

A Transcriptome Based Nonparametric Method to Deconvolute Immune Cells and Cancer Subtypes

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Abstract: The molecular characterization of immune cells as well as cancer subtypes is important for understanding the disease developments and searching effective treatment. A handful models and methods have been developed and shown power in estimating the composition of immune cells or cancer subtypes based on several signatures or the whole transcriptome. However, signature-based methods are easily influenced by between-dataset variations while transcriptome-based methods suffer from measurement noises. Weighted regression improves the estimation but require the distribution assumptions and a sufficient knowledge for weight inference. Given the high complexity of biological system and the small size of experiments, we proposed a non-parametric method by integrating the information from both signatures and transcriptome, which showed significantly improved robustness on simulation and real datasets.