

Statistical analysis of coupled single-cell RNA-seq and immune profiling data

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Abstract: We present an analytical framework for analyzing coupled single-cell transcriptome (scRNA-seq) and T cell receptor sequencing (scTCR-seq) data. The framework provides key functions for preprocessing, aligning cells from different samples, detecting differential gene expression across biological conditions, analyzing sequence features in T cell repertoire, and linking sequence features to gene expression signatures. We demonstrate this framework by analyzing single-cell data both from public databases and from a neoadjuvant immunotherapy clinical trial for non-small cell lung cancer.