[BIOINFO 2024]

Comparative Evaluation of Deconvolution Methods for Bulk RNA-Sequencing in Blood Samples

Na Young Kwon[1], Jimin Seo[1], Heeje Cho[1], and Young-Jun Jeon[1,*]

[1]*Department of Integrative Biotechnology, Sungkyunkwan University*
**Corresponding author: jeon2020@skku.edu*

Bulk RNA sequencing offers valuable insights into overall gene expression but lacks the resolution to observe RNA expression in individual cell types. To address this limitation, computational deconvolution methods are used to estimate cell type proportions within bulk RNA-seq data using reference datasets. This approach is particularly useful for understanding changes in cell type proportions in disease conditions or tracking gene expression changes in specific cell populations. In this study, multiple deconvolution tools will be evaluated, including CIBERSORTx, Bisque, BayesPrism, DWLS, and Scaden, to determine the most effective method for estimating immune cell type proportions in blood samples. Pseudobulk data will be used to test the accuracy of each method in correctly estimating cell fractions. The results aim to provide a clearer understanding of how these tools perform in a blood-specific context, ultimately enhancing our ability to interpret bulk RNA-seq data in immune-related research, such as observing immunotherapy responses in cancer patients.