

Recurrent Event Analysis with R packages **reda** and **reReg**

Recurrent event data arise when the event of interest, such as hospital admissions, infections, or tumor recurrences, can recur in the same individual during follow-up. The standard “time-to-first” event analysis cannot capture the cumulative experience of the recurrent events and could lead to invalid inferences. The R packages **reda** (Wang et al., 2020) and **reReg** (Chiou and Huang, 2020) provide a collection of methods for exploring and analyzing recurrent event data.

Consider a random sample of n subjects and let $N_i(t)$ be the number of events the i th subject experienced over the interval $[0, t]$. Let D be the failure time of interest that could either be a terminal event (e.g., death) or a non-terminal event (e.g., treatment failure). Let C be the potential censoring time for reasons other than the failure event (e.g., study dropouts). The observed data are independent and identically distributed copies $\{N_i(t), Y_i, X_i; t \leq Y_i, i = 1, \dots, n\}$, where $Y_i = \min(D, C)$, $\Delta_i = I(D \leq C)$, $I(\cdot)$ is the indicator function, X_i is a co-variate vector, and $N_i(\cdot)$ is observed up Y_i . We illustrate the key features of **reda** and **reReg** with the rehospitalization data from the **frailtypack** package (Rondeau et al., 2019).

The `Recur()` function prepares the recurrent event data into a `Recur` object used in the packages **reda** and **reReg**. The `Recur` object is an S4 class object that bundles together a set of recurrent times, failure time, and censoring status. The `Recur` object is also used as the formula response for many key functions in **reda** and **reReg**. The following commands create a `Recur` object corresponding to the rehospitalization data:

```
library(reda); library(reReg)
data(readmission, package = "frailtypack")
with(readmission, Recur(t.stop, id, event, death))
```

Error: Subjects having multiple terminal events:
60, 109, 280.

The `Recur()` internally checks whether the specified data fits into the recurrent event data framework and detected a possible issue on the data structure. The `show()` method for `Recur` objects presents recurrent events in intervals, where events happened at end of the recurrent episodes with censoring due to (or not) terminal indicated by a trailing + (or *). The following prints the `Recur` object for the first five subjects.

```
with(readmission[1:14,], Recur(t.stop, id, event, death))
```

```
[1] 1: (0, 24], (24, 457], (457, 1037+]
[2] 2: (0, 489], (489, 1182+]
[3] 3: (0, 15], (15, 783*]
[4] 4: (0, 163], (163, 288], ..., (686, 2048+]
[5] 5: (0, 1134], (1134, 1144+]
```

An easy way to glance at recurrent event data is by event plots, which can be created by applying the generic function `plot()` to the `Recur` object when the **reReg** package is loaded. Additionally, the `plotEvents()` function from the **reReg** package allows users to stratify the event plots by discrete variables. The following codes produces event plots with and without stratifying by whether the patients received chemotherapy.

```
df0 <- subset(readmission, !(id %in% c(60, 109, 280)))
obj <- with(df0, Recur(t.stop, id, event, death))
plot(obj, legend = "bottom") ## Fig. 1
fn <- Recur(t.stop, id, event, death) ~ chemo
plotEvents(fn, data = df0, legend = "bottom") ## Fig. 2
```

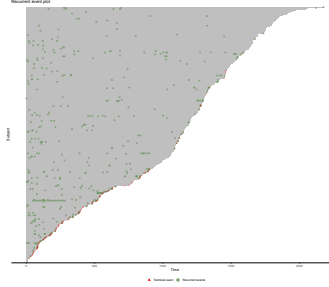


Fig. 1: No stratification

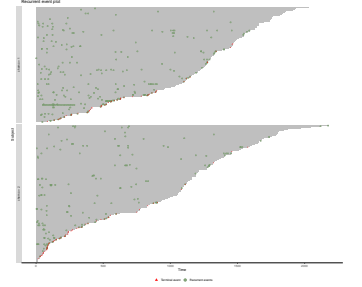


Fig. 2: Stratified by ‘chemo’.

The mean cumulative function (MCF) is often the focus in the nonparametric analysis of recurrent events. Let $M_i(t) = \mathbb{E}\{N_i(t)\}$ denote the MCF of $N_i(t)$. The Nelson-Aalen estimator (Nelson, 2003) for the MCF takes the form

$$\widehat{M}(t) = \int_0^t \frac{dN(s)}{\delta(s)},$$

where $dN(s) = \sum_{i=1}^k dN_i(s)$, $\delta(s) = \sum_{i=1}^k \delta_i(s)$, $dN_i(s)$ and $\delta_i(s)$ is, respectively, the jump size and at-risk indicator of process i at time s . The MCF can be visualized by plotting the `Recur` object with argument `mcf = TRUE` when the **reReg** package is active, e.g., `plot(obj, mcf = TRUE)`. Alternatively, the `mcf()` function from the **reda** package provides a more sophisticated approach to plot MCFs and make inference. The following example uses the `mcf()` function to visualize MCF estimates stratified by whether the patients received chemotherapy.

```
re_mcf <- mcf(fn, data = df0)
plot(re_mcf, conf.int = TRUE, lty = 1:2) +
  ggplot2::theme(legend.position = "bottom") ## Fig. 3
```

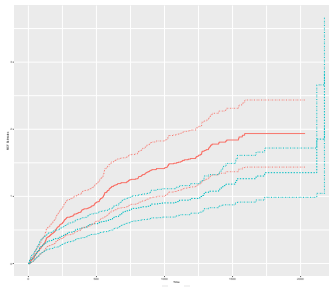


Fig. 3: Stratified by ‘chemo’

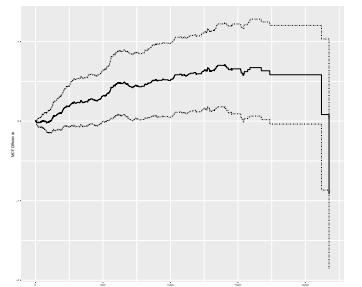


Fig. 4: MCF difference

The MCF difference between two groups can be tested via `mcfDiff.test()`, which implements the two-sample pseudo-score tests of (Cook et al., 1996). The following results indicate the MCF estimates are statistically different at a significance level of 0.05. The MCF difference can be plotted directly by `plot(mcfDiff(re_mcf))`, as shown in Fig. 4.

```
mcfDiff.test(re_mcf)
```

Two-Sample Pseudo-Score Tests:

	Statistic	Variance	Chisq	DF	Pr(>Chisq)
Constant Weight	47.49	416.71	5.41	1	0.020 *
Linear Weight	36.56	263.59	5.07	1	0.024 *

Signif. codes:

0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Variance Estimator: robust

When the study interest is to evaluate the covariate effect on the recurrent event process and/or the terminal event, the `reReg()` function from the **reReg** package fits semiparametric regression models to recurrent event data. A general joint model for the rate of the recurrent event process and the hazard of the failure time can be formulated as follow:

$$\lambda(t) = Z\lambda_0(te^{X^\top\alpha})e^{X^\top\beta}; h(t) = Zh_0(te^{X^\top\eta})e^{X^\top\theta}, \quad (1)$$

where Z is a latent shared frailty variable to account for association between the two types of outcomes, $\lambda_0(\cdot)$ is the baseline rate function, $h_0(\cdot)$ is the baseline hazard function, and the regression coefficients (α, η) and (β, θ) correspond to the shape and size parameters of the rate function and hazard function, respectively. In contrast to many shared-frailty models that require a parametric assumption, following the idea of Wang et al. (2001), the `reReg()` function implements semiparametric estimation procedures that do not require the knowledge about the frailty distribution. As a result, the dependence between recurrent events and failure event is left unspecified and the proposed implementations accommodate informative censoring.

Model (1) includes several popular semiparametric models as special cases, which can be specified via the `method` argument with the rate function and hazard function separated by `"|"`. For examples, the joint Cox model proposed by Huang and Wang (2004) is a special case of (1) when $\alpha = \eta = 0$ and can be called by `method = "cox|cox"`; the joint Accelerated Mean model proposed by Xu et al. (2017) is a special case when $\alpha = \beta$ and $\eta = \theta$ and can be called by `method = "am|am"`. When the primary interest is in the covariate effects on the risk of recurrent events and treating the terminal event as nuisances, i.e., $\eta = \theta = 0$, model (1) reduces to the generalized scale-change model proposed in Xu et al. (2019), called by `method = "sc|."`. Users can mixed and match the `method` arguments depending on the application. For example, `method = "cox|ar"` postulate a Cox proportional model for the recurrent event rate function and an accelerated rate model for the terminal event hazard function, i.e., this assumes $\alpha = \theta = 0$ in (1). For inference, the asymptotic variance is estimated from an efficient resampling-based sandwich estimator motivated by Zeng and Lin (2008). The resampling approach is faster than the conventional bootstrap method as it only requires evaluating perturbed estimating equations rather than solving them. The following code fit the joint Cox model with 200 (default) resampling replicates:

```
system.time(fit <- reReg(fn, df0, method = "cox|cox"))
```

user	system	elapsed
1.884	0.016	1.903

The `summary()` method prints the results of the model fits:

```
summary(fit)
```

Call:

```
reReg(formula = fn, data = df0, method = "cox|cox")
```

Recurrent event process:

	Estimate	StdErr	z.value	p.value
chemoTreated	-0.189	0.244	-0.778	0.437

Terminal event:

	Estimate	StdErr	z.value	p.value
chemoTreated	0.519	0.286	1.815	0.07

After a model is fitted, the baseline rate function and hazard function can be visualized by plotting the `reReg()` object. Methods proposed by authors Lin et al. (2000), Ghosh and Lin (2002), and Ghosh and Lin (2003) are also implemented in **reReg**. See wenjie-stat.me/reda/ and www.sychiou.com/reReg/ for the full package documents.

Reference

- Chiou, S. H. and Huang, C.-Y. (2020), **reReg: Recurrent Event Regression**, R package version 1.3.0.
- Cook, R. J., Lawless, J. F., and Nadeau, C. (1996), "Robust Tests for Treatment Comparisons Based on Recurrent Event Responses," *Biometrics*, 52, 557–571.
- Ghosh, D. and Lin, D. (2003), "Semiparametric analysis of recurrent events data in the presence of dependent censoring," *Biometrics*, 59, 877–885.
- Ghosh, D. and Lin, D. Y. (2002), "Marginal regression models for recurrent and terminal events," *Statistica Sinica*, 663–688.
- Huang, C.-Y. and Wang, M.-C. (2004), "Joint modeling and estimation for recurrent event processes and failure time data," *Journal of the American Statistical Association*, 99, 1153–1165.
- Lin, D. Y., Wei, L.-J., Yang, I., and Ying, Z. (2000), "Semiparametric regression for the mean and rate functions of recurrent events," *Journal of the Royal Statistical Society: Series B (Statistical Methodology)*, 62, 711–730.
- Nelson, W. B. (2003), *Recurrent events data analysis for product repairs, disease recurrences, and other applications*, Society for Industrial and Applied Mathematics.
- Rondeau, V., Gonzalez, J. R., Mazroui, Y., Mauguen, A., Diakite, A., Laurent, A., Lopez, M., Król, A., and Sofeu, C. L. (2019), *frailtypack: General Frailty Models: Shared, Joint and Nested Frailty Models with Prediction; Evaluation of Failure-Time Surrogate Endpoints*, R package version 3.0.3.
- Wang, M.-C., Qin, J., and Chiang, C.-T. (2001), "Analyzing recurrent event data with informative censoring," .
- Wang, W., Fu, H., and Yan, J. (2020), **reda: Recurrent Event Data Analysis**, R package version 0.5.1.
- Xu, G., Chiou, S. H., Huang, C.-Y., Wang, M.-C., and Yan, J. (2017), "Joint scale-change models for recurrent events and failure time," *Journal of the American Statistical Association*, 112, 794–805.
- Xu, G., Chiou, S. H., Yan, J., Marr, K., and Huang, C.-Y. (2019), "Generalized scale-change models for recurrent event processes under informative censoring," *Statistica Sinica*.

Zeng, D. and Lin, D. (2008), “Efficient resampling methods for nonsmooth estimating functions,” *Biostatistics*, 9, 355–363.



Wenjie Wang
Research Scientist
Machine Learning, Artificial
Intelligence, and Connected Care
Advanced Analytics and Data Sciences
Eli Lilly and Company
Email: wang-wenjie@lilly.com



Sy Han Chiou
Assistant Professor
Department of Mathematical Sciences
University of Texas at Dallas
Email: schiou@utdallas.edu