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Title: Flexible Models for Survival Data

Abstract:

Classical linear regression involves introducing predictor variables through the mean of the response variable, whereas the variance is a constant common to all individuals. However, there is no reason believe that this should be true in practice – just as the mean varies with predictor variables, so too can the variance (albeit the constant variance assumption leads to elegant classical theory). A more flexible "multi-parameter regression" (MPR) approach is to allow both mean and variance parameters to depend on predictor variables; this is known as "heteroskedastic regression" in econometrics.

In the field of survival analysis, Cox's "proportional hazards" (PH) regression model reigns supreme (especially in medical applications) – and the "accelerated failure time" (AFT) model is also very much used (especially in engineering applications). Both the PH and AFT models assume that a scale parameter depends on predictor variables, whereas the shape does not. In the PH model, this implies that the hazards for any two individuals have exactly the same shape (e.g., increasing or decreasing over time), differing only in terms of the overall size (small or large hazards). Just like the classical linear model, this leads to nice theoretical properties, but, in practice, we often observe hazards with different shapes such that they converge or cross in time.

We examine flexible MPR modelling of survival data through simultaneous scale and shape regression. Our unified framework generalises both the PH and AFT models, and includes all of the most popular parametric baseline distributions (log-logistic, Burr, Weibull, exponential, Gompertz) and hazard shapes (constant, increasing, decreasing, up-then-down, down-then-up); cure models, where a proportion of the population is non-susceptible or cured, are also contained within the framework. Further robustness can be achieved by leaving the baseline unspecified (as is done in the Cox model), i.e., semi-parametric MPR modelling. We apply these models to data arising in lung cancer, melanoma, and kidney function studies, demonstrating their flexibility and discussing their interpretation.