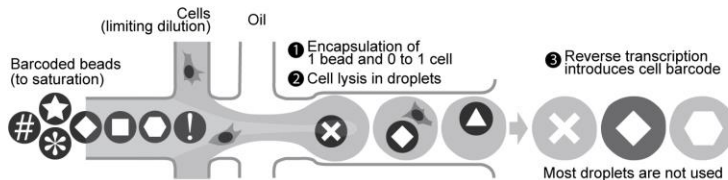


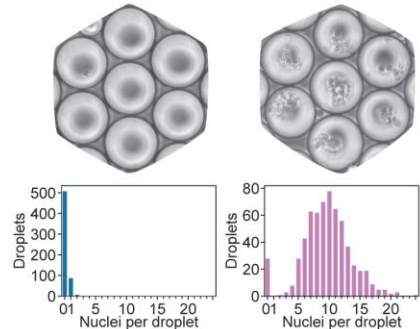
scifi - single-cell combinatorial fluidic indexing

A method to unlock the full potential of droplet generators for massive-scale single-cell profiling

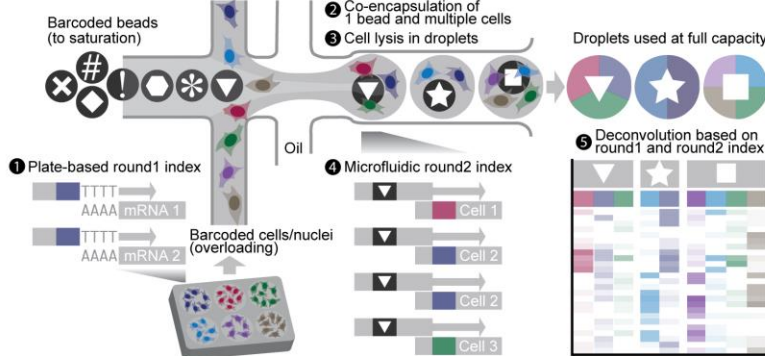
Standard single-cell RNA-seq in microfluidic droplets



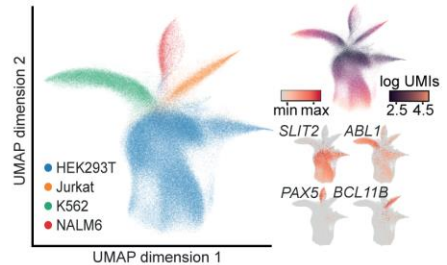
Scifi enables massive droplet overloading



Single-cell combinatorial fluidic indexing RNA sequencing (scifi-RNA-seq)



151,788 single cells in a single microfluidic channel



Applications

- Ultra-high throughput scRNA-seq by droplet overloading
- Multiplexing for hundreds of experimental conditions
- Cell Atlas Projects
- Perturbation screens in single-cells (drug screens and CRISPR screens)
- Compatibility with other single-cell assays (e.g. scATAC-seq)

Competitive Advantage

- Easy, efficient, 15x-fold increase in throughput

Intellectual Property

- Priority application filed at the EPO: Sep 6, 2019

Lead Researchers

Christoph Bock and Paul Datlinger joined CeMM in 2012. They have developed a method for high-throughput DNA methylation mapping, the popular CROP-seq assay for CRISPR screens at single-cell resolution, and more recently the scifi barcoding strategy for single-cell analyses at ultra-high throughput.

Ce-M-M

CeMM is an interdisciplinary research institute of the Austrian Academy of Sciences committed to advancing the understanding of human diseases through basic and biomedical research. Located in a tailor-made building in the midst of the campus of the Medical University of Vienna