

# A framework for leveraging machine learning tools to estimate personalized survival curves

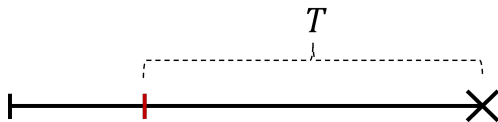
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# Background

In this project, we study  $T$ , the time between an initiating event and a terminating event.

- Example: time from **disease onset** to **death**



$T$  may be right-censored due to loss to follow-up, end of study, etc.

# Full and observed data

The **full-data** world:

$X$		covariates
$T$		time to event
$C$		time to censoring

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The **observed-data** world:

$X$		covariates
$Y := \min\{T, C\}$		observed follow-up time
$\Delta := \mathbb{1}(T \leq C)$		event indicator

# Machine learning for conditional survival curves

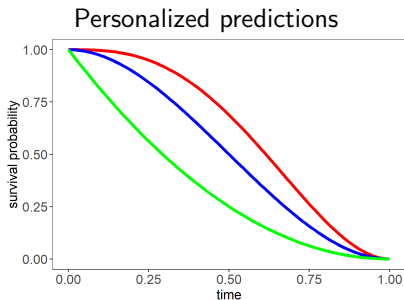
**Goal:** Use machine learning tools to estimate the conditional survival function of  $T$  subject to right censoring.

Desired properties:

1. Incorporate off-the-shelf machine learning methods (not adapted for censoring)
2. Estimate the entire survival function over some interval (not just at a single time-point)

# The conditional survival function

Our goal is to estimate  $S(\tau | x) := P(T > \tau | X = x)$ . Why is this quantity of interest?



Nuisance parameter in non- and semiparametric problems

$$\mathbb{E}[S(\tau | X)]$$

# Loss functions

Machine learning methods rely on loss functions for

1. Optimization: e.g., gradient boosting, neural nets
2. Tuning parameter selection: comparing predictions to observations

For estimating  $S(\tau | x)$ , we might use familiar squared-error loss:

$$L(x, t, \theta) = \{\mathbb{1}(t > \tau) - \theta(x)\}^2$$

In fact, the minimizer of this loss is  $\theta(x) = S(\tau | x)$ . Unfortunately:

- We can't evaluate this because we don't observe  $T$ .
- This only targets a single time  $\tau$ , rather than an entire survival curve.

# Estimation at a single time point

What if there were no censoring? Then  $S(\tau | x)$  can be viewed as a binary regression (or classification) problem.

$$\begin{pmatrix} X & T \\ \hline X_1 & T_1 \\ X_2 & T_2 \\ X_3 & T_3 \\ \vdots & \vdots \\ X_n & T_n \end{pmatrix} \longrightarrow \begin{pmatrix} X & \text{outcome} \\ \hline X_1 & \mathbb{1}(T_1 > \tau) \\ X_2 & \mathbb{1}(T_2 > \tau) \\ X_3 & \mathbb{1}(T_3 > \tau) \\ \vdots & \vdots \\ X_n & \mathbb{1}(T_n > \tau) \end{pmatrix}$$

# Estimation on a grid (global stacking)

Choose a time grid  $\mathcal{C} := \{\tau_1, \dots, \tau_J\}$ .

$$\begin{array}{c}
 \left( \begin{array}{cc}
 X & T \\
 \hline
 X_1 & T_1 \\
 X_2 & T_2 \\
 X_3 & T_3 \\
 \vdots & \vdots \\
 X_n & T_n
 \end{array} \right) \xrightarrow{\text{stack}} \left( \begin{array}{ccc}
 X & \text{time} & \text{outcome} \\
 \hline
 X_1 & t_1 & \mathbb{1}(T_1 > \tau_1) \\
 X_2 & t_1 & \mathbb{1}(T_2 > \tau_1) \\
 \vdots & \vdots & \vdots \\
 X_n & t_1 & \mathbb{1}(T_n > \tau_1) \\
 X_1 & t_2 & \mathbb{1}(T_1 > \tau_2) \\
 X_2 & t_2 & \mathbb{1}(T_2 > \tau_2) \\
 \vdots & \vdots & \vdots \\
 X_n & t_2 & \mathbb{1}(T_n > \tau_2) \\
 X_1 & t_3 & \mathbb{1}(T_1 > \tau_3) \\
 X_2 & t_3 & \mathbb{1}(T_2 > \tau_3) \\
 \vdots & \vdots & \vdots
 \end{array} \right)
 \end{array}$$



## A discrete approach (local stacking)

Alternatively, we could treat  $T$  as discrete, such that it can **only** take values in  $\mathcal{C}$ .

$$P(T > \tau | X = x) = \prod_{\tau_i < \tau} \{1 - P(T = \tau_i | T > \tau_{i-1}, X = x)\}$$

Each of these probabilities can be estimated using binary regression, or can be estimated jointly by stacking the data matrices.

Unlike in the previous approach, the choice of  $\mathcal{C}$  determines the number of events in each time bin.

- Coarse grid: more events in each bin, but potential loss of information since all events in same bin are treated equally
- Fine grid: fewer events in each bin, more difficult estimation problem

# Loss functions under censoring

Possible solutions to the censoring problem:

- Adapt the loss function to account for censoring.

$$L(x, y, \delta, \theta) = \frac{\delta}{P(C > y | X = x)} \{\mathbb{1}(y > \tau) - \theta(x)\}^2$$

- Use an loss that doesn't depend on actual event times (e.g., the negative Cox partial likelihood).

# Hazards

The conditional hazard function  $\lambda(\tau | x)$  is the instantaneous event rate at time  $\tau$  conditional on  $X = x$ .

$$\lambda(\tau | x) = \lim_{\epsilon \rightarrow 0} \frac{P(\tau \leq T \leq \tau + \epsilon | T \geq \tau, X = x)}{\epsilon}$$

The cumulative hazard is  $\Lambda(\tau | x) = \int_0^\tau \lambda(u | x) du$ .

The hazard and survival functions are linked via the product integral:

$$S(\tau | x) = \prod_{u \in (0, \tau]} \{1 - \Lambda(du | x)\}$$

# Hazards

Hazards allow us to identify the survival function in the presence of conditionally independent right censoring.

In the discrete case,

$$P(T = \tau \mid T \geq \tau, X = x) = P(Y = \tau, \Delta = 1 \mid Y \geq \tau, X = x).$$

Therefore, the discrete local stacking approach is still valid, even with censoring.

# Hazards

However, we don't need to artificially discretize time. It turns out we can decompose the cumulative hazard conveniently as

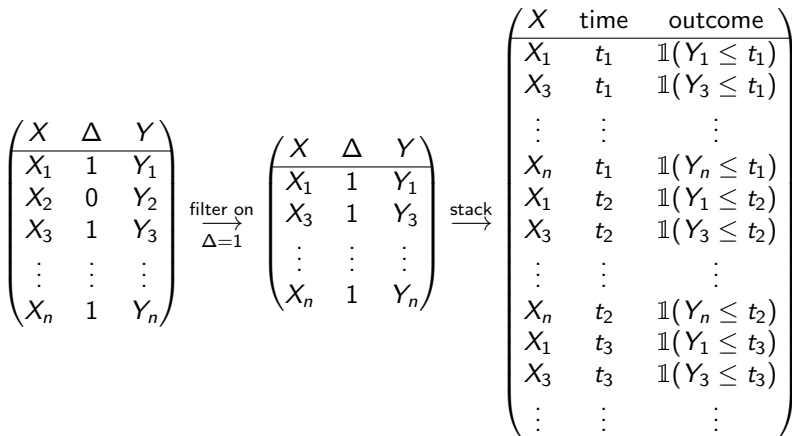
$$\Lambda(du | x) = \frac{\pi(x)F_{Y,1}(du | x)}{\pi(x)\{1 - F_{Y,1}(u | x)\} + \{1 - \pi(x)\}\{1 - F_{Y,0}(u | x)\}}$$

Three components to estimate:

- $\pi(x) := P(\Delta = 1 | X = x)$  conditional event probability
- $F_1(u | x) := P(Y \leq u | \Delta = 1, X = x)$  conditional CDF of  $Y$  among the uncensored
- $F_0(u | x) := P(Y \leq u | \Delta = 0, X = x)$  conditional CDF of  $Y$  among the censored

## CDF estimation

Same as before, but this time we stratify on  $\Delta$ :



# Computational concerns

The stacked matrix for CDF estimation can be quite large, with dimension depending on sample size and the time grid  $\mathcal{C}$ .

- Time and memory usage are potential issues.

**Solution:** Adopt stochastic gradient descent.

1. Mini-batch over sample indices  $\{1, \dots, n\}$ .
2. Mini-batch over times in the grid  $\mathcal{C} = \{\tau_1, \dots, \tau_J\}$ .

## Extra information

- Global survival stacking implemented in R package `survML`:  
<https://github.com/cwolock/survML>.
- Manuscript available on arXiv [Wolock et al., 2022].



# References

Craig, E., Zhong, C., and Tibshirani, R. (2021).

Survival stacking: casting survival analysis as a classification problem.  
[arXiv:2107.13480](https://arxiv.org/abs/2107.13480).

van der Laan, M. J. and Rose, S. (2011).

*Targeted Learning: Causal Inference for Observational Data*.  
Springer.

Westling, T., Luedtke, A., Gilbert, P. B., and Carone, M. (2021).

Inference for treatment-specific survival curves using machine learning.  
[arXiv:2106.06602](https://arxiv.org/abs/2106.06602).

Wolock, C. J., Gilbert, P. B., Simon, N., and Carone, M. (2022).

A framework for leveraging machine learning tools to estimate personalized survival curves.  
[arXiv:2211.03031](https://arxiv.org/abs/2211.03031).

## Extra slides

# Local survival stacking

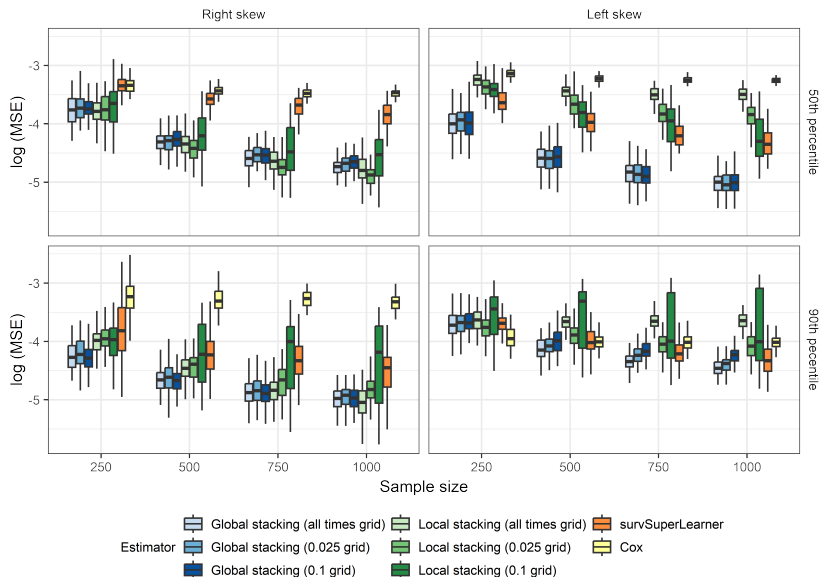
$$\begin{array}{c}
 \left( \begin{array}{ccc}
 X & \Delta & Y \\
 \hline
 X_1 & 1 & Y_1 \\
 X_2 & 0 & Y_2 \\
 X_3 & 1 & Y_3 \\
 \vdots & \vdots & \vdots \\
 X_n & 1 & Y_n
 \end{array} \right)
 \xrightarrow{\text{stack}}
 \left( \begin{array}{ccc}
 X & \text{time} & \text{outcome} \\
 \hline
 X_1 & Y_1 & 1 \\
 X_2 & Y_1 & 0 \\
 \vdots & \vdots & \vdots \\
 X_n & Y_1 & 0 \\
 X_3 & Y_3 & 1 \\
 X_4 & Y_3 & 0 \\
 \vdots & \vdots & \vdots \\
 X_n & Y_3 & 0 \\
 \vdots & \vdots & \vdots
 \end{array} \right)
 \end{array}$$

# Simulations: setup

Compare the performance of the following:

1. **Proposed method (global survival stacking)**: Using Super Learner for binary regression, three time grids (fine, medium, coarse)
2. **Discrete hazards (local) survival stacking**: [van der Laan and Rose, 2011, Craig et al., 2021] Using Super Learner for binary regression, three time grids (fine, medium, coarse)
3. **survSuperLearner**: [Westling et al., 2021] Ensemble method for survival-specific estimators (Cox, Kaplan-Meier, parametric regression, random survival forest)
4. **Cox proportional hazards model**

# Simulation results



# STEP trial

- Phase IIB trial for Ad5 HIV vaccine, 1,836 individuals assigned male sex at birth in Central and South America
- Some evidence of increased risk of infection among vaccine recipients, particularly among those who were (1) uncircumcised or (2) had baseline Ad5 neutralizing antibodies

