

RTNsurvival: An R package for making survival analyses and plots from transcriptional networks

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Transcriptional networks are important objects of study to better understand the complexity of interactions between genes such as how some key transcriptional factors act in a specific phenotype. Several methods can be used to reconstruct and understand these networks, one is the RTN package, an R tool to build transcriptional network of regulons centered around any regulatory element, such as transcription factors and miRNAs. These regulons can be used to interpret a wide variety of data, including clinical information. However, there is currently no simple tool to integrate survival analysis with reconstructed transcriptional networks ("TNI" objects) from RTN. Here we show the RTNsurvival, which is an R package for making survival analyses and plots from "TNI" object. The package takes transcriptional networks generated by RTN and integrates it with survival data from the same cohort, the methods consist in a Kaplan-Meier curve and a Proportional Hazards Regression model (Cox) analysis, which are regulon-specific, and their respective plots. The package was used to analyse data from a cohort of breast cancer (BRCA) patients from the METABRIC database with a previously computed 'TNI' with transcription factor regulons. It confirmed that the regulon centered around of the estrogen receptor gene (ESR1) is predictive of survival in BRCA patients, with patients with active regulons having higher survival and patients with a repressed regulon having lower survival. RTNsurvival will be submitted to Bioconductor and integrate the RTN-family of R packages, with the intent of facilitating further survival analyses of transcriptional networks provided by RTN package.