COMET : Combinatorial Marker Detection from Single-Cell Transcriptomic Data

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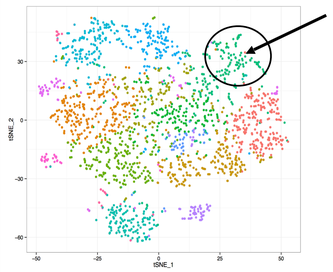
Motivation

t-SNE Plot from scRNA-seq data



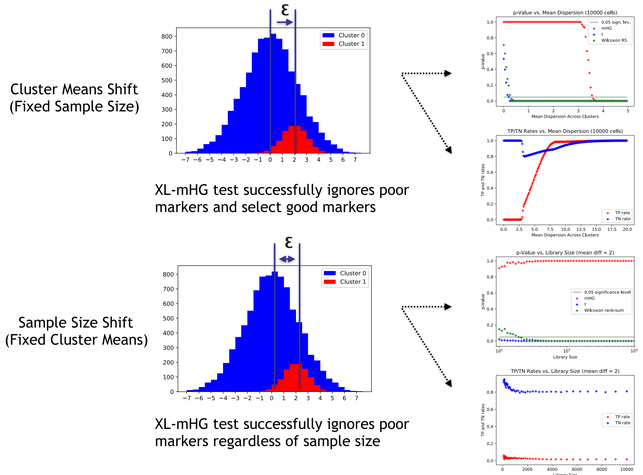
Identification of novel, functional genetic marker panels

1. Clustering of scRNA-seq data
2. Marker Identification with COMET
3. Isolation by flow cytometry-based assay
4. Functional Analysis

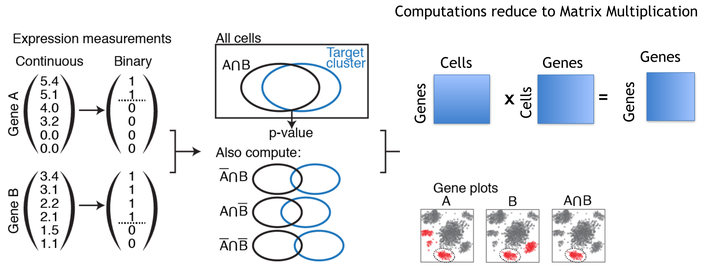
Utilizing the XL-mHG test for candidate marker detection

The XL-mHG test identifies, for each cluster, the optimal way in which a gene can isolate that cluster. For each gene and each cluster, an expression threshold is determined.

Statistical Performance of XL-mHG test

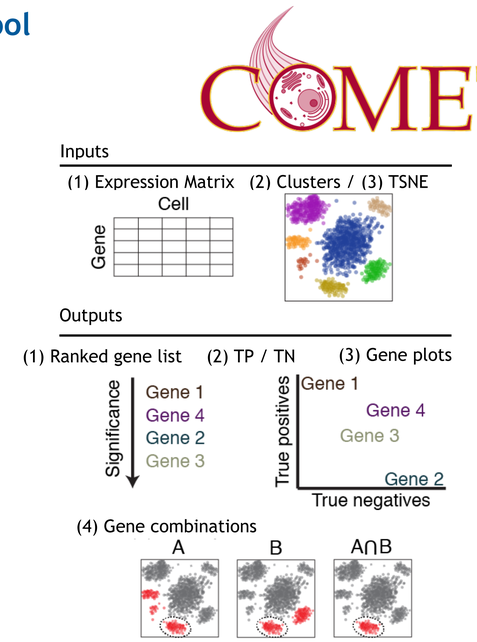


Combinatorics of potential gene markers

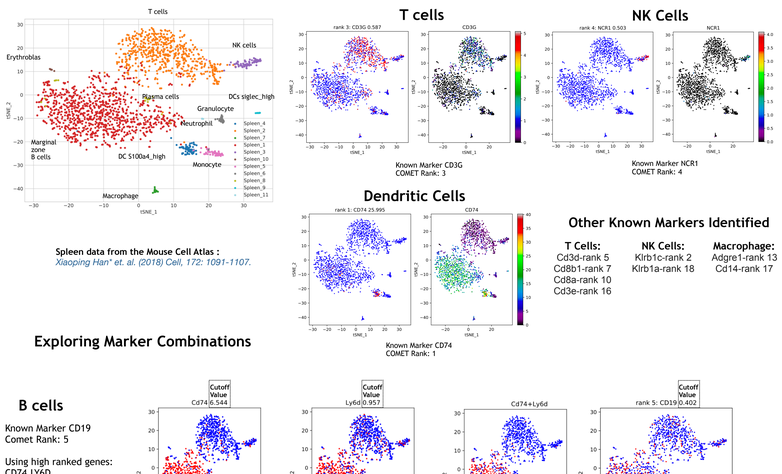


Computations reduce to Matrix Multiplication

Comet tool



Results



Spleen data from the Mouse Cell Atlas : *Xiaoping Han* et. al. (2018) Cell, 172: 1091-1107.*

Other Known Markers Identified

T Cells:	NK Cells:	Macrophage:
Cd3d-rank 5	Klrb1c-rank 2	Adgre1-rank 13
Cd8b1-rank 7	Klrb1a-rank 18	Cd14-rank 17
Cd8a-rank 10		
Cd3e-rank 16		

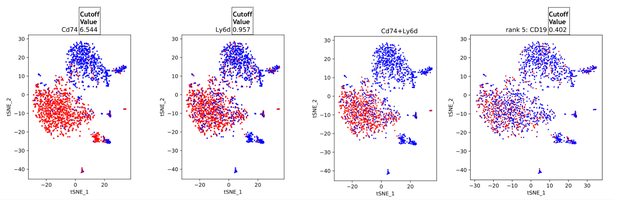
Exploring Marker Combinations

B cells

Known Marker CD19
Comet Rank: 5

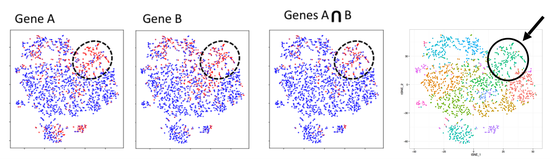
Using high ranked genes: CD74,LY6D

CD74+LY6D identifies B-Cells with good statistics, currently being experimentally verified

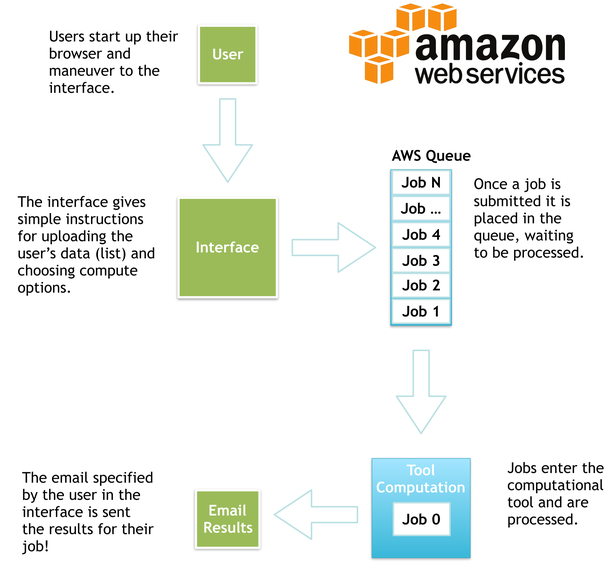


True Positive	0.74	0.92	0.69	0.42
True Negative	0.84	0.83	0.96	0.90

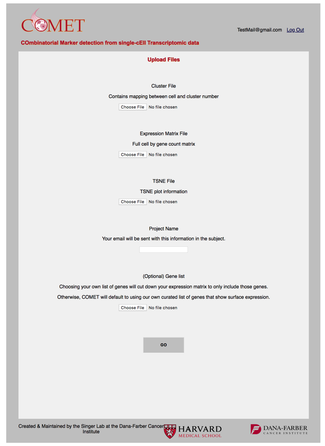
Initial identification of markers for a CD8⁺ Tumor Infiltrating Lymphocyte sub-population



Tool Interface & Deployment



The COMET Web Interface



Discussion / Future Work

Future work includes running COMET on tissues from the single-cell mouse atlas

We plan on having an operational web interface and downloadable package for this tool within the next month.

We are actively looking for Beta users to test the tool and give valuable suggestions to improve the user experience! Let us know if you are interested.