Dynamic RMST from Predicted Survival Curves with tvrmst

A methodological note on dynamic restricted mean survival time as an interpretable summary of individualized survival predictions.

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Restricted mean survival time (RMST) summarizes a survival curve on the time scale of the outcome. For a survival function $S(t) = P(T > t)$, the RMST up to horizon τ is

$$\mu(\tau) = \int_0^\tau S(t)\, dt.$$

When the input is an individualized survival matrix, each row is a predicted survival curve $S_i(t_j)$ for patient i at grid time t_j. The individual dynamic RMST curve is

$$\hat{\mu}_i(\tau_k) = \sum_{j=1}^{k} \frac{S_i(t_{j-1}) + S_i(t_j)}{2}(t_j - t_{j-1}),$$

using the trapezoidal rule on the prediction grid. The population summary is then

$$\hat{\mu}(\tau_k) = \frac{1}{n}\sum_{i=1}^{n} \hat{\mu}_i(\tau_k).$$

For two groups, a clinically readable contrast is the RMST difference

$$\Delta(\tau) = \hat{\mu}_B(\tau) - \hat{\mu}_A(\tau),$$

which can be read as the difference in expected event-free time up to τ. This is often easier to explain than a hazard ratio when proportional hazards is doubtful.[1]

Example

The `tvrmst` package works with survival matrices and computes RMST over one or several horizons.[2]

```
library(tvrmst)

set.seed(1)
time <- seq(0, 24, by = 1)

control <- outer(
  1:6, time,
  function(i, t) exp(-0.035 * t) * (1 - 0.015 * i)
)

treatment <- outer(
  1:6, time,
  function(i, t) exp(-0.025 * t) * (1 - 0.010 * i)
)

control_mat <- as_survmat(
  control,
  time = time,
  id = paste0("C", 1:6),
  group = rep("Control", 6)
)

treatment_mat <- as_survmat(
  treatment,
  time = time,
  id = paste0("T", 1:6),
  group = rep("Treatment", 6)
```

[1] Royston, P., & Parmar, M. K. B. (2013). Restricted mean survival time: an alternative to the hazard ratio for the design and analysis of randomized trials with a time-to-event outcome. *BMC Medical Research Methodology*, 13, 152.

[2] `tvrmst` package documentation, CRAN: https://CRAN.R-project.org/package=tvrmst.

```
)

control_rmst <- rmst_dynamic(control_mat, tau = c(6, 12, 18, 24))
treatment_rmst <- rmst_dynamic(treatment_mat, tau = c(6, 12, 18, 24))

treatment_rmst$at_tau
```

```
  tau  estimate
1   6  5.376952
2  12 10.004938
3  18 13.988282
4  24 17.416778
```

The dynamic RMST values increase with the horizon because they accumulate survival probability over time. A group contrast is computed from the two survival matrices:

```
delta <- rmst_delta(control_mat, treatment_mat, tau = c(6, 12, 18, 24))
delta$at_tau
```

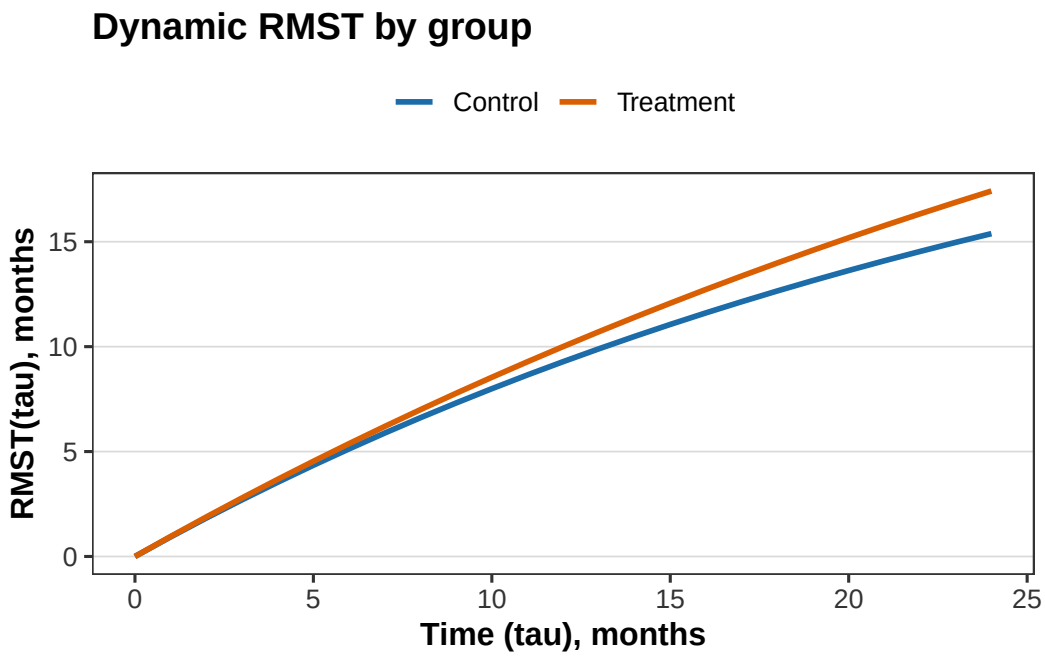
```
  tau    rmst_A    rmst_B     delta
1   6  5.128279  5.376952 0.2486736
2  12  9.285180 10.004938 0.7197575
3  18 12.654699 13.988282 1.3335825
4  24 15.385978 17.416778 2.0307995
```

In this example, the treatment survival curves stay above the control curves. The absolute RMST gain grows as the horizon increases: the estimated difference is about 0.25 months at 6 months and about 2.03 months at 24 months. The interpretation is direct: by 24 months, the treatment profile has about two additional months of expected event-free time within the restricted follow-up window.

Figures

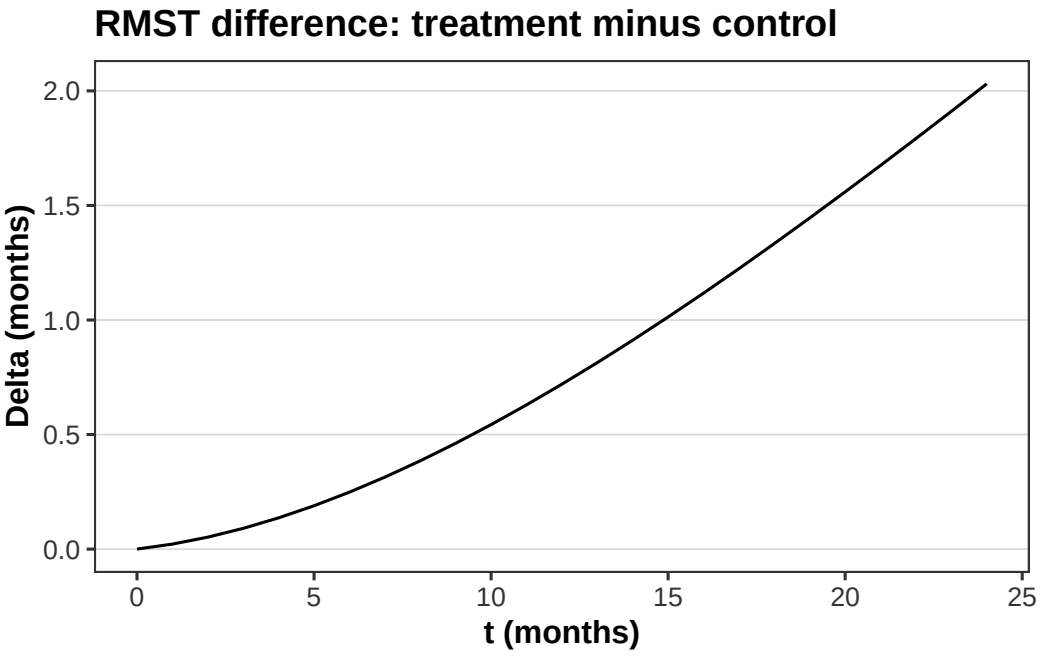
The dynamic RMST curves show how expected event-free time accumulates over the follow-up horizon.

```r
plot_rmst_two_arms(
  control_mat,
  treatment_mat,
  labels = c("Control", "Treatment"),
  title = "Dynamic RMST by group",
  x_unit = "months",
  y_unit = "months"
)
```



The delta curve makes the horizon-dependent treatment-control contrast explicit.

```r
delta_curve <- rmst_delta(control_mat, treatment_mat)
plot_delta_curve(
  delta_curve$time,
  delta_curve$delta,
  title = "RMST difference: treatment minus control",
  x_unit = "months",
  y_unit = "months"
)
```



Practical Notes

- Report the prediction time grid and the maximum horizon.
- Avoid extrapolating beyond the time support of the fitted survival model.
- Prefer several clinically meaningful horizons when the timing of separation matters.
- Interpret RMST contrasts as descriptive summaries unless the comparison is embedded in a valid causal design.