\cdot)$ satisfying $1/\zeta \le p(x) \le \zeta$ for all x and some $\zeta \ge 1$.*

We also set a restriction on the tuning parameter k, the minimum terminal node size, which may grow with n and dimension d.

Assumption 3. *Assume that k is bounded below so that*

$$\lim_{n\to\infty} \frac{\log(n)\max\{\log(d),\log\log(n)\}}{k} = 0. \tag{4.12}$$

Then we have the adaptive bound for our tree estimator in the following theorem. The proof is collected in Appendix S3.

Theorem 2. *Suppose the training data $\mathcal{D}_n$ satisfy Assumptions 1 and 2, and the rate of the sequence (n,d,k) satisfies Assumption 3. Then all valid trees concentrate on a censoring contaminated tree:*

$$\sup_{t<\tau,\, x\in[0,1]^d,\, \mathscr{A}\in\mathcal{V}_{\alpha,k}(\mathcal{D}_n)} \left|\widehat{\Lambda}_{\mathscr{A},n}(t\mid x) - \Lambda^*_{\mathscr{A},n}(t\mid x)\right|$$

$$\leq M_1 \sqrt{\frac{\log(n/k)[\log(dk)+\log\log(n)]}{k\log((1-\alpha)^{-1})}},$$

with probability larger than $1-2/\sqrt{n}$, for some universal constant M_1.

The above theorem holds for all single tree partitions in $\mathcal{V}_{\alpha,k}(\mathcal{D}_n)$. Consequently, we have a similar result for the forest estimator in Corollary S1 in Appendix S3.

Remark 1. In a moderately high-dimensional setting, i.e., $d \sim n$, the rate is $\log(n)/k^{1/2}$. In an ultra high-dimensional setting, for example, $\log(d) \sim n^\vartheta$,

where $0 < \vartheta < 1$, the rate is close to $n^{\vartheta}/k^{1/2}$. The rate that k grows with n cannot be too slow in order to achieve the bound in the ultra high-dimensional setting. This is quite intuitive since if k grows too slowly then we are not able to bound all possible nodes.

The results established in this section essentially address the variance component in a fitted random forest. We chose not to use the true within-node population averaged quantity $\Lambda_{\mathcal{A}}^*(t)$ (see Equation 3.6), or its single tree and forest versions as the target of the concentration. This is because such a result would require bounded density function of the failure time T. However, when $f(t)$ is bounded, the results can be easily generalized to $\left|\widehat{\Lambda}_{\mathcal{A},n}(t) - \Lambda_{\mathcal{A}}^*(t)\right|$. Lemma 2 in Section 4.3 provides an analog of Theorem 1 in this situation.

With the above concentration inequalities established, we are now in a position to discuss consistency results. We consider two specific scenarios: a finite-dimensional case where the splitting rule is generated randomly, and a high-dimensional case using the marginal difference of Nelson-Aalen estimators as the splitting rule.

4.2   Consistency under random splitting rules when d is finite

Assume that the dimension d of the covariates space is fixed and finite. At each internal node we choose the splitting variable randomly and uniformly from all covariates [5, 25]. When the splitting variable is chosen, we choose the splitting point uniformly at random such that both child nodes contain at least α proportion of the samples in the parent node. We will bound the bias term

$$\sup_{t<\tau} E_X \left| \Lambda^*_{\{\mathscr{A}_{(b)}\}_1^B, n}(t \mid X) - \Lambda(t \mid X) \right|.$$

It should be noted that in Section 4.1, we did not treat the tree and forest structures ($\mathscr{A}$ and $\{\mathscr{A}_{(b)}\}_1^B$) as random variables. Instead, they were treated as elements of the valid structure sets. However, in this section, once a particular splitting rule is specified, these structures become random variables associated with certain distributions induced from the splitting rule. When there is no risk of ambiguity, we inherit the notation $\widehat{\Lambda}_{\mathscr{A},n}$ to represent a tree estimator, where the randomness of $\mathscr{A}$ is understood as part of the randomness in the estimator itself. A similar strategy is applied to the forest version. Before presenting the consistency results, we make an additional smoothness assumption on the hazard function:

Assumption 4. *For any fixed time point t, the CHF $\Lambda(t \mid x)$ is L_1-Lipschitz*

continuous in terms of x, and the hazard function $\lambda(t \mid x)$ is L_2-Lipschitz

continuous in terms of x, i.e., $|\Lambda(t \mid x_1) - \Lambda(t \mid x_2)| \leq L_1\|x_1 - x_2\|$ and

$|\lambda(t \mid x_1) - \lambda(t \mid x_2)| \leq L_2\|x_1 - x_2\|$, respectively, where $\|\cdot\|$ is the Euclidean

norm.

We are now ready to state our main consistency results for the proposed

survival tree model. Theorem 3 provides the pointwise consistency result.

The proof is collected in Appendix S4.

Theorem 3. *Under Assumptions 1–4, the proposed survival tree model with*

random splitting rule is consistent, i.e., for each $x \in [0,1]^d$,

$$\sup_{t<\tau} \left|\widehat{\Lambda}_{\mathscr{A},n}(t \mid x) - \Lambda(t \mid x)\right| = O\left(\sqrt{\frac{\log(n/k)[\log(dk) + \log\log(n)]}{k\log((1-\alpha)^{-1})}} + \left(\frac{k}{n}\right)^{\frac{c_1}{d}}\right),$$

with probability at least $1 - w_n$, where

$$w_n = \frac{2}{\sqrt{n}} + d\exp\left\{-\frac{c_2^2 \log_{1/\alpha}(n/k)}{2d}\right\} + d\exp\left\{-\frac{(1-c_2)c_3c_4^2 \log_{1/\alpha}(n/k)}{2d}\right\},$$

and $c_2, c_4 \in (0,1)$, $c_3 = (1 - 2\alpha)/8$ and $c_1 = c_3(1-c_2)(1-c_4)/\log_{1-\alpha}(\alpha)$.

Remark 2. The first part $\sqrt{\frac{\log(n/k)[\log(dk)+\log\log(n)]}{k\log((1-\alpha)^{-1})}}$ in the bound comes

from the concentration results and the second part $(k/n)^{c_1/d}$ comes from

the bias. We point out that the optimal rate is obtained by setting $k =$

$n^{c_3/[c_3 + d\log_{1-\alpha}(\alpha)/2]}$, and then the optimal rate is close to $n^{-c_3/[2c_3 + d\log_{1-\alpha}(\alpha)]}$.

If we further assume that we always split at the middle point at each inter-

nal node, then the optimal rate degenerates to $n^{-1/(d+2)}$ obtained by setting

$k \sim n^{d/(d+2)}$.

The consistency result can be easily extended to survival forests with

B trees. Theorem 4 presents an integrated version, which can be derived

from Theorem 3. The proof is collected in Appendix S4.

Theorem 4. *Under Assumptions 1-4, the proposed survival forest is con-*

sistent, i.e.,

$$
\lim_{B \to \infty} \sup_{t < \tau} E_X |\widehat{\Lambda}_{\{\mathscr{A}_{(b)}\}_1^B, n}(t \mid X) - \Lambda(t \mid X)|
$$
$$
= O\left(\sqrt{\frac{\log(n/k)[\log(dk) + \log\log(n)]}{k \log((1-\alpha)^{-1})}} + \left(\frac{k}{n}\right)^{\frac{c_1}{d}} + \log(k) w_n \right),
$$

where w_n is a sequence approaching to 0 as defined in Theorem 3, $c_2, c_4 \in$

$(0, 1)$, $c_3 = (1 - 2\alpha)/8$ and $c_1 = c_3(1 - c_2)(1 - c_4)/\log_{1-\alpha}(\alpha)$.

4.3   Consistency under adaptive splitting rules

We have so far established consistency results for both survival trees and

forests for finite dimension d. In this section, we allow the dimension d to

go to infinity with sample size n while the covariates are possibly corre-

lated. We note that this is not a commonly used setting in the literature

because it can be difficult to control the marginal distribution of a noise

variable. We first provide several definitions. We assume that there are

d_0 important variables involved in the failure time distribution, and denote $\mathscr{M}_F$ the set of their indices, hence $\mathscr{M}_F \subset \{1, \ldots d\}$. Precisely, we have $T \perp X | X_{\mathscr{M}_F}$. The number of features involved in either the failure time and censoring time distributions is $d_0 + d_1$, where d_0 and d_1 are fixed, and denoted $\mathscr{M}_{FC}$ their indices. However, this does not imply that there are only d_1 variables for the censoring distribution because the failure variables and censoring variables may share some common indices. For example, age, as a commonly used demographic variable, can be informative for both the clinical outcome of interest (failure) and the lost to follow-up (censoring). However, splitting such variables is necessary as long as they are involved in the failure distribution. The splits that we may want to avoid is on the variables in the set $\mathscr{M}_C$ defined as $\mathscr{M}_{FC} \backslash \mathscr{M}_F$, making $d_1 = |\mathscr{M}_C|$. However, our later analysis indicates that this may not be avoidable because of the biasedness caused by censoring. Lastly, we define the set of noise variables' indices as $\mathscr{M}_N = \{1, \ldots d\} \setminus \mathscr{M}_{FC}$. We make the following assumption on the weak dependencies between noise variables and variables in $\mathscr{M}_{FC}$.

Assumption 5. *We assume that the conditional distribution of the failure and censoring covariates $X_{\mathscr{M}_{FC}}$ has weak dependencies on any univariate*

noise variable, in the sense that for some constant $\gamma > 1$, we have

$$\gamma^{-1} < \frac{p(X_{\mathcal{M}_{FC}} = x | X^{(j)} = x_1)}{p(X_{\mathcal{M}_{FC}} = x | X^{(j)} = x_2)} < \gamma,$$

for any $x_1, x_2 \in [0, 1]$, $(d_0 + d_1)$-dimensional vector x and any $j \in \mathcal{M}_N$.

Assumption 5 relaxes the commonly used independent covariate assumption in the literature [5, 43, 35, 38]. However, this poses significant difficulties when evaluating the marginal signal carried by a noise variable, meaning that the difference between the two potential child nodes may not be 0. A large threshold is necessary to prevent the noise variables from entering the model, as shown in the later results. However, as the correlation reduces to 0, i.e., $\gamma = 1$, the threshold will naturally degenerate to 0. We further need an assumption on the effect size of the failure variable.

Assumption 6. *(Marginal signal of the failure distribution) Let $\mathcal{A}$ be any internal node, and $j \in \mathcal{M}_F$ be an index of a variable that has never been split, i.e., the range of $X^{(j)}$ in node $\mathcal{A}$ is $[0, 1]$. Let $\mathcal{A}_j^+$ and $\mathcal{A}_j^-$ be defined as $\mathcal{A}_j^+(c) = \{X : X^{(j)} \geq c\}$ and $\mathcal{A}_j^-(c) = \{X : X^{(j)} < c\}$, respectively. We further define*

$$\ell^+(j, t, c) = \int_0^t \frac{E_{X \in \mathcal{A}_j^+(c)} f(s \mid X)}{E_{X \in \mathcal{A}_j^+(c)}[1 - F(s \mid X)]} \, \mathrm{d}s,$$

$$\ell^-(j, t, c) = \int_0^t \frac{E_{X \in \mathcal{A}_j^-(c)} f(s \mid X)}{E_{X \in \mathcal{A}_j^-(c)}[1 - F(s \mid X)]} \, \mathrm{d}s.$$

Then there exists a time point $t_0 \in [0, \tau]$, a constant $c_0 \in (0, 1)$, and minimum effect size $\ell > 2(\gamma^2 - \gamma^{-2})\tau L/M^2$, such that

$$M\ell^+(j, t_0, c_0) - M^{-1}\ell^-(j, t_0, c_0) > \ell, \quad if \quad \ell^+(j, t_0, c_0) > \ell^-(j, t_0, c_0),$$

$$or \quad M\ell^-(j, t_0, c_0) - M^{-1}\ell^+(j, t_0, c_0) > \ell, \quad if \quad \ell^+(j, t_0, c_0) < \ell^-(j, t_0, c_0),$$

where τ and M are defined in Assumption 1, γ is defined in Assumption 5, and L is an upper bound of $f(t|x)$ for all $x \in [0, 1]^d$.

This assumption can be interpreted as the following. First, $\ell^+(j, t, c)$ and $\ell^-(j, t, c)$ are the averaged CHFs on the left and right-hand side, respectively, of a split at the jth variable. The constant M and its reciprocal can be understood as the minimum and maximum contamination, respectively, of the censoring distribution on these CHFs. The assumption requires that if the difference of these contaminated versions is sufficiently large at some time point t_0 and some cut-point c_0. Note that M is a lower bound of $\mathrm{pr}(C \geq \tau \mid X = x)$, this essentially bounds below the signal size regardless of any dependency structures between C and T. However, in some trivial cases, such as when the G_i's are identical, the constant M can be removed from the assumption due to the independence between T and C. A simplified version will be provided in Assumption 7 in Section 5. Furthermore, ℓ can be an arbitrarily small constant if $\gamma = 1$, which is essentially the

independent covariates case.

Another important observation of this assumption is that t_0 can be arbitrary. Hence, we essentially allow the CHFs of different subjects to cross each other. As a comparison, we note that in many popular survival models, such as the Cox proportional hazard model, the CHF is a monotone function of X on the entire time domain. Hence the survival curve of any subject can only be completely above or below that of another subject. However, when the survival curves cross each other, a log-rank test may not be effective [17, 16]. When we incorporate the splitting rule that detects the maximum differences on $[0, \tau)$, our model is capable of detecting non-monotone signals of the CHF as a function of both X and t, making our approach more powerful than the traditional log-rank test splitting rule.

Finally, to make a splitting rule concrete, we provide Algorithm 2 in Appendix S1, which marginally compares the estimated CHF over all time points and uses the difference to select the best split. Based on this algorithm, Lemma S6 in Appendix S5 shows that our d dimensional survival forest is equivalent to a $(d_0 + d_1)$ dimensional survival forest with probability larger than $1 - 3/\sqrt{n}$. This means that with a large probability, we shall never split on the noise variable set $\mathscr{M}_N$. We highlight here that $\Lambda^*_{\mathcal{A},n}(t)$ is an essential tool to prove Lemma S6. The intuition here is that when the

failure distribution doesn't depend on the variable j, the quantity

$$\int_0^t \frac{E_{X \in \mathcal{A}_j^+(x)}[1 - G(s \mid X)]\mathrm{d}F(s \mid X)}{E_{X \in \mathcal{A}_j^+(x)}[1 - G(s \mid X)][1 - F(s \mid X)]}$$
$$- \int_0^t \frac{E_{X \in \mathcal{A}_j^-(x)}[1 - G(s \mid X)]\mathrm{d}F(s \mid X)}{E_{X \in \mathcal{A}_j^-(x)}[1 - G(s \mid X)][1 - F(s \mid X)]}$$

is bounded by a small constant under weak dependency. However, this is

quantity will degenerate to 0 as long as the dependency vanishes, i.e., $\gamma =$

1, since $dF(s|X)/[1 - F(s|X)]$ separates regardless of what the censoring

distribution is. The proof is indeed beautiful and neat, which is deferred to

Appendix S5.

Notice that $\Lambda_{\mathcal{A},n}^*(t)$ is a sample version of the asymptotic distribution

of the terminal node $\mathcal{A}$. In Lemma 2, we show the bound of the difference

of $\Lambda_{\mathcal{A},n}^*(t)$ and its integrated version $\Lambda_{\mathcal{A}}^*(t)$ across all valid nodes $\mathcal{A}$, where

$\Lambda_{\mathcal{A}}^*(t)$ is as defined in Equation (3.6). The proof is given in Appendix S5.

Lemma 2. *Under Assumptions 1-3 and further assume that the conditional*

density function $f(t \mid x)$ of the failure time T is bounded by L for all

$x \in [0,1]^d$. The difference between $\Lambda_{\mathscr{A},n}^*(t)$ and $\Lambda_{\mathscr{A}}^*(t)$ is bounded by

$$\sup_{t<\tau,\, x\in[0,1]^d,\, \mathscr{A}\in\mathcal{V}_{\alpha,k}(\mathcal{D}_n)} \left|\Lambda_{\mathscr{A},n}^*(t \mid x) - \Lambda_{\mathscr{A}}^*(t \mid x)\right|$$
$$\leq M_2\sqrt{\frac{\log(n/k)[\log(dk) + \log\log(n)]}{k\log((1-\alpha)^{-1})}},$$

with probability larger than $1 - 1/\sqrt{n}$.

Based on Lemma S6 provided in Appendix S5, we essentially only split on $(d_0 + d_1)$ dimensions with probability larger than $1 - 3/\sqrt{n}$ on the entire tree. The consistency holds from Theorem 3. The following result shows the consistency of the proposed survival forest. The proof is almost identical to Theorem 4.

Theorem 5. *Under Assumptions 1-6, the proposed survival tree using the splitting rule specified in Algorithm 2 is consistent, i.e., for any x,*

$$
\sup_{t < \tau} |\widehat{\Lambda}_{\mathscr{A},n}(t \mid x) - \Lambda(t \mid x)|
$$
$$
= O\left(\sqrt{\frac{\log(n/k)[\log\{(d_0 + d_1)k\} + \log\log(n)]}{k \log((1-\alpha)^{-1})}} + \left(\frac{k}{n}\right)^{\frac{c_1}{d_0 + d_1}} \right),
$$

with probability at least $1 - w_n$, where

$$
w_n = \frac{3}{\sqrt{n}} + (d_0 + d_1)\left[\exp\left\{ -\frac{c_2^2 \log_{1/\alpha}(n/k)}{2(d_0 + d_1)} \right\} + \exp\left\{ -\frac{(1 - c_2)c_3 c_4^2 \log_{1/\alpha}(n/k)}{2(d_0 + d_1)} \right\} \right],
$$

$c_2, c_4 \in (0, 1)$, $c_3 = (1 - 2\alpha)/8$ and $c_1 = c_3(1 - c_2)(1 - c_4)/\log_{1-\alpha}(\alpha)$.

Consequently, the proposed survival forest is consistent, i.e.,

$$
\lim_{B \to \infty} \sup_{t < \tau} E_X |\widehat{\Lambda}_{\{\mathscr{A}_{(b)}\}_1^B, n}(t \mid X) - \Lambda(t \mid X)|
$$
$$
= O\left(\sqrt{\frac{\log(n/k)[\log\{(d_0 + d_1)k\} + \log\log(n)]}{k \log((1-\alpha)^{-1})}} + \left(\frac{k}{n}\right)^{\frac{c_1}{d_0 + d_1}} + \log(k)w_n \right).
$$

Although we have developed a result where d can grow exponentially fast with n in this section, the splitting rule implemented was not completely the same as practice because it essentially checks only the signal where the candidate variables have never been used. This is made possible with Assumption 6 that the difference between two potential child nodes resulted from $X^{(j)} < c_0$ versus $X^{(j)} \geq c_0$ is sufficiently large. Once a variable is used, it will be automatically included as a candidate in subsequent splits. The idea is similar to the protected variable set used in [43], where the protected set serves as the collection of variables that have been used in previous nodes.

Remark 3. We provide a consistency result for survival trees and forests under weak dependency framework. We highlight that our results hold naturally if X is uniformly distributed with $\zeta = \gamma = 1$. Notice that when variables are uncorrelated, our results are still meaningful and constructive: the biasedness is not due to correlated variables but the entanglement between failure time and censoring time marginally. For example, if censoring time shares one common variable with failure time, then all other censoring variables also play a role in the limiting distribution, so there is no guarantee to split only on failure variables.

5. A bias-corrected survival forest

Recall that in Section 3, we investigated the estimation bias in the comparison of two potential child nodes. This is caused by ignoring the within-node heterogeneity of the censoring distribution while it is entangled with the failure distribution. A closer look at Equation (3.5) motivates us to perform a weighted version of the Nelson-Aalen estimator to correct this bias and estimate the true within-node averaged CHF. Hence, we consider

$$\widetilde{\Lambda}_{\mathcal{A},n}(t) = \sum_{s \leq t} \frac{\sum_{i=1}^{n} \mathbb{1}(\delta_i = 1)\mathbb{1}(Y_i = s)\mathbb{1}(X_i \in \mathcal{A})/[1 - \widehat{G}(s|X_i)]}{\sum_{i=1}^{n} \mathbb{1}(Y_i \geq s)\mathbb{1}(X_i \in \mathcal{A})/[1 - \widehat{G}(s|X_i)]}, \quad (5.13)$$

where $\widehat{G}(s|X_i)$ is an estimated conditional censoring distribution function. Note that this estimator resembles a form of the inverse probably weighting strategy [33], which is an extensively studied technique in the survival analysis and missing data literature [32]. There have been many different forms of inverse probably weighted estimators under a variety of contexts. For example, [20] uses $\delta_i/(1 - \widehat{G}(Y_i|X_i))$ as the subject-specific weight to fit regression random forests. One can also transform the censored observations into fully observed ones using, e.g., [34], and then fit a regression model with the complete data [29, 36, 37]. Similar ideas have also been used for imputing censored outcomes [42] when learning an optimal treatment strategy [14].

However, our proposal is fundamentally different from these existing methods. We estimate and compare an inverse probably weighted hazard function using weight $\delta_i/(1 - \widehat{G}(s|X_i))$ and repeatedly performing this at each internal node. A key observation is that the comparison is over the entire domain of the survival time instead of fitting regression forests based on complete observations. This is a unique advantage because the distribution function contains richer information than the within-node means. This makes our approach more sensitive for detecting differences between two potential child nodes at all quantile levels of the survival time. It also advocates the goal of a typical survival analysis model, where the survival function is the target of interest rather than the expected survival time. The intuition has a close connection with the sup-log-rank test statistic [17, 16], which can be used to detect any distributional difference of T of the two potential child nodes. Furthermore, with the following modified algorithm, we can achieve an improved convergence rate that depends only the size of $\mathscr{M}_F$.

Algorithm 2 can be modified accordingly to incorporate this new procedure. In particular, at each internal node $\mathcal{A}$, we use the weighted CHF estimator $\widetilde{\Lambda}_{\mathcal{A},n}(t)$ defined in Equation (5.13). We then pick the splitting point $\tilde{c}$ with the rule such that both child nodes contain at least proportion

α of the samples at $\mathcal{A}$:

$$\tilde{c} = \arg\max_{c} \Delta_2(c),$$

where $\Delta_2(c) = \max_{t<\tau} \left| \widetilde{\Lambda}_{\mathcal{A}_j^+(c),n}(t) - \widetilde{\Lambda}_{\mathcal{A}_j^-(c),n}(t) \right|$, $\mathcal{A}_j^+(c) = \{X : X^{(j)} \geq c\}$, and $\mathcal{A}_j^-(c) = \{X : X^{(j)} < c\}$, $X^{(j)}$ is the j-th dimension of X.

Note that the threshold of $\Delta_2(c)$ in this bias-corrected version is the same as the one used for $\Delta_1(c)$ in Algorithm 2. The intuition is that after removing the censoring bias, variables in $\mathscr{M}_C$ play the same role as noise variables in $\mathscr{M}_N$. In addition, the signal size Assumption 6 can be relaxed to the following.

Assumption 7. *(Marginal signal of the failure distribution) Let* $\ell^+(j, t_0, c_0)$, $\ell^-(j, t_0, c_0)$ *and effect size* l *be as defined in Assumption 6. Then, there exists a time point* t_0 *and a cutting point* c_0 *such that, for any* $j \in \mathscr{M}_F$,

$$\left| \ell^+(j, t_0, c_0) - \ell^-(j, t_0, c_0) \right| > \ell.$$

Note that this is essentially removing the censoring contaminated part (M and its reciprocal) from Assumption 6. Of course, this is at the cost of plugging-in a consistent estimator of the censoring distribution G to correct the bias. On the other hand, we need an additional assumption on the dependency structures.

Assumption 8. *We assume that the conditional distribution of the failure and censoring covariates $X_{\mathscr{M}_{FC}}$ has weak dependencies on any univariate censoring variable, in the sense that for constant $\gamma > 1$, we have*

$$\gamma^{-1} < \frac{p(X_{\mathscr{M}_{FC}\setminus\{j\}} = x | X^{(j)} = x_1)}{p(X_{\mathscr{M}_{FC}\setminus\{j\}} = x | X^{(j)} = x_2)} < \gamma,$$

for any $x_1, x_2 \in [0, 1]$, $(d_0 + d_1 - 1)$-dimensional vector x and any $j \in \mathscr{M}_C$.

This is an analog of Assumption 5 to further prevent the censoring variables from carrying strong marginal signals due to correlations. It will again degenerate to the commonly used independent covaraite case when $\gamma = 1$. Finally, we show that consistency can be established based on our new model fitting procedure, with convergence rate depends only on the number of variables in $\mathscr{M}_F$.

Theorem 6. *Under Assumptions 1-5, 7 and 8, assuming that $\widehat{G}$ in Equation (5.13) is a consistent estimation of the censoring distribution, the proposed bias-corrected survival tree is consistent, i.e., for any x,*

$$\sup_{t < \tau} |\widehat{\Lambda}_{\mathscr{A},n}(t \mid x) - \Lambda(t \mid x)|$$
$$= O\left(\sqrt{\frac{\log(n/k)[\log(d_0 k) + \log\log(n)]}{k\log((1-\alpha)^{-1})}} + \left(\frac{k}{n}\right)^{\frac{c_1}{d_0}}\right),$$

with probability at least $1 - w_n$, where

$$w_n = \frac{3}{\sqrt{n}} + d_0 \exp\left\{-\frac{c_2^2 \log_{1/\alpha}(n/k)}{2d_0}\right\} + d_0 \exp\left\{-\frac{(1-c_2)c_3 c_4^2 \log_{1/\alpha}(n/k)}{2d_0}\right\},$$

$c_2, c_4 \in (0,1)$, $c_3 = (1-2\alpha)/8$ and $c_1 = c_3(1-c_2)(1-c_4)/\log_{1-\alpha}(\alpha)$.

Consequently, the proposed survival forest is consistent, i.e.,

$$\lim_{B\to\infty} \sup_{t<\tau} E_X |\widehat{\Lambda}_{\{\mathscr{A}_{(b)}\}_1^B, n}(t \mid X) - \Lambda(t \mid X)|$$
$$= O\left(\sqrt{\frac{\log(n/k)[\log(d_0 k) + \log\log(n)]}{k \log((1-\alpha)^{-1})}} + \left(\frac{k}{n}\right)^{\frac{c_1}{d_0}} + \log(k)w_n \right).$$

In Appendix S7, we perform simulation studies to show that by actively correcting the bias, the prediction error can be significantly reduced. Interestingly, we want to highlight that as can be seen from simulations, the biasedness is mainly caused by the splitting rather than terminal node estimation. This is intuitive and in line with our theory that the splitting bias-correction procedure can enjoy a potentially faster convergence rate than the non-bias-corrected version. One might not expect a good prediction if trees are partitioned inefficiently regardless of what kind of terminal node estimation is used. After the tree is constructed, there is not much room to correct the bias if previous splits were chosen on noise or censoring variables.

6. Discussion

In this paper, we provided insights into survival forest and tree models and developed several fundamental results analyzing the impact of split-

ting rules. We first investigated the within-node Nelson-Aalen estimator of the CHF and established a concentration inequality for independent but non-identically distributed samples. By introducing a new concept called the censoring contamination, we can exactly quantify the bias of existing splitting rules. Based on this, we also developed a concentration inequality that bounds the variance component of survival trees and forests. We further analyzed in detail how such bias can affect consistency. In particular, we show that for a commonly used marginal comparison splitting rule strategy, the convergence rate depends on the total number of variables involved in the failure and censoring distribution. However, by appropriately correcting the bias, the convergence rate depends only on the number of failure variables. Essentially, the new bias correction procedure can be understood as untangling the failure and censoring distributions.

In addition to analyzing this entanglement, our result is based on a weak dependency structure, which bounds the marginal signal of any noise variable. This is a generalization of the commonly used independent covariate setting in the literature. A univariate split has a disadvantage when dealing with noise variables because if they are systematically selected in the splitting rule, the convergence rate will suffer. We believe that similar weak dependency assumptions are inevitable, because otherwise, any correlation

structure may carry signals into the noise variables. It would be interesting to investigate whether more advanced splitting rules can overcome this drawback.

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