PgmNr 1419: The investigation of cell separation-induced gene expression via a penalized deconvolution approach.

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Recently, there has been increasing interest in studying genomics and transcriptomics at the single cell level. One of the keys to single-cell study is the success of developing cell sorting technology that is used to separate cells according to their type. However, the process of cell isolation changes the cell microenvironment that affects the gene activity, and thus, the gene expression change induced by cell separation can bias the conclusion of the single-cell study. To address the perturbation of the gene expression caused by cell sorting, we proposed the statistical deconvolution approach, named PEACH, to decompose the cell type-specific expression from bulk tissue and at the same time identify the genes that are expressed differentially to the pure cell samples that were affected by the cell sorting procedure. In this study, PEACH uses cell type-specific samples as the reference to estimate the underlying cell proportions of bulk samples with immune-related diseases and to identify the genes changing in its expression. As a result, the genes we identified are related to biological functions such as stress-responsive transcription factors, cellular metabolism, ribosomal proteins, and human leukocyte antigen. Our study illustrates that genes sensitive to the cell sorting process are biological meaningfully and non-negligible, and it may provide new insight into single cell study for transcriptomic analysis.