

Mixture Nonuniqueness of the Bivariate Survival NPMLE

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Abstract

The nonparametric maximum likelihood estimator of the survival function (NPMLE) given bivariate censored data is nonunique in some situations, in spite of being consistent in Hellinger distance. This nonuniqueness can arise as so-called representational (or R -) nonuniqueness and mixture (or M -) nonuniqueness. We adapt known optimization techniques to quantify M -nonuniqueness and produce an algorithm to obtain the M -nonuniqueness polytope. We provide a worked example, explicitly dealing with M -nonuniqueness. We produce simulation results indicating that, for moderately sized data sets, M -nonuniqueness can remain a significant nature of the NPMLE, both as regards its probability of occurring and the extent of the M -nonuniqueness.