Random survival forests for the analysis of recurrent events for right-censored data, with or without a terminal event

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- 1. Motivating example
- 2. Growing decision trees and ensemble random forests
- 3. Application based on open-source data

Motivating example

What survival data are made of



Figure 1: Readmission dataset (source: frailtypack, R)

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How to predict the number of hospital readmissions over time for each patient?

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- Focus on time to recurrent readmission with a terminal event

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The objective for today is to introduce a new approach to **model recurrent events using ensemble methods**.

Growing decision trees and ensemble random forests

Background on recurrent events survival analysis

Let N(t) the cumulative number of events over the interval $[0, t], t \in [0, T]$ with T the longest follow-up time overall

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- Without a terminal event We use the Nelson-Aalen MCF estimator

$$\hat{\mu}(t) = \int_0^t \frac{dN(u)}{Y(u)} \tag{1}$$

with $N(t) = \sum_i N_i(t)$, and $Y(t) = \sum_i Y_i(t)$ the number of individuals at risk at time t

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• With a terminal event - We incorporate the Kaplan-Meier estimator of the survival function of the terminal event

$$\hat{\mu}(t) = \int_{0}^{t} \hat{S}(u) \frac{\sum_{i} Y_{i}(u) dN_{i}(u)}{\sum_{i} Y_{i}(u)}$$
(2)



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Bucket list:

- A **splitting** rule at each node
- A terminal node **estimator**
- A **pruning** strategy

Growing survival decision trees



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	Without a terminal event	With a terminal event
Splitting rule	Maximize the test statistic	
At each node, $m \in \mathbb{N}$ predictors	Pseudo-score test	Wald test
are randomly selected	from np estimates	from Ghosh-Lin model
Terminal node estimator	$\hat{\mu}_b(t \mathbf{x})$	$\hat{\mu}_b(t \mathbf{x})$
for tree b	$= \int_0^t \frac{dN_b(u)}{Y_b(u)}$	$= \int_{0}^{t} \hat{S}_{b}(u) \frac{\sum_{i} Y_{b,i}(u) dN_{b,i}(u)}{\sum_{i} Y_{b,i}(u)}$
Pruning strategy	A minimal number of events	
	and/or a minimal number of individuals	

Aggregating to build random forests





Performance evaluation - (a) The concordance index

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The proposed C-index is based on event occurrence rate to tackle inter-individual heterogeneity

$$\hat{\mathbb{C}}_{\text{rec}} = \frac{\sum_{i=1}^{n} \sum_{j=1}^{n} \mathbb{1}_{r_i > r_j} \times \mathbb{1}_{\hat{r}_i > \hat{r}_j}}{\sum_{i=1}^{n} \sum_{j=1}^{n} \mathbb{1}_{r_i > r_j}}$$
(3)

with $r_i = \frac{N_i(T_i)}{T_i}$ and $\hat{r}_i = \frac{\hat{\mu}(T_i|\mathbf{x}_i)}{T_i}$ the observed and predicted event occurrence rates, respectively.

Performance evaluation - (b) The mean square error

- No MSE metric for recurrent events framework until very lately (Bouaziz, 2023)
- We adapted for an ensemble framework

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For each tree *b*,

$$\widehat{MSE}_{b}(t,\hat{\mu}_{b}) = \frac{1}{n} \sum_{i=1}^{n} \left(\int_{0}^{t} \frac{dN_{i}(u)}{\hat{G}_{c}(u|\mathbf{x})} - \hat{\mu}_{b}(t|\mathbf{x}) \right)^{2}$$
(4)

Where $\hat{G}_c(u|\mathbf{x}) = 1 - \hat{G}(u - |\mathbf{x})$ is an estimator of $G_c(u|\mathbf{x}) = 1 - G(u - |\mathbf{x})$ the conditional cumulative distribution function of the censoring variable *C* given \mathbf{x} .

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Thus:

$$\widehat{MSE}\left(t,\hat{M}\right) = \frac{1}{B} \sum_{b=1}^{B} \widehat{MSE}_{b}(t,\hat{\mu}_{b})$$
(5)

Performance evaluation - (c) The score

But

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We introduce a score to represent the prediction gain compared to a reference estimator and we define for each tree *b*

$$Score_b(t, \hat{\mu}_b, \hat{\mu}_{b,0}) = \widehat{MSE}_b(t, \hat{\mu}_{b,0}) - \widehat{MSE}_b(t, \hat{\mu}_b)$$
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Thus:

$$Score\left(t,\hat{M}\right) = \frac{1}{B}\sum_{b=1}^{B}Score_{b}\left(t,\hat{\mu}_{b},\hat{\mu}_{b,0}\right)$$
(7)

Performance evaluation - Integrated counterparts

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$$\begin{cases} \widehat{IMSE}(\tau_1, \tau_2, \hat{M}) &= \frac{1}{\tau_2 - \tau_1} \int_{\tau_1}^{\tau_2} \widehat{MSE}(t, \hat{M}) dt \\ IScore(\tau_1, \tau_2, \hat{M}) &= \frac{1}{\tau_2 - \tau_1} \int_{\tau_1}^{\tau_2} Score(t, \hat{M}) dt \end{cases}$$

(8)

With $\tau_1 = 0$ and τ_2 the maximum event time on the original sample.

Application

- Readmission dataset from R was used
- Multiple rehospitalizations after surgery in 403 patients diagnosed with colorectal cancer, with 199 patients with no admission and a total of 106 deaths
- Available factors: sex (M/F), chemotherapy treatment (Yes/No), Dukes' tumoral stage (with levels A-B, C, and D), and time-dependent comorbidity Charlson's index (with levels 0, 1-2, and 3)
- Predictions from np estimator and Ghosh-Lin models were used for comparison

Metric	C-index ↑	IMSE ↓	IScore ↑
Np	0.58 (0.05)	7 883.50 (6 229.47)	ref.
GL1	0.53 (0.08)	7 843.99 (6 106.36)	39.41 (230.6)
GL2	0.48 (0.08)	8 361.16 (6 292.29)	-477.67 (348.48)
GL3	0.48 (0.07)	8 229.08 (6 478.35)	-345.62 (432.6)
GL4	0.45 (0.05)	9 981.50 (6 064.23)	-2 098.44 (541.59)
RecForest	0.80 (0.04)	706.02 (508.96)	188.22 (89.00)
GL*	0.60 (0.06)	7 934.28 (6 606.23)	51.33 (142.63)

Table 1: Means and standard deviations over the 10-fold cross-validation

Variable importance



Figure 3: Variable importance of RecForest computed on the C-index and the opposite of the integrated MSE. Charlson refers to Charlson comorbidity index, Dukes refers to tumoral Dukes stage.

Predictions



Figure 4: Expected cumulative number of recurrent events with RecForest for two patients, one in orange with the highest Charlson comorbidity score, and the other in blue with the lowest. Data points outside the prediction curves are observed data. Triangle indicates the patient died.

Discussion & Conclusion

To wrap-up

Take home messages

- Our approach is simple and easily accessible;
- **RecForest** handles longitudinal factors, terminal events, high-dimensionality, and missing data;
- Insight of interpretability with feature importance;
- Solid baseline for many extensions.

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Take home messages

- Our approach is simple and easily accessible;
- **RecForest** handles longitudinal factors, terminal events, high-dimensionality, and missing data;
- Insight of interpretability with feature importance;
- Solid baseline for many extensions.

For these reasons, the approach we propose is a **valuable contribution** for analysing recurrent events in medical research. Thank you for your attention!

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