Single-Index Mixture Cure Models in R: An Application to a Cardiotoxicity Dataset with the Sicure Package

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Abstract

Standard survival models assume that, in the absence of censoring, all individuals will experience the event of interest. However, sometimes this is not realistic. For example, if the event is a cancer therapy-related adverse effect, there will be a fraction of patients (considered as cured) who will never experience it. Mixture cure models address this by estimating both the probability of cure and the survival function for the uncured subjects (known as latency). In the literature, nonparametric estimation of these functions focuses on continuous univariate covariates. However, in clinical practice, it is common to collect several patient characteristics and medical imaging data. The R package sicure implements single-index mixture cure models, that can handle a vector covariate under the assumption that the survival function depends on it through an unknown linear combination estimable via maximum likelihood techniques. These models can be easily extended to functional covariates. Additionally, the package incorporates the implementation of a nonparametric density estimator for the uncured population. The use of this package is illustrated with a cardiotoxicity dataset, demonstrating its practical application in medical research.

Keywords

Dimension reduction, functional data, kernel estimation, survival analysis.