FEM: mining biological meaning from cell level in Single-cell RNA sequencing data

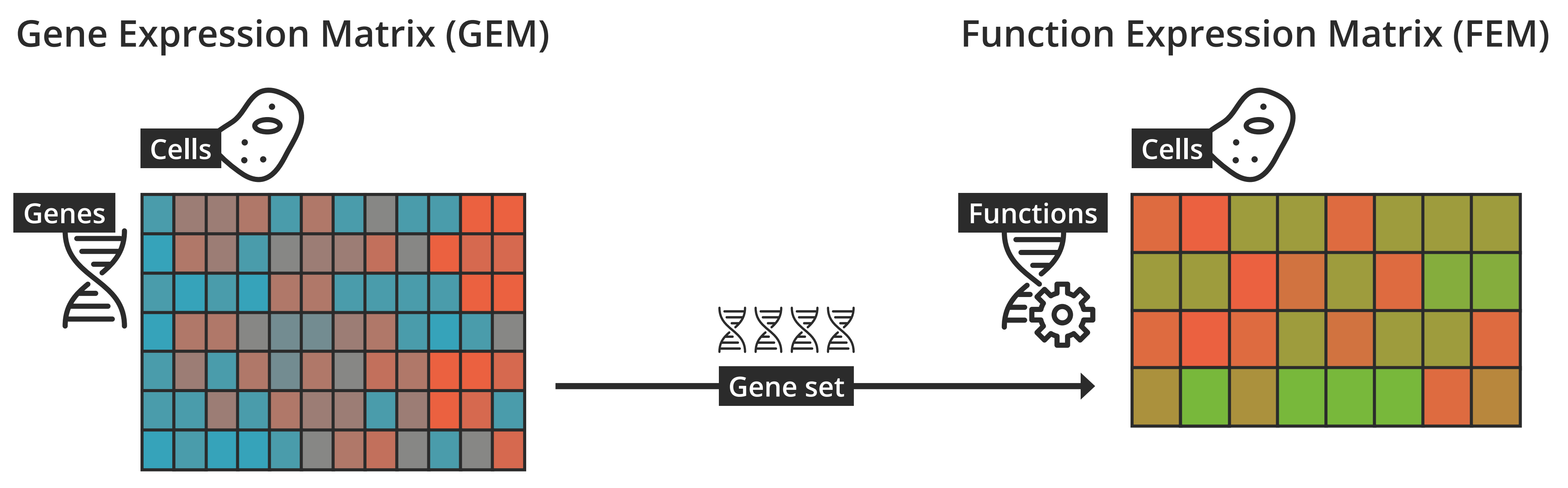
BACKGROUND

One goal of expression data analysis is to discover the biological significance or function of genes that are differentially expressed. Gene Set Enrichment (GSE) analysis is one widely-used tool for function mining. However, **every gene expressed in a cell is valuable information in the GSE analysis of single-cell RNA sequencing (scRNA-SEQ) data and should not be discarded.**

METHODS

We developed the functional expression matrix (FEM) algorithm to utilize the information from all expressed genes. The algorithm converts the gene expression matrix (GEM) into a FEM.

PATHWAY OR FUNCTION ACTIVITY SCORE CAN PROVIDE A NEW PERSPECTIVE ON SINGLE-CELL RNA SEQUENCING (SCRNA-SEQ) DATA

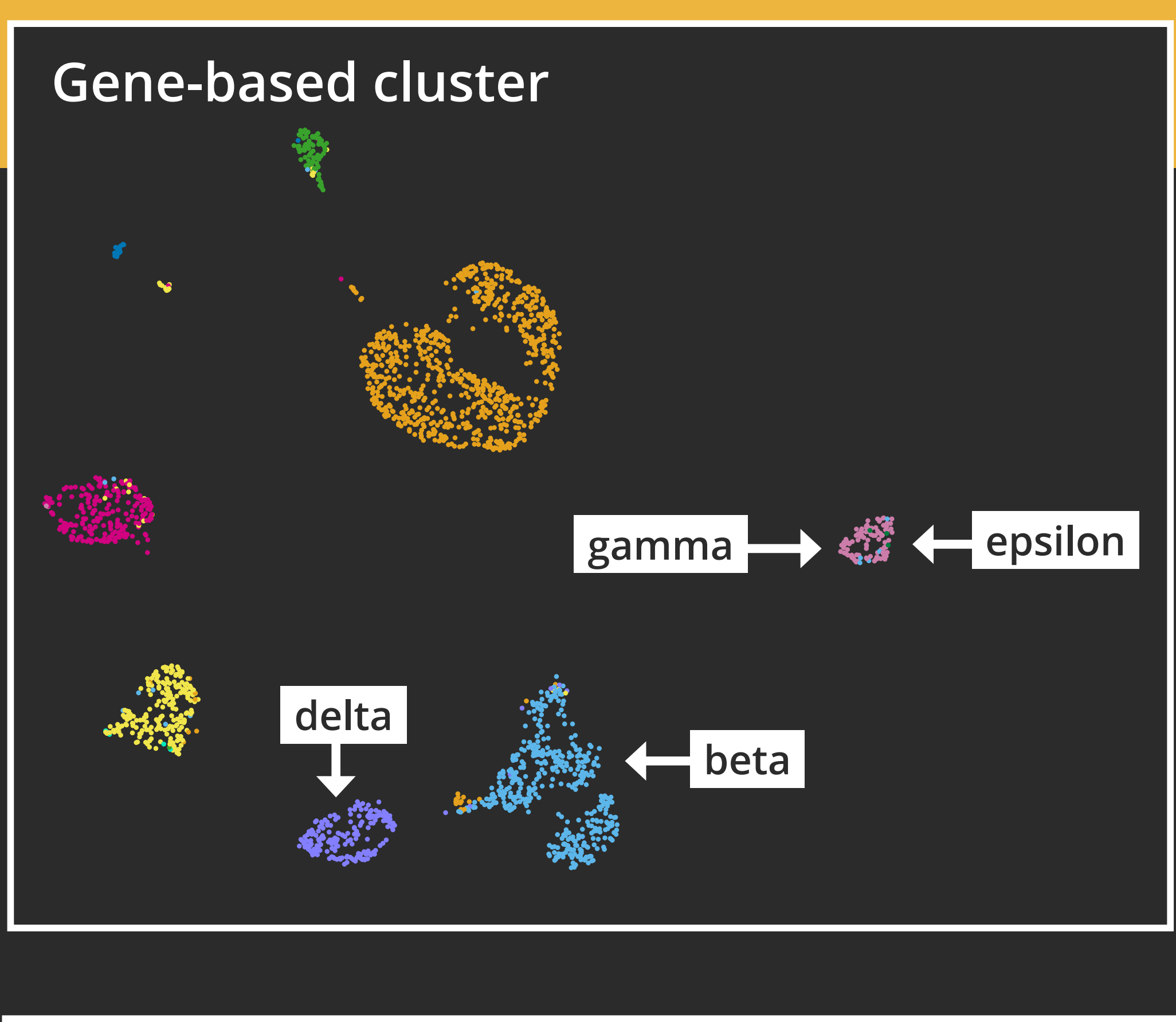


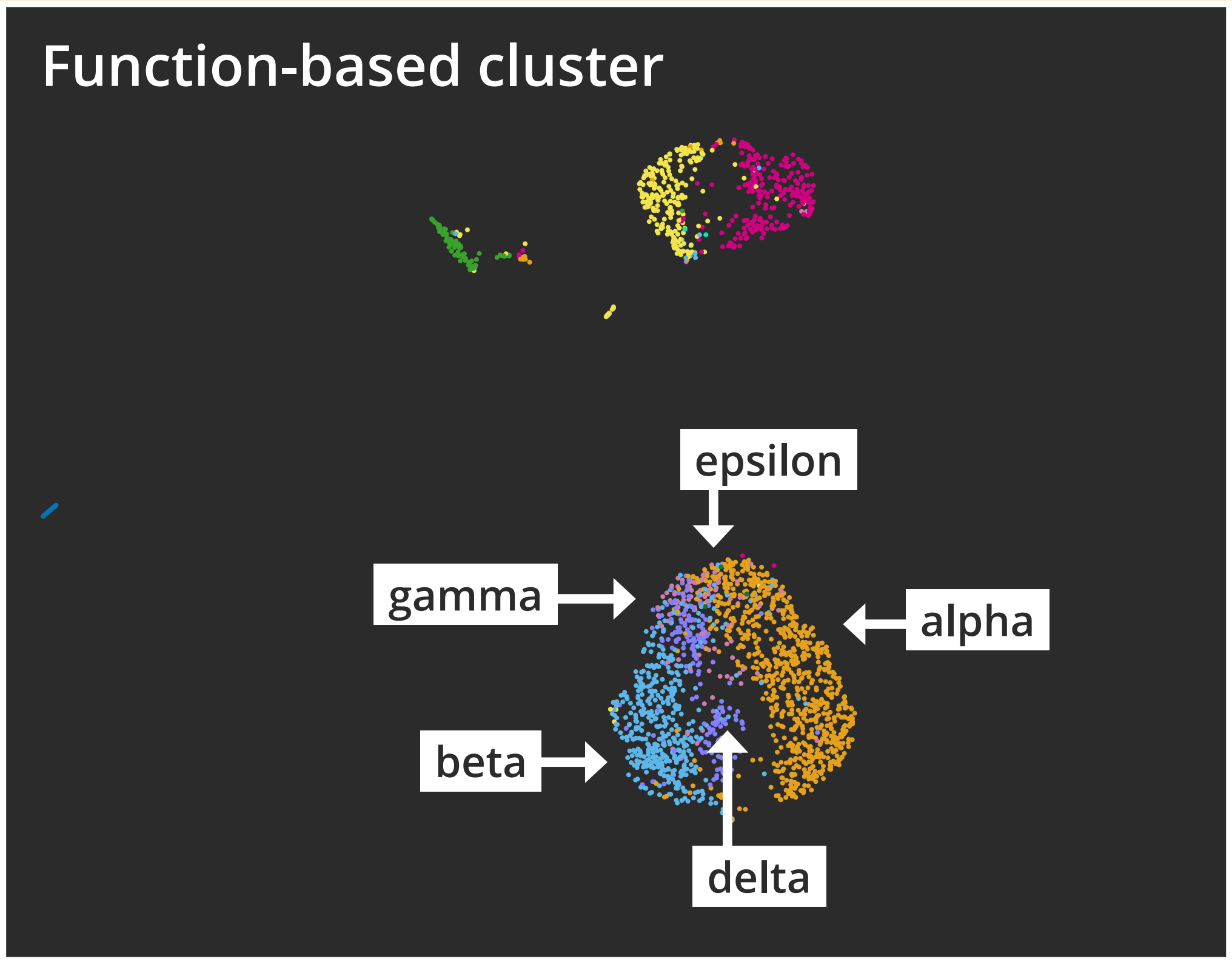
The FEM algorithm can provide insight on the biological significance of a single cell. It can also integrate with GEM for downstream analysis.

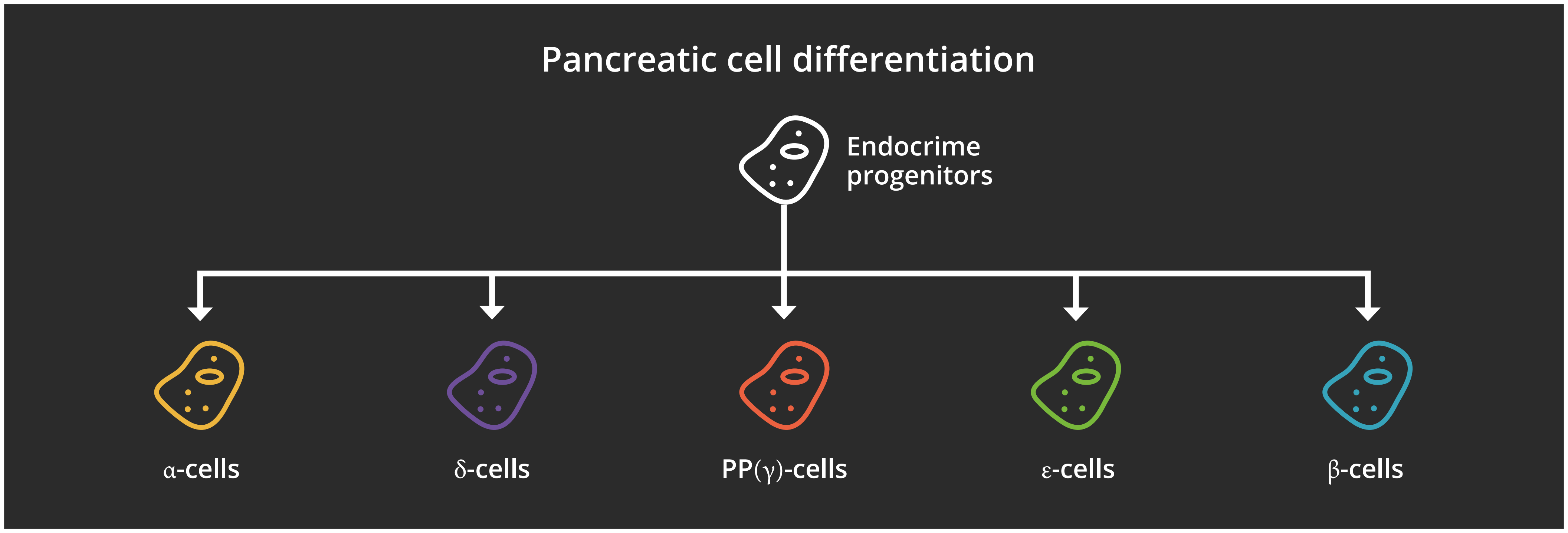
RESULTS

We found that FEM performed well with cell clustering and cell-type specific function annotation in three datasets (peripheral blood mononuclear cells, human liver, and human pancreas).

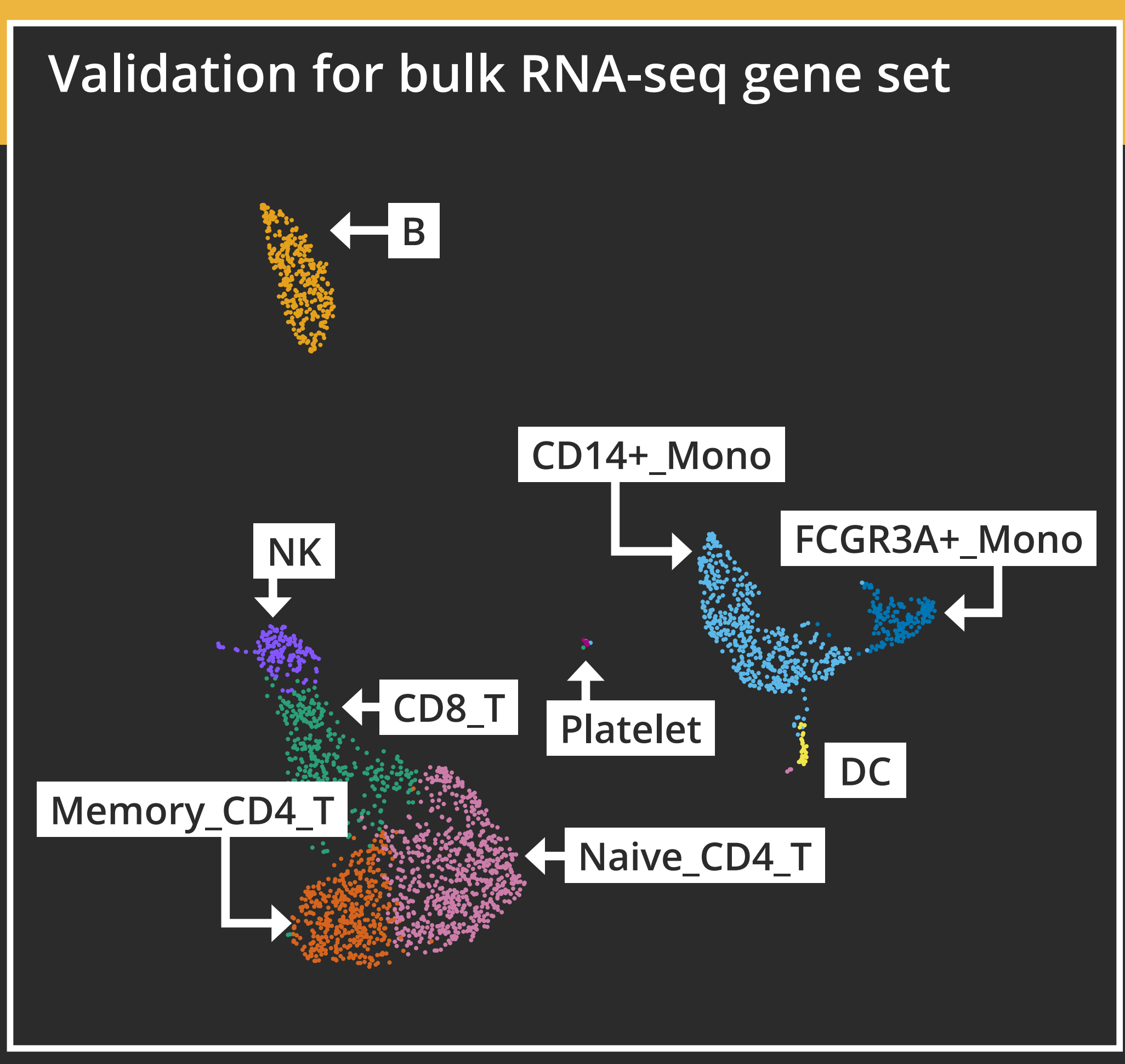
THE FEM METHOD CAN HELP DETERMINE FUNCTIONAL SIMILARITIES BETWEEN DIFFERENT CELL TYPE

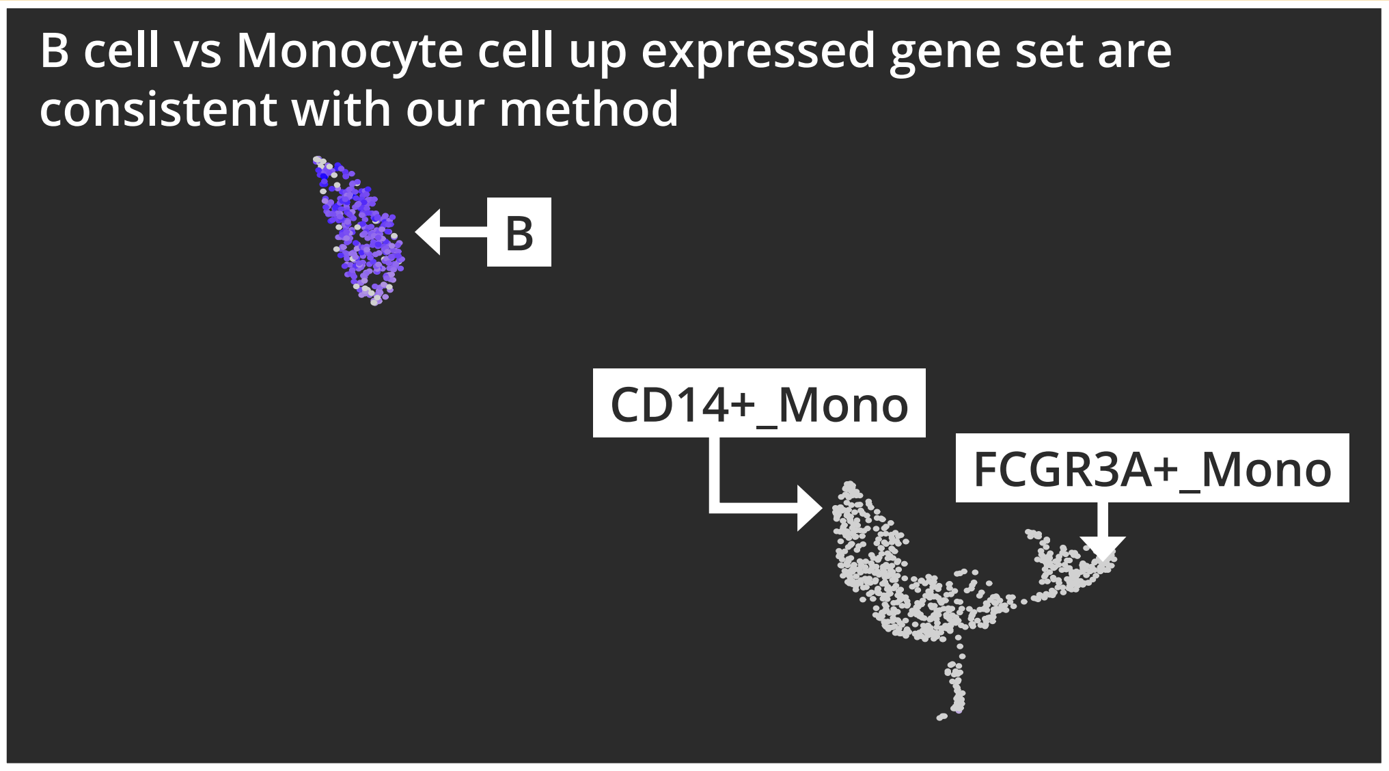

Gene-based cluster

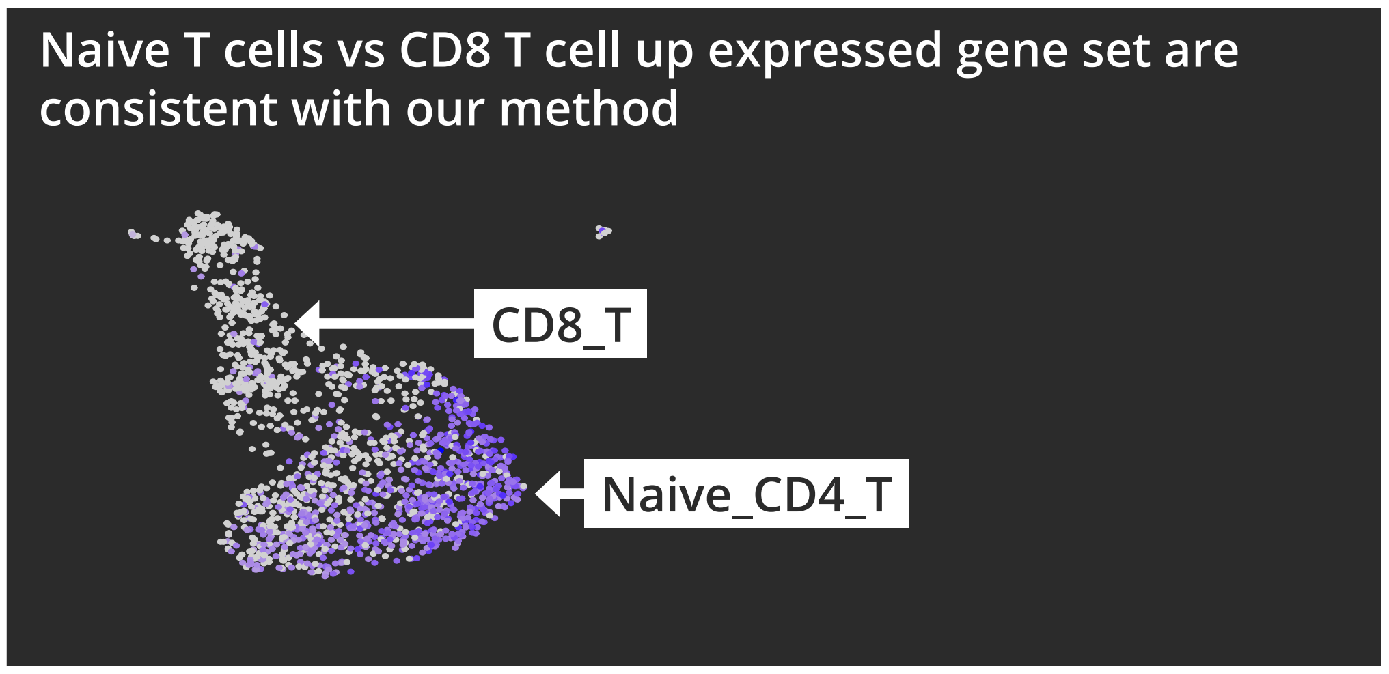

Function-based cluster


Pancreatic cell differentiation

THE DIFFERENCE BETWEEN THE CELLS OBTAINED BY THE BULK RNA-SEQ METHOD AND OUR METHOD IS CONSISTENT


Validation for bulk RNA-seq gene set


B cell vs Monocyte cell up expressed gene set are consistent with our method


Naive T cells vs CD8 T cell up expressed gene set are consistent with our method

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