Mass General Brigham
Mass Eye and Ear

Schepens Eye Research Institute

The Technology Seminar Series Presents:

"COMBINATORIAL BARCODING for scRNA-seq up to 1M CELLS PER RUN"

Anna Malinkevich, MS

Field Application Scientist

Parse Biosciences

Monday, September 30, 2024

12:00 Pm– 1:00 pm

MEE 243 Charles Street Boston, MA, The Meltzer Auditorium (3rd Floor)

Zoom:

https://masseyeandear.zoom.us/j/86924632435?pwd=flovzpbBSJEybUMd9SWSmIK3FINlzv.1

HARVARD MEDICAL SCHOOL
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Summary of Anna's talk:

Split pool combinatorial barcoding utilizes the fixed cell (or nucleus) itself as a reaction compartment, eliminating the need for specialized instrumentation for capturing cells in droplets or microwells. An exponentially large number of barcode combinations makes it possible to label up to 1M cells or nuclei in parallel for a single experiment, while still allowing for the option and flexibility of initial sample collection and processing on different days. Optimized workflow strategies allow you to pair whole transcriptome library analysis with concurrently-generated TCR libraries, BCR libraries, CRISPR-based assay libraries, and focused gene-enrichment libraries to produce rich datasets for new experimental insights.

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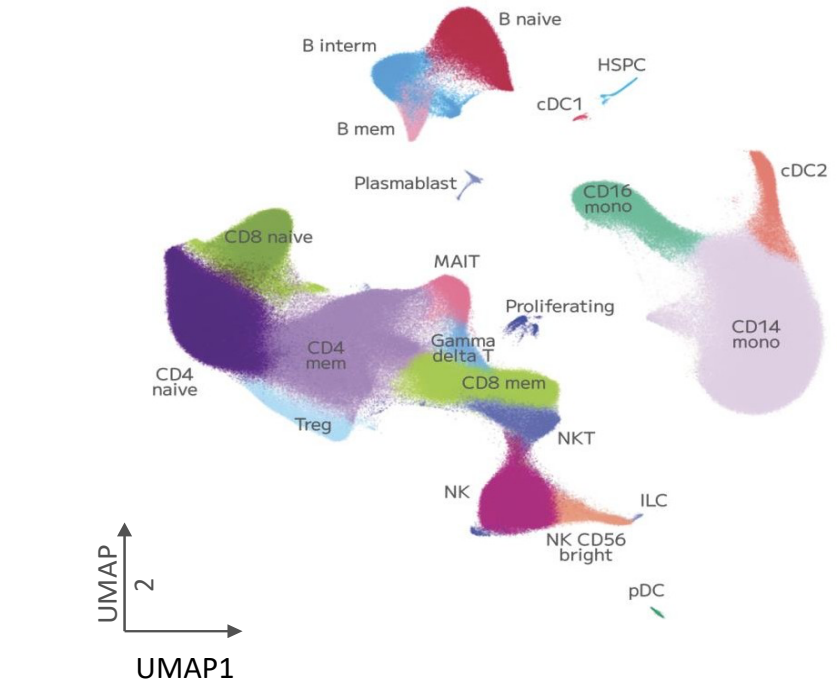
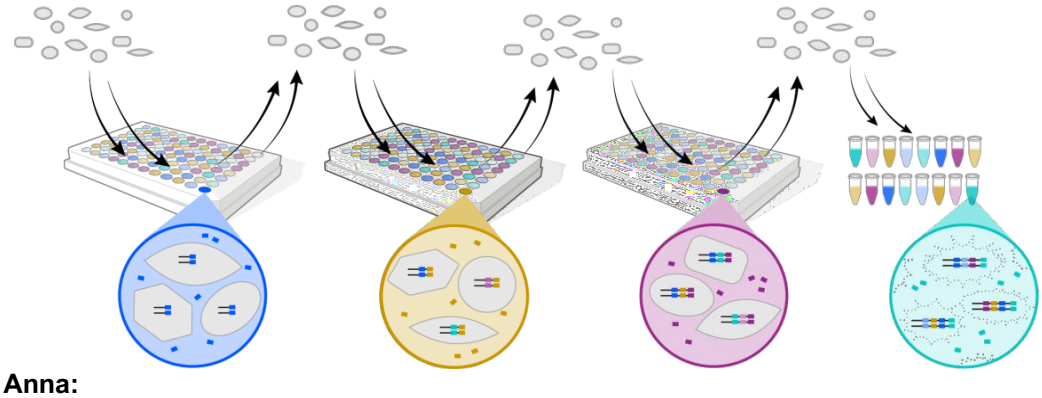
COMBINATORIAL BARCODING for scRNA-seq up to 1M CELLS PER RUN





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About Anna:

Anna Malinkevich is a Field Application Scientist (FAS) with Parse Biosciences, currently focusing on the New England region. Anna joined Parse in 2020 as the very first FAS on board and has since helped grow and develop both the Field Application Team and company's product portfolio. Prior to Parse, Anna has held numerous technical roles with start-up and large company teams, across fields ranging from genetic engineering to disease modeling to the immune-based assay space.