COMBATTING FUTURE BIOLOGICAL THREATS – HOST-DIRECTED INTERVENTIONS TO EMERGING THREATS FOR RAPID RESPONSE

An Automated 10x scRNA-seq Workflow

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Single cell transcriptomic (scRNA) analysis is a powerful tool to analyze immune response, among other applications. However, the analysis of the single cell transcriptomic data is not standardized and can be subjective. We compared the performance of different tools and parameter settings using a 10X data set collected from human peripheral blood mononuclear cells (PBMC). Peripheral blood mononuclear cells were collected from healthy donors and donors diagnosed with Burkholderia pseudomallei by collaborators. This study examines human gene expression and bacterial genomes in parallel for insights on patient outcome while building a novel analysis pipeline. Data was analyzed using Kallisto-Bustools, Cell Ranger, Scanpy, SCVI-tools, leiden clustering, py-DeSeq2, and PhaME. Our analysis revealed the importance of removing different types of low-quality data and the challenges of standardizing tool parameters. The results, combined with further research, can help to better understand which methods are the most effective for scRNA-seq analysis. Our results suggest scRNA may be a promising tool to develop biomarkers for predicting clinical outcome.

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