

BART-Survival: A Bayesian machine learning approach to survival analyses in Python

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Summary

BART-Survival is a Python package that allows time-to-event (survival) analyses in discrete-time using the non-parametric machine learning algorithm, Bayesian Additive Regression Trees (BART). BART-Survival combines the performance of the BART algorithm with the complementary data and model formatting required to complete the survival analyses. The library contains a convenient application programming interface (API) that allows a simple approach when using the library for survival analyses, while maintaining capabilities for added complexity when desired. The package is intended for analysts exploring use of flexible non-parametric alternatives to traditional (semi-)parametric survival analyses.

Statement of need

Survival analyses are a cornerstone of public health and clinical research in such diverse fields as cancer, cardiovascular disease, and infectious diseases (Altman & Bland, 1998; Bradburn et al., 2003). Traditional parametric and semi-parametric statistical methods, such as the Cox proportional hazards model, are commonly employed for survival analyses (Cox, 1972). However, these methods have several limitations, particularly when applied to complex data. One major issue is the need for restrictive assumptions, such as proportional hazards and predefined functional forms, which may not hold true in complex, real-world healthcare data (Harrell, 2015; Ishwaran et al., 2008). Additionally, these methods often struggle with high-dimensional datasets, leading to problems with over-fitting, multi-collinearity, and dealing with complex interactions (Ishwaran et al., 2008; Joffe et al., 2013).

More recently, non-parametric machine learning approaches have been introduced to address the limitations of the traditional methods (Harrell, 2015; Ishwaran et al., 2008). BART is one such approach that has demonstrated exceptional performance across a variety of analytic settings, typically outperforming the traditional methods in terms of predictive accuracy. BART's performance is linked to its ability to flexibly model complex non-linear and variable interactions within the data, while being inherently regularized to reduce issues of over-fitting. The BART method is fully non-parametric and can adaptively model data complexities without prior knowledge or specification of a particular functional form. Finally, the method is generally accepted as being a user-friendly machine learning approach, as it typically requires minimal hyperparameter tuning and the outcomes can be easier to interpret than those produced by other similar methods (Chipman et al., 2010; R. Sparapani et al., 2021; R. A. Sparapani et al., 2016).

Currently, the only BART survival algorithm readily available exists as part of the BART R package, which contains a library of various BART-based approaches in addition to a BART survival analysis application (R. Sparapani et al., 2021; R. A. Sparapani et al., 2016). The

BART-Survival package described here combines the survival analysis approach outlined in the BART R package with the foundational Python-based probabilistic programming language library, PyMC (Abril-Pla et al., 2023), and the accompanying BART algorithm from the PyMC-BART library (Quiroga et al., 2023). Our aim in developing BART-Survival is to provide accessibility to the BART survival algorithm within the Python programming language. This contribution is beneficial for analysts when Python is the preferred programming language, the analytic workflow is Python-based, or when the R language is unavailable for analyses.

The need for a complete BART-Survival python package is given by the simple fact that the BART survival algorithm is non-trivial to implement. Both the required data transformations and the internal model definition requires precise implementations to ensure generation of accurate survival models. Our BART-Survival library provides accessibility to these precise methods while removing the technical barriers that would limit user adoption of the BART survival approach.

More specifically, the BART-Survival library abstracts away the complexities of generating the proper training and inference datasets, which are conceptually complex and prone to being specified incorrectly if implemented from scratch. Similarly, the BART-Survival library provides a pre-specified internal Bayesian model using the PyMC probabilistic programming language. This pre-specified model is primarily accessed through the BART-Survival API removing the requirement for users to have more than a cursory knowledge of the PyMC or PyMC-BART libraries. Since the BART-Survival package is intended for students and professional in the public health and clinical fields, it is expected that users of the BART-Survival library will not have extensive programming expertise, adding to the need for a fully self-contained and accessible approach.

In summary, the BART-Survival package provides a simple and accessible approach to implementing the BART survival algorithm. The provided approach can be beneficial for users who are looking for non-parametric alternatives to traditional (semi-)parametric survival analysis. The BART survival algorithm can be especially useful in large, complex healthcare data, where machine learning methods can demonstrate improved performance over the traditional methods.

Methods

The following sections provides details on the methods employed by the BART-Survival library, focusing specifically on the discrete-time survival algorithm used. For review of the BART algorithm we refer to associated PyMC-BART publication (Quiroga et al., 2023).

Background

The BART-Survival package provides a discrete-time survival method which aims to model survival as a function of a series of probabilities that indicate the probability of event occurrence at each discrete time. For clarity, the probability of event occurrence at each discrete time will be referred to as the risk probability.

In combination with a structural configuration of the data, the discrete-time algorithm allows for flexible modeling of the risk probabilities as a non-parametric function of time and observed covariates. The series of probability risks can then be used to derive the survival probabilities, along with other estimates of interest.

The foundation of the method is simple and is based off the well-defined Kaplan-Meier Product-Limit estimator. While a full review of the Kaplan-Meier method can be found elsewhere (Stel Vianda S., 2011), the following example demonstrates the fundamental concepts of discrete-time survival analysis that motivates its application within the BART-Survival method.

1. Starting with a simple event-time dataset, create a sequence of time intervals that represent the unique discrete-time intervals observed in the data. Each interval is

represented as a t_j , where $j = 1, \dots, k$ and k is the length of the set of unique observed times.

For example if the observed event-time data is:

event status	event time
1	1
0	2
1	2
1	4
1	4
1	5

Then the set of unique observed times is $[1, 2, 4, 5]$ with $k = 4$ indices and the corresponding t_j intervals are:

index	interval
t_1	$(0, 1]$
t_2	$(1, 2]$
t_3	$(2, 4]$
t_4	$(4, 5]$

In the table above the intervals are denoted with the properties, "(" indicating exclusive times and "]" indicating inclusive times in an interval. Additionally, the **event status** column is defined as (1 = event, 0 = censor)

2. Then with the constructed time intervals t_1, \dots, t_k , tally the following for each interval:

- the number of observations with an event
- the number of observation censored
- the total number of observations eligible to have an event (at risk) at the start of the interval

Continuing the above example, the corresponding frequencies for each interval are:

index	interval	event	censor	at risk
t_1	$(0, 1]$	1		6
t_2	$(1, 2]$	1	1	5
t_3	$(2, 4]$	2		3
t_4	$(4, 5]$	1		1

3. Finally, the risk of event occurrence within each interval t_j can simply be derived as:

$$P_{t_j} = \frac{n \text{ events}_{t_j}}{n \text{ at risk}_{t_j}},$$

and the survival probability at a time-index j , can be derived as:

$$S(t_j) = \prod_{q=1}^j (1 - P_{t_q}).$$

Applied to our example the risks of event P_{t_j} are:

index	interval	event	censor	at risk	P_{t_j}
t_1	(0, 1]	1		6	0.167
t_2	(1, 2]	1	1	5	0.2
t_3	(2, 4]	2		3	0.667
t_4	(4, 5]	1		1	1.0

106 And the corresponding survival estimates at times [1, 2, 4, 5] are:

index	time	survival
t_1	1	.83
t_2	2	.67
t_3	4	.22
t_4	5	0

107 BART-Survival builds off this simple foundation by replacing each naively derived P_{t_j} with a
 108 probability risk prediction, $p_{t_j|x_{ij}}$ yielded from the BART regression model. The x_{ij} values are
 109 the associated covariate values for each observation i at each discrete time j . The predicted
 110 values $p_{t_j|x_{ij}}$ can be further transformed into survival probability estimates or other estimands
 111 of interest. Formally, the survival probability estimate for a single observation i at time-index j
 112 can be derived as:

$$S(t_j|x_i) = \prod_{q=1}^j (1 - p_{t_q|x_{iq}}).$$

113 Data Preparation

114 As displayed in the above example, survival data is typically given as paired (*event status*,
 115 *event time*) outcomes, along with a set of covariates x_i for each observation. In this setup,
 116 *event status* is typically a binary variable, with 1 = **event** and 0 = **censored**.

117 Obtaining the $p_{t_j|x_{ij}}$ values and subsequent survival estimates is a two-step process. Each step
 118 of the process requires generating a specialized augmented datasets from the generic survival
 119 data. The first step in the process involves training the BART model which requires the
 120 **training augmented dataset (TAD)**. The second step involves generating the $p_{t_j|x_{ij}}$ predictions
 121 from the trained BART model, which requires the **predictive augmented dataset (PAD)**.

122 The **TAD** is created by transforming each single observation row into a series of rows representing
 123 the observation over a time series. When transformed a single observation's information is
 124 represented as a series of tuples, each tuple containing the augmented values of *status* and
 125 *time*, as well as replicates of the covariates x . The series of tuples is constructed using the
 126 k distinct times from the generic dataset. These times are represented by t , which can be
 127 indexed by j , where j is in the set $1, \dots, k$. Then for each observation's *event time* _{i} there is an
 128 index j in $1, \dots, k$ where $t_j = \text{event time}_i$. This special index j is denoted as m_i and can be
 129 defined as:

$$t_{m_i} = t_j = \text{event time}_i.$$

130 For each observation, a set of tuples is created containing a total of m_i tuples which are used
 131 to represent that observation's information. Each tuple is created for a specific time t_j where
 132 $j = 1, \dots, m_i$. Additionally, for all tuples with times $t_j < t_{m_i}$ the value of *status* is set to 0

133 and for the time $t_j = t_{m_i}$ the value of *status* is set to the value *event status_i*. Covariate
134 information is simply replicated across tuples.

135 For example if the survival data is:

observation	status	time	unique times (k=6)
— — —	— — —	— — —	
1	1	4	with 4 6 7 8 12 14
2	0	6	
3	1	6	
4	1	7	
5	1	8	
6	0	8	
7	1	12	
8	1	14	

136 Then the transformation for observation 7 would be represented in the *augmented* dataset as
137 the sequence of rows:

observation	status	time
— — —	— — —	— — —
7	0	4
7	0	6
7	0	7
7	0	8
7	1	12

138 Similarly, the transformation for observation 6 would be represented as:

observation	status	time
— — —	— — —	— — —
6	0	4
6	0	6
6	0	7
6	0	8

139 It is important to reiterate that for each observation i , the new set of rows created only include
140 the time points $t_j \leq t_{m_i}$. For observation 7, the $t_{m_i} = 12$ and the corresponding times in
141 the **TAD** are 4, 6, 7, 8, 12. For observation 6, the $t_{m_i} = 8$ and the corresponding times in the
142 **TAD** are 4, 6, 7, 8.

143 The utility of the **TAD** is that it unlinks *event time* from the *event status*. In this setup, the
144 constructed *status* variable (which is a simple binary variable taking values 1 or 0) represents
145 the outcome and *time* is a covariate. Then treating each row of the **TAD** as an independent
146 observation, the outcome can be modeled as a binary regression of *status* over *time* and any
147 additional covariates x . The trained regression model from this dataset can be used to yield
148 probability predictions for each time t_j for j in $1, \dots, k$. These probability predictions hold the
149 interpretation as being the probability risk of event occurrence at each time conditional on the
150 event not having already occurred at a previous time. The predictions for each observation i
151 and time t_j can be used to yield the various analytic targets, such as survival probabilities.

152 To generate the predictions of probability risks over the observed times, the **PAD** dataset
153 is used. The **PAD** transformation is similar to the **TAD**, but is simpler in that for each
154 observation a set of size k tuples is created. Each tuple in the set contains the time t_j for
155 $j = 1, \dots, k$ and any additional covariates x .

156 Continuing the examples above, there are $k = 6$ the unique times. For $j = 1, \dots, k$ the resulting
157 distinct times are $t_j = 4, 6, 7, 8, 12, 14$ and the **PADs** for observations 6, and 7 would be:

observation	time
6	4
6	6
6	7
6	8
6	12
6	14
7	4
7	6
7	7
7	8
7	12
7	14

158 Notably the **TAD** and **PAD** lengths can differ. **PAD** length is simple to calculate. If n is
 159 the number of observations in the generic dataset and k is the number of the unique times
 160 observed in the generic dataset, then the length of the **PAD** is simply $n * k$. In the example
 161 data above it would be $(8 * 6) = 48$.

162 The **TAD** length can be calculated using each observation's m_i , which again is defined as
 163 being the index that resolves $t_{m_i} = \text{event time}_i$. The **TAD** length can be calculated as:

$$\text{TAD}_{\text{length}} = \sum_{i=1}^n m_i.$$

164 This can be demonstrated with the example dataset, where the **TAD** length can be found as
 165 the sum of the m_i column which resolves to a **TAD** length of 27:

observation	event time _{<i>i</i>}	m_i
1	4	1
2	6	2
3	6	2
4	7	3
5	8	4
6	8	4
7	12	5
8	14	6
		27

166 While the **PAD** and **TAD** lengths are not important for generating the models, they are helpful
 167 to keep in mind when completing an analysis. Specifically, the fact that the **TAD** and **PAD**
 168 can be far larger in length than the generic dataset. For example the generic dataset used
 169 above is only 8 rows in length, but the **TAD** and **PAD** dataset are 27 and 48 rows respectively.

170 When the length of the two datasets become large enough to make computation difficult it is
 171 recommended to downscale the *event time* values, which will reduce the length of the two
 172 augmented datasets. The downscaling algorithm we provide in the library takes the *event time*,
 173 divides by a scaling factor and then takes the "ceiling" truncation to create the new *scaled*
 174 *event time*. Below the downscaling algorithm is demonstrated with the example dataset using
 175 a scaling factor of 4:

time	downscaled time	rescaled time
4	1	4
6	2	8
6	2	8
7	2	8
8	2	8
8	2	8
12	3	12
14	4	16

Downscaling the *event time* values causes loss of granularity in the set of discrete times analyzed. As shown in the example above, after downscaling (and then rescaling) the analytic targets can only be derived for the times 4, 8, 12 and 16, which is reduced from the original set of times, 4, 6, 7, 8, 12, 14. While the analytic targets cannot be returned for the times 6, 7, 14, the training information contributed by the observations with these *event times* is maintained through subsequent contribution at the downscaled times. Since there is no loss of event information, the probability of event at the downscaled times 4, 8, 12, 16 will be equal to the probability of event from a non-downscaled dataset at the select time 4, 8, 12, 16.

Downscaling can be safely applied to datasets without loss of precision of estimates at the downscaled times. The only consideration required when using a downscaling procedure is to ensure that the downscaled times granularity fulfills the needs of the analysis. For example, in a multi-year health-outcomes study, downscaling from days to months could significantly reduce computational burden without a meaningful loss of information in the outcome. However, if that same study reduced time from days to years, this could lead to loss of meaningful information in the outcome. The considerations for downscaling need to be made on a study-to-study basis and no general recommendation on selecting a downscaling factor can be provided.

Model

The BART-Survival algorithm is two-step algorithm. First, the **TAD** is used to train a non-parametric regression model of *status* on *time* and covariates. Then the **PAD** is used to yield predicted probabilities at each discrete time. These probability of event predictions can be used generate all additional estimates useful for statistical inference.

To motivate the use of the **TAD** in training the regression model, an example **TAD** is displayed below. Here, *status* can be represented as the outcome vector of y_{ij} values and *time* is represented by the t_{ij} values. Additional covariates are represented by a vector of x_{ij} values. The subscript i refers to the i^{th} observation of the generic dataset and the subscript j refers to the j^{th} index of the unique set of discrete times previously defined as t . In the **TAD** and **PAD**, the i, j indices can be thought of as multi-indices over the rows.

i	j	y	t	x
1	1	0	3	x_{11}
1	2	0	4	x_{12}
1	3	1	6	x_{13}
2	1	0	3	x_{21}
2	2	1	4	x_{22}
3	1	0	3	x_{31}
3	2	0	4	x_{32}
3	3	1	6	x_{33}

When using the **TAD**, each y_{ij} value can then be treated as independent draw of a *Bernoulli* distribution parameterized with the probability of event p_{ij} for observation i at time index j . The p_{ij} values are collected as the latent values yielded from a *probit* regression of y on t and x . Formally the model is defined as:

$$\begin{aligned} y_{ij}|p_{ij} &\sim \text{Bernoulli}(p_{ij}), \\ p_{ij}|\mu_{ij} &= \Phi(\mu_{ij}), \\ \mu_{ij} &\sim \text{BART}(t_{ij}, x_{ij}), \end{aligned}$$

where Φ is the normal cumulative distribution function and BART is the ensemble of regression trees that yield the μ_{ij} value for a given t_{ij} , x_{ij} combination.

Regarding the BART algorithm, in brief BART is a Bayesian approach to the ensemble regression trees class of non-parametric models. BART uses a combination of Bayesian priors placed on the tree generating components and a Markov Chain Monte Carlo sampling algorithm to iteratively generate tree ensembles. These tree ensemble are collected as samples of the posterior distribution. The samples of the posterior distribution are subsequently used to generate distinct posterior predictive distributions for a given set of observations.

This implies that for each t_{ij} , x_{ij} combination, the algorithm first returns a distribution of p_{ij} values, denoted as p_{ij}^{dist} . Each value in the p_{ij}^{dist} is a prediction mapped from a single tree ensemble of the posterior distribution. Point estimates and uncertainty intervals can be easily obtained from the p_{ij}^{dist} as simple estimates from that distribution. For example the mean can be derived as the empirical average of p_{ij}^{dist} . Similarly, the even-tailed 95% credible interval can be derived as the 5th and 95th percentiles of the p_{ij}^{dist} . Of note, any reference to p_{ij} used in this article is referring to the mean point estimate of the p_{ij}^{dist} .

Further details regarding the BART implementation used in the BART-Survival algorithm can be found in PyMC-BART repository and the accompanying publication (Quiroga et al., 2023).

Survival

A trained BART-Survival model is used along with the **PAD** to generate the vector of p_{ij} predictions. To generate survival estimates the p_{ij} vector is grouped by the i indices. Then using the following equation the survival probability at discrete times can be constructed:

$$S(t_q|x_{iq}) = \prod_{j=1}^q (1 - p_{ij}),$$

where q is the index of the time for the desired estimate. As described in the previous section a full posterior predictive distribution is returned for each $S_{t_q, x_{iq}}$. Point estimates and credible intervals can be obtained through the empirical mean and percentile functions of the returned posterior predictive distribution for each $S(t_q|x_{iq})$.

Marginal Effects

BART-Survival provides capabilities to evaluate covariate effects through use of partial dependence functions which yield marginal effect estimates. The partial dependence function method involves generating predictions of p for the observations in a **partial dependence augmented dataset (PDAD)**. Using variations of the **PDAD** yields different sets of predictions p . These sets can then be contrasted to yield marginal effect estimates, including marginal Hazard Ratios which have similar interpretation as the Cox Proportional Hazard Model's conditional Hazard Ratios.

PDADs can be created through further augmentation of the previously described **PAD**. As a reminder, the **PAD** contains the generated time covariate t and k replicates of each x_i from

the generic dataset, where k is the length of the uniquely observed *event times*. Importantly x_i can be defined generically as the set of covariates $\{x_{1_i}, x_{2_i}, \dots, x_{m_i}\}$, where m is the index of the last included covariate.

Then, starting with the **PAD**, the **PDAD** is generated through selection of a specific covariate $x_{[I]}$, from the set of covariates $\{x_1, x_2, \dots, x_m\}$ and setting that covariate to a deterministic value for all observation i and evaluated times j . The bracketed notation $[I]$ is used to define the index of the covariate selected and convey that the selected covariate is set to a deterministic value. Expanding the notation, $x_{[I]=v}$ indicates that covariate of index I is selected and deterministically set to value v .

In the following example the second covariate from a set of covariates $\{x_1, x_2, x_3\}$ is of interest for evaluating marginal effects. This covariate is binary and takes the values 0, 1. Evaluation of this covariate can be completed by creating **PDADs** for possible values of the selected covariate. In each **PDAD** all of the observations and times are set to a deterministic values selected from the range of the covariate. The two generated **PDADs** can be defined by the covariate index and set values: $x_{[2]=0}$ and $x_{[2]=1}$.

	i	j	t	x_1	x_2	x_3
	—	—	—	—	—	—
PAD:	1	1	2	1.2	0	10
	1	2	3	1.2	0	10
	1	3	5	1.2	0	10
	2	1	2	2.4	1	12
	2	2	3	2.4	1	12
	2	3	5	2.4	1	12
	3	1	2	1.9	0	3
	3	2	3	1.9	0	3
	3	3	5	1.9	0	3

	i	j	t	x_1	x_2	x_3
	—	—	—	—	—	—
PDAD _{$x_{[2]=1}$}	1	1	2	1.2	1	10
	1	2	3	1.2	1	10
	1	3	5	1.2	1	10
	2	1	2	2.4	1	12
	2	2	3	2.4	1	12
	2	3	5	2.4	1	12
	3	1	2	1.9	1	3
	3	2	3	1.9	1	3
	3	3	5	1.9	1	3

	i	j	t	x_1	x_2	x_3
	—	—	—	—	—	—
PDAD _{$x_{[2]=0}$}	1	1	2	1.2	0	10
	1	2	3	1.2	0	10
	1	3	5	1.2	0	10
	2	1	2	2.4	0	12
	2	2	3	2.4	0	12
	2	3	5	2.4	0	12
	3	1	2	1.9	0	3
	3	2	3	1.9	0	3
	3	3	5	1.9	0	3

From the two **PDADs** the predicted probabilities, $p_{x_{[2]=1}}$, $p_{x_{[2]=0}}$ and survival probabilities $S_{x_{[2]=1}}$, $S_{x_{[2]=0}}$, can be generated:

i	j	$p_{x_{[2]}=1}$	$S_{x_{[2]}=1}$	$p_{x_{[2]}=0}$	$S_{x_{[2]}=0}$
1	1	.20	.80	.10	.90
1	2	.25	.60	.15	.77
1	3	.18	.49	.08	.70
2	1	.10	.90	.08	.92
2	2	.13	.78	.11	.81
2	3	.12	.69	.10	.74
3	1	.20	.80	.15	.92
3	2	.28	.58	.23	.82
3	3	.23	.44	.18	.74

The marginal expectations of $p_{x_{[t]}}$ and $S_{x_{[t]}}$ at a specific time can be further derived by taking the average of the estimates over observations i for the specified time t indexed by j :

$$E_i[p_{x_{[t]}}|t_j] = \frac{1}{n} \sum_{i=1}^n p_{ij,x_{[t]}},$$

$$E_i[S_{x_{[t]}}(t_j)] = \frac{1}{n} \sum_{i=1}^n S_{i,x_{[t]}}(t_j),$$

where E_i is the expectation over i, \dots, n observations. From the above example, this yields the expectations for time indices $j = 1, 2, 3$.

j	t	$E_i[p_{x_2=1}]$	$E_i[S_{x_2=1}]$	$E_i[p_{x_2=0}]$	$E_i[S_{x_2=0}]$
1	2	0.17	0.83	0.11	0.91
2	3	0.22	0.65	0.16	0.8
3	5	0.18	0.54	0.12	0.73

These expectations can be further used to make comparisons between the evaluation of various values of $x_{[t]}$ across multiple PDADs. Common marginal effect estimates derived from these predicted values include:

- Marginal difference is survival probability at time t :

$$\text{Surv. Diff.}_{\text{marg}}(t_j) = E_i[S_{x_{[t]}=v_2}(t_j)] - E_i[S_{x_{[t]}=v_1}(t_j)].$$

- Marginal Risk Ratio at time t :

$$\text{RR}_{\text{marg}}(t_j) = \frac{E_i[p_{j,x_{[t]}=v_2}]}{E_i[p_{j,x_{[t]}=v_1}]}.$$

- Marginal Hazard Ratio (expectation over i and times up to t):

$$\text{HR}_{\text{marg}}(t_j) = \frac{E_{ij}[p_{x_{[t]}=v_2}]}{E_{ij}[p_{x_{[t]}=v_1}]}.$$

Continuing the example, the marginal effect of x_2 as measured by difference in survival probability when $x_{[2]} = 1$ and $x_{[2]} = 0$ at the times 2, 3, 5 can be examined below:

j	t	Surv.Diff.
1	2	−0.08
2	3	−0.15
3	5	−0.19

274 These results can be conveniently interpreted. For example, at time $t = 5$ the increase of x_2
 275 from 0 to 1 leads to an average change in the survival probability of -0.19 , where survival
 276 probability is in the range 0-1. Additionally, as mentioned in the previous sections, all estimates
 277 of the model will first be yielded as posterior predictive distributions. The empirical mean
 278 and percentile function of this distribution yield the point estimates described above and their
 279 respective credible intervals.

280 Demonstration

281 The following is a brief demonstration on how to use the BART-Survival library. In the
 282 demonstration the *rossi* survival dataset from the lifelines library is used. The dataset contains
 283 one year of follow-up observation on 432 convicts who were released from Maryland state
 284 prisons in the 1970s. The primary event measured in this dataset is observation of a “new
 285 arrest” within that year and the associated “time to arrest” is given in weeks (Rossi & Lenihan,
 286 1980).

```
from lifelines.datasets import load_rossi
from bart_survival import surv_bart as sb
import numpy as np
```

```
#####
# Load rossi dataset from lifelines
rossi = load_rossi()
names = rossi.columns.to_numpy()
rossi = rossi.to_numpy()
```

287 After loading the libraries and data, the first step is to generate the **TAD** and **PAD** datasets.
 288 In this step, the time (originally in weeks) is downsampled by a factor of 4, setting time to be
 289 measured in months.

```
#####
# Transform data into 'augmented' dataset
# Requires creation of the training dataset and a predictive dataset for inference
# TAD
trn = sb.get_surv_pre_train(
    y_time=rossi[:,0],
    y_status=rossi[:,1],
    x = rossi[:,2:],
    time_scale=4
)

# PAD
post_test = sb.get_posterior_test(
    y_time=rossi[:,0],
    y_status=rossi[:,1],
    x = rossi[:,2:],
    time_scale=4
)
```

290 Below the *trn* object is displayed. The *trn* object generated in this step is a dictionary of
 291 arrays containing the **TAD** components. The *y* and *x* components are the corresponding
 292 outcome and covariates of the **TAD**. The *w* object is an array of weight values generated by the
 293 *get_surv_pre_train* function. By default all weights are set to 1 and do not contribute to
 294 model training. For general use, the weighting functionality can be ignored. In more complex
 295 study designs, observation level weights can be provided which allows weighted contribution to
 296 the likelihood function during model training. Weighting the likelihood function is currently

297 experimental, but we plan to evaluate this utility further in future work. Finally, the coord
 298 object contains the observation identifier for each row of the **TAD**, making it easy to identify
 299 the rows associated with a single or set of observations from the **TAD**.

```
# {'y': array([[0.],
#             [0.],
#             [0.],
#             ...,
#             [0.],
#             [0.],
#             [0.]])},
# 'x': array([[ 1.,  0., 27., ...,  0.,  1.,  3.],
#            [ 2.,  0., 27., ...,  0.,  1.,  3.],
#            [ 3.,  0., 27., ...,  0.,  1.,  3.],
#            ...,
#            [11.,  1., 24., ...,  0.,  1.,  1.],
#            [12.,  1., 24., ...,  0.,  1.,  1.],
#            [13.,  1., 24., ...,  0.,  1.,  1.]])},
# 'w': array([[1.],
#            [1.],
#            [1.],
#            ...,
#            [1.],
#            [1.],
#            [1.]])},
# 'coord': array([ 0,  0,  0, ..., 431, 431, 431])}
```

300 The next step is to initialize the model, which involves setting several parameter values. The key
 301 considerations when initializing the models is number of trees and the split rules. The number of
 302 trees controls how many regression trees will be used. Typically 50 trees is a good default, but
 303 it can be adjusted to assist in model performance. Split rules is a specific PyMC-BART parameter
 304 and is used to designate the how the regression trees are constructed. The one requirement
 305 of the split rules is that the time covariate has to be set as a `pmb.ContinuousSplitRule()`.
 306 Otherwise, continuous variables can be assigned `pmb.ContinuousSplitRule()` and categorical
 307 variables assigned `pmb.OneHotSplitRule()`. It is recommended to review the PyMC-BART
 308 literature for more information regarding parameterization of the models.

```
#####
# Instantiate the BART models
# model_dict defines specific model parameters
model_dict = {"trees": 50,
              "split_rules": [
                  "pmb.ContinuousSplitRule()", # time
                  "pmb.OneHotSplitRule()", # fin
                  "pmb.ContinuousSplitRule()", # age
                  "pmb.OneHotSplitRule()", # race
                  "pmb.OneHotSplitRule()", # wexp
                  "pmb.OneHotSplitRule()", # mar
                  "pmb.OneHotSplitRule()", # paro
                  "pmb.ContinuousSplitRule()", # prio
              ]
}
# sampler_dict defines specific sampling parameters
sampler_dict = {
    "draws": 200,
    "tune": 200,
```

```

        "cores": 8,
        "chains": 8,
        "compute_convergence_checks": False
    }
    BSM = sb.BartSurvModel(
        model_config=model_dict,
        sampler_config=sampler_dict
    )
309 The model can then be trained with the TAD input and predicted  $p_{ij}$  values yielded with the
310 PAD input.

#####
# Fit Model with TAD
BSM.fit(
    y = trn["y"],
    X = trn["x"],
    weights=trn["w"],
    coords = trn["coord"],
    random_seed=5
)

# Get posterior predictive for evaluation using the PAD
post1 = BSM.sample_posterior_predictive(
    X_pred=post_test["post_x"],
    coords=post_test["coords"]
)
311 Finally, the survival probability can be derived from the  $p_{ij}$  estimates.

# Convert to SV probability.
sv_prob = sb.get_sv_prob(post1)
print(sv_prob["sv"].shape)
# (1600, 432, 13)
312 The sv_prob object above is a dictionary containing numpy arrays of both the  $p_{ij}$  and  $s_{ij}$ 
313 estimates, labeled "prob" and "sv" respectively. The  $p, s$  arrays are three dimensional with the
314 dimensions of the arrays being:
315     ■ axis 0 = draws of the posterior predictive distribution: 1600
316     ■ axis 1 = observations  $i$ : 432
317     ■ axis 2 = times  $j$ : 13
318 These arrays can be easily reduced down to point estimates and credible intervals using basic
319 numpy methods. For example to get the estimate of the mean over all observations, first get
320 the mean over the observations (axis 1) followed by the mean over the posterior draws (axis
321 0). The results being the estimated mean survival over the 13 time intervals.
322 Similarly the 0.05-0.95 credible interval for the estimated mean survival can be returned as the
323 quantile evaluations of the same mean-over-axis-1 array. This yields a (2,13) array with the
324 lower and upper bounds (rows) of the credible interval defined for each time point (columns).

# get the mean value across observations for each time within each draw of the posterior
ave_obs = sv_prob["sv"].mean(axis=1)
print(ave_obs.shape)
# (1600, 13)

# get the average across the posterior draws
ave_obs_draws = ave_obs.mean(0)

```

```
print(ave_obs_draws)
#[0.98282867 0.96457594 0.94578149
# 0.92613075 0.90503023 0.88429523
# 0.86382304 0.84376736 0.82281631
# 0.80169965 0.78080675 0.75948555
# 0.73816541]

# get the .05 and .95 percentiles of the mean across posterior draws
ci_obs_draws = np.quantile(ave_obs, [0.05, 0.95], axis=0)
print(ci_obs_draws)
# lower bound
# [0.97813492 0.95597036 0.93449701
# 0.91273325 0.88996273 0.86803963
# 0.84529644 0.82373944 0.8013158
# 0.77941446 0.75844137 0.73615453
# 0.71387    ]
# upper bound
# [0.9879464 0.97269846 0.95684153
# 0.93988969 0.91999613 0.90054844
# 0.8815908 0.86294746 0.84339772
# 0.82276706 0.80264632 0.78084766
# 0.76145384]
```

325 Examples of generation of marginal effect estimates can be found in the example notebooks
326 provided in the repository documentation.

327 Conclusion

328 BART-Survival provides the computational methods required for completing non-parametric
329 discrete-time survival analysis. This approach can have several advantages over alternative
330 survival methods. These advantages include capabilities to incorporate non-linear and interac-
331 tion effects into the model, naturally ability to regularize the model (which reduces the risk of
332 over-fitting) and of being robust to issues of multi-collinearity. The BART-Survival approach
333 is especially useful when the assumptions of alternative survival methods are violated.

334 Our BART-Survival algorithm has been tested in a rigorous simulation study, with additional
335 applications to real-world data. While the manuscript for this work is currently under develop-
336 ment, the results indicate similar performance as the the R-based BART survival method across
337 settings of varied complexity. Both methods demonstrate the previously describe advantages
338 over other survival approaches (such as Cox Proportional Hazard Models) when the relationships
339 within the data becomes more complex or assumptions of the these other models are violated.
340 A comparison of the R-based method and our BART-Survival algorithm is included in the
341 [examples folder of the github repository](#).

342 Our library provides a convenient API for completing discrete-time survival analysis, along with
343 the functionality to customize the methodology as needed. The associated API documentation
344 can be found [here](#), along with the associated github repository [BART-Survival](#).

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