Title:
Meta-analysis of gene expression and survival data using the R packages SurvComp and genefu

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Abstract:
Gene expression survival analysis is a major research field of biomarker discovery in the war against cancer and seeks to identify prognostic gene expression profiles which predict the probability of events such as patient relapse or survival. A number of gene signatures have been translated into the clinic to guide clinical decision making and therapy. We present the R packages SurvComp and genefu. SurvComp provides tools for meta-analysis and visualization of survival data, enabling statistical comparison of the performance of various risk prediction models. Survcomp performs meta-analysis of multiple genes across multiple gene expression datasets, even across different technologies (e.g. Affymetrix, Agilent). The R package genefu is designed for breast cancer research, and has methods to robustly identify the breast cancer molecular subtypes and computes the prevalence of transcripts with respect to these subtypes. Both R packages are open source and are available in bioconductor.org and CRAN (cran.r-project.org) respectively.