New Cell Type Detection via a Universal Single-Cell Gene Expression Algorithm

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Detecting rare cell types would allow very early disease diagnosis (e.g., cancer, infection), identification of new cell types, and deepen our understanding of cell differentiation. We developed a universal algorithm to identify rare cell types from single-cell gene expression data. Our algorithm discovered a putative new hippocampal (brain) cell type. The state-of-the-art computational method to analyze single-cell gene expression data has serious limitations, including that it requires data from a very large number of genes. Our method overcomes this and other limitations. We validated our algorithm on three datasets which highlight the universality of the method: single-cell qPCR data from mouse hematopoietic cells, single-cell RNA-seq data from human glioblastoma tumors cells, and seq-FISH data from mouse hippocampus cells. The latter could not be analyzed using any existing algorithm, since the dataset contained only a small number of genes. Ours is the first algorithm able to analyze this data, in which we detected a putative new hippocampal cell type. Our validated method can now be applied to a wide range of genomic and transcription data to detect the early onset of diseases and discover new cell types.

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