

Reconstructing physical cell interaction networks from single-cell data using Neighbor-seq

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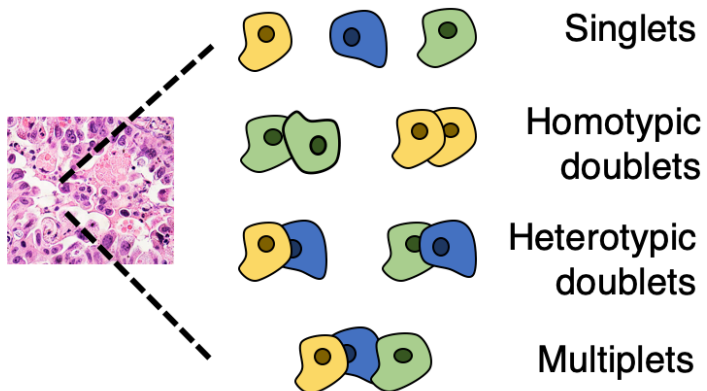
New Brunswick, NJ 08901, USA.



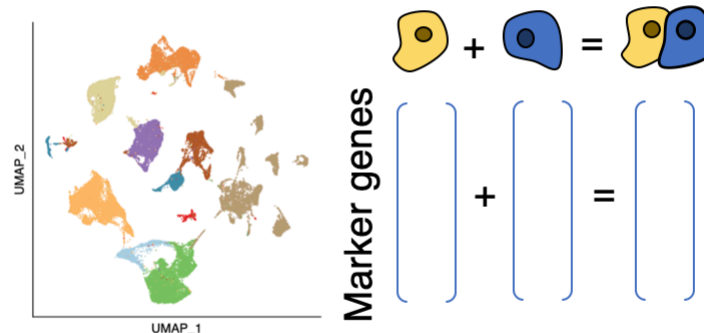
Background

- Spatial context affects cellular and tissue function
- There are limited methods to probe both the full transcriptional identity and spatial organization of cells
- Neighbor-seq detects physically interacting cells by analyzing naturally occurring cell doublets in single-cell RNA-seq data

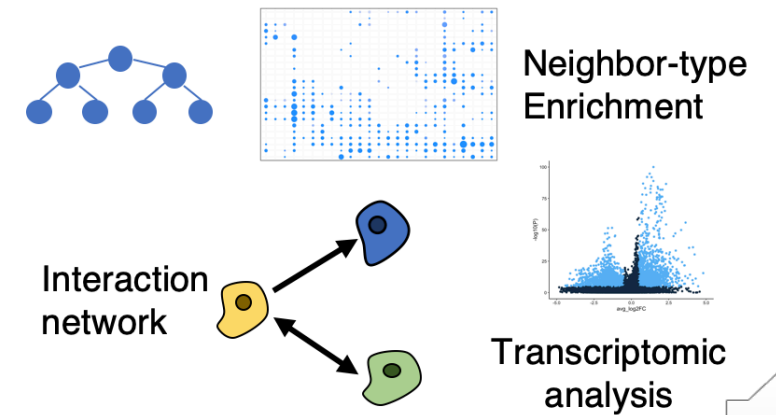
scRNAseq



Clustering + artificial multiplet construction

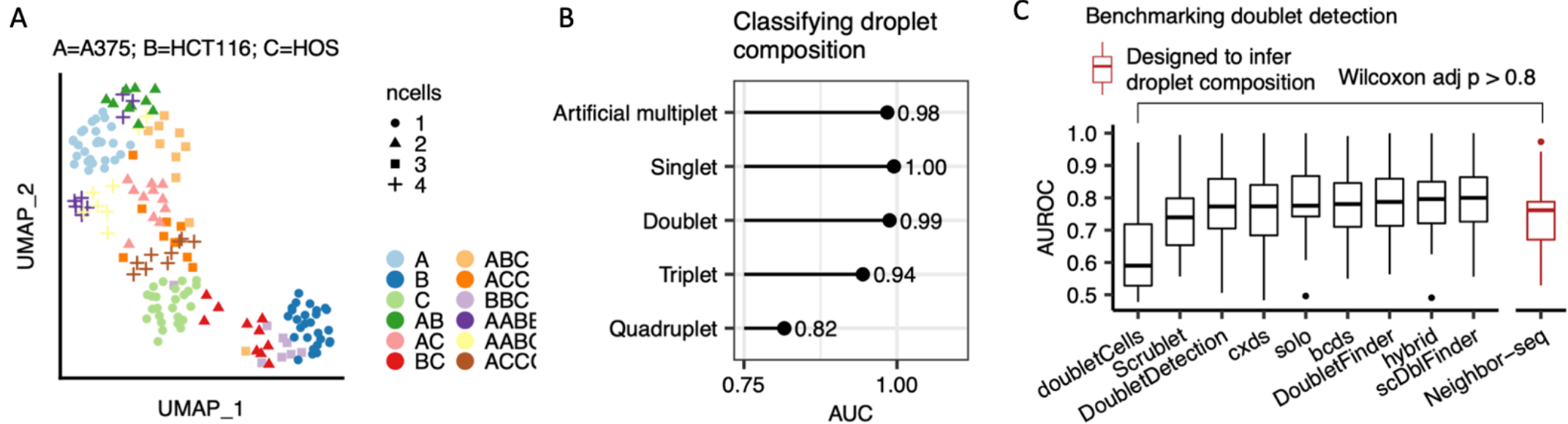


Classification, prediction, statistical analysis



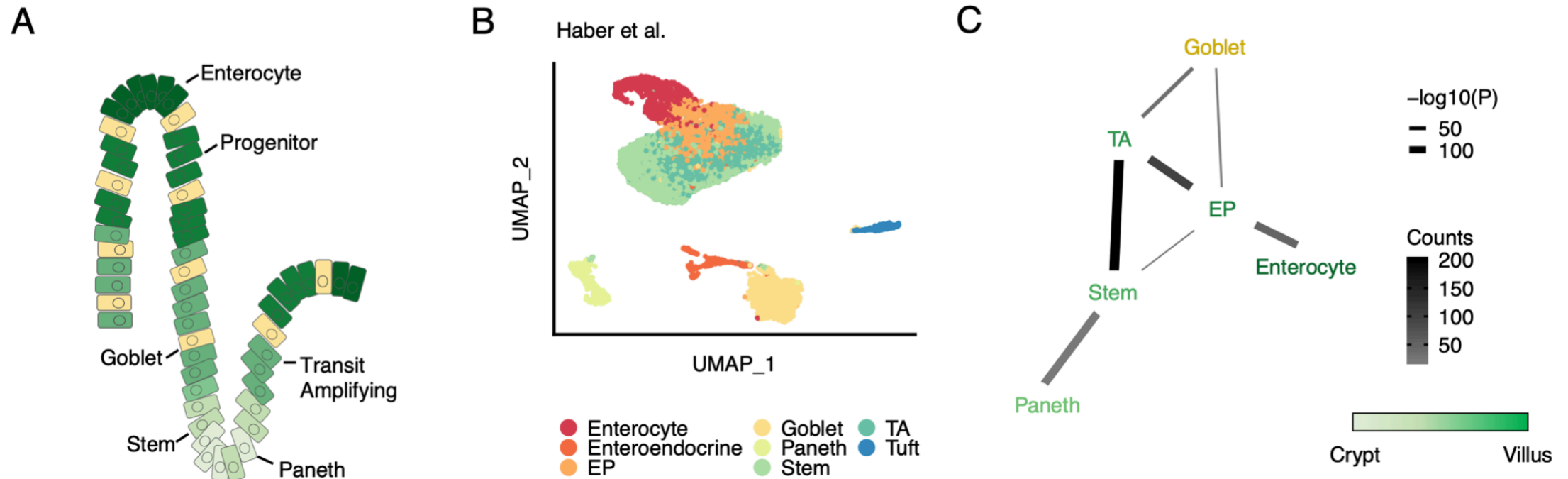
Benchmarking Neighbor-seq

Neighbor-seq annotates cell-line multiplets of known composition (3 cell lines, FACS sorted) and identifies real experimentally annotated doublets in diverse tissues



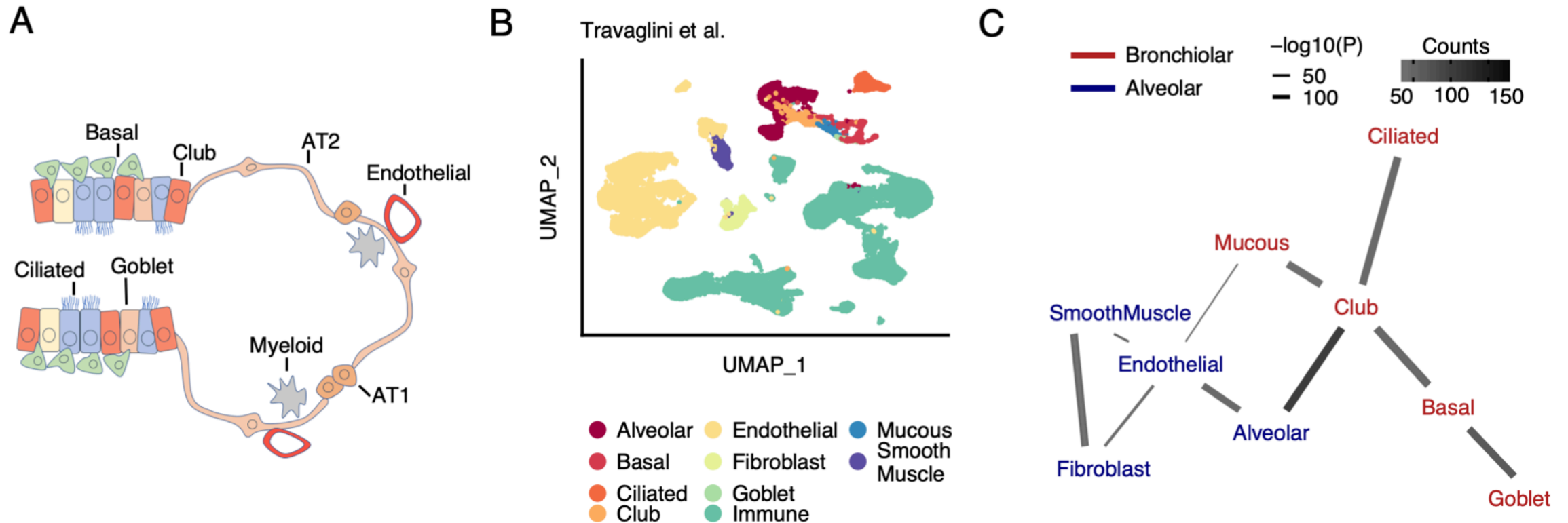
Testing Neighbor-seq

Neighbor-seq analyzes doublets in small intestine, lung, and spleen samples and recovers known tissue structures.



Testing Neighbor-seq

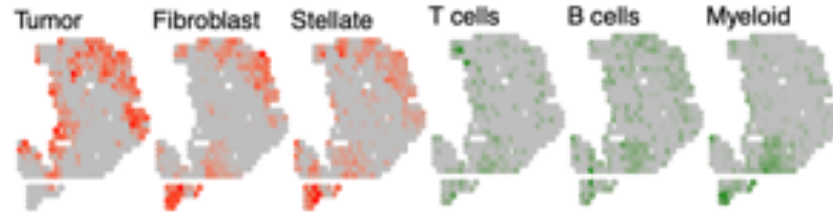
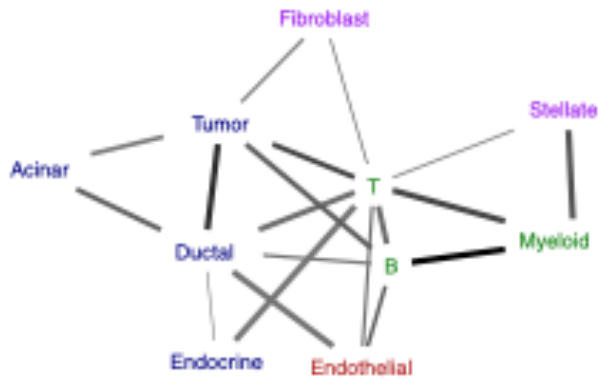
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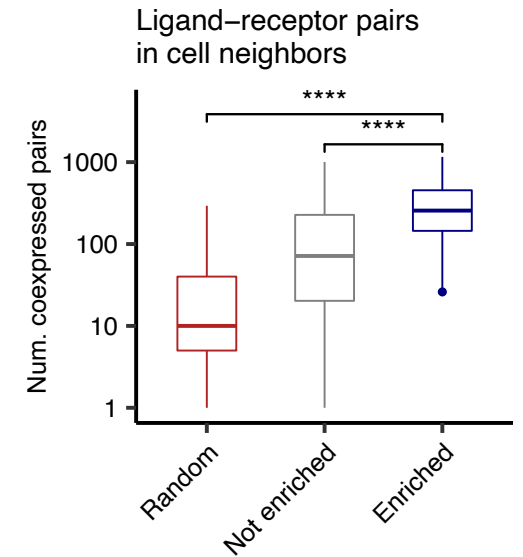
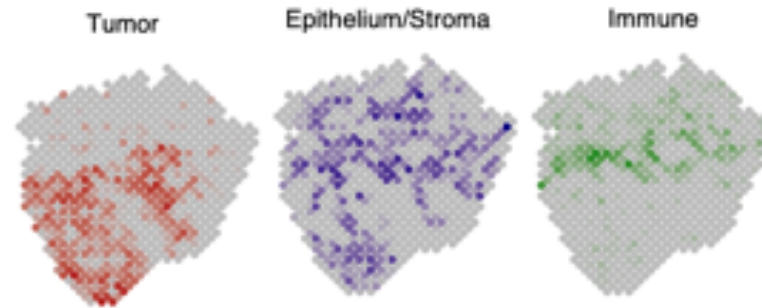
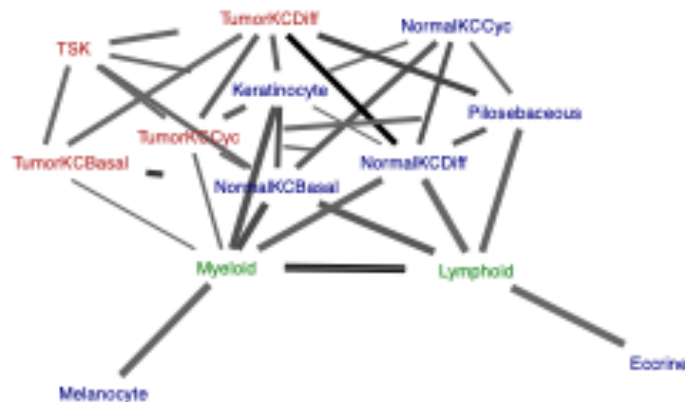
Applying Neighbor-seq to pancreatic and skin cancer

- Neighbor-seq identifies differing tumor-immune interactions in the two cancer types
- Interacting cells express high levels of ligand-receptor pairs
- Inferred interaction network matches spatial transcriptomic data

Pancreas cancer



Skin cancer



In conclusion, Neighbor-seq identifies directly interacting cells in standard scRNA-seq data and can be used to study cell interactions in tumors.

There are open positions in our group – interested candidates, please contact Dr. De.

Thank you!