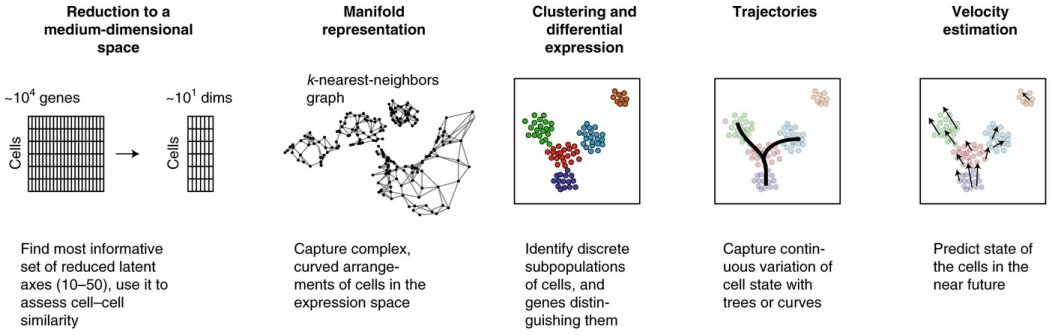
Single Cell Transcriptomics

Newsletter August 2021

Paper 1

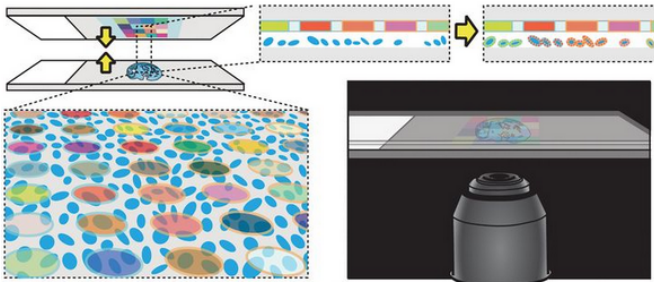
Kharchenko P. [The triumphs and limitations of computational methods for scRNA-seq](), *Nature Methods, 2021*



A very nicely written review by Peter Kharchenko from Harvard Medical School discusses the current state of the field with the focus on computational analysis. It's not the kind of a review that lists all methods for all existing questions, focusing instead on statistical ideas, underlying most of these developed methods. Though he explains in detail what gold standard methods are used now and why they work. So this paper can be used as a beginner-friendly description of how things work in scRNA-seq!

Paper 2

Srivatsan SR *et al.* [Embryo-scale, single-cell spatial transcriptomics](), *Science, 2021*

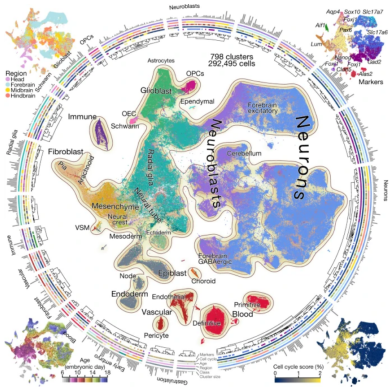


Scientists from the University of Washington published a protocol (sci-Space) for spatial transcriptomic measurements on the level of single cells together with its results on mouse E14 sagittal sections. The protocol works by having a 18x18mm grid with ~73µm spots, which are used to pull cells in. In contrast to 10x Visium or Slide-seq, it pulls actual cells, but not their molecular content, which allows attaching both position and cell barcodes. Thus, single-cell precision and no need for deconvolution. The authors applied protocol to E14 mouse embryos getting ~122k cells with 1231 genes per cell on average. They were able to get detailed cell type annotation and seemingly aligned well with the published scRNA-seq data for mouse embryos. The spot coverage of the protocol is really sparse though (see Supp. Figures 12 and 13), so many replicas of the experiment could be needed.

Papers 3,4

La Manno, G *et al.* [Molecular architecture of the developing mouse brain](), *Nature, 2021*

The Tabula Sapiens Consortium, Quake SR. [The Tabula Sapiens: a single cell transcriptomic atlas of multiple organs from individual human donors](), *biorXiv, 2021*



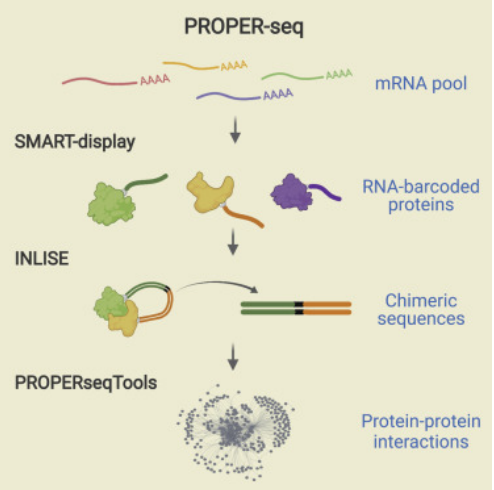
Expanding on the topic of the previous paper, the first one reports an atlas of the embryonic mouse brain between gastrulation and birth. Gioele La Manno, et al produced 93 samples and 292k cells, measuring each day between E7 and E18 and identified almost 798 cellular states that describe a developmental program. To capture spatial patterns they additionally measured 119 genes using in situ sequencing. So check the paper to find out about their biological findings, and don't miss the aesthetics of cell state visualization on Figure 1!

And speaking about atlases, the CZI Consortium just published a preprint with 500k cells from 24 human tissues and organs.

Paper 5

Johnson, KL. *et al.* [Revealing protein-protein interactions at the transcriptome scale by sequencing](), *Molecular Cell, 2021*

The publication presents a method for high-throughput mapping of protein-protein interactions using RNA-sequencing, called PROPER-seq. The protocol works by (i) labeling individual proteins with RNA barcodes to generate a library, then (ii) mixing two such libraries together, (iii) purifying interacting protein pairs and (iv) sequencing the RNA barcode pairs. The authors applied PROPER-seq to three lines of human cells: HEK293T, Jurkat, and human umbilical vein cells (HUVECs), which revealed 210,518 pairs of interacting proteins involving 8,635 proteins. These results are available through a web-interface. The publication also shows that among the 1,273,679 computationally predicted and previously uncharacterized protein-protein interactions they found 17,638 (which could not happen by chance, $p < 2.2 \times 10^{-16}$).



Next Single Cell Seminar

Date: 27th Aug 2021, Maersk Tower top floor, Faculty Lounge 7.15.107B

9:00 – 9:40

Viktor Petukhov, BRIC

Cacoa – new tool for comparison of single-cell data between health and disease

10:00 – 10:40

Nicola Meola, Bio-Techne

RNAscopeTM HiPlex v2: Enhancing Spatial Mapping In Your Research...and more stories

10:40 – 11:00

Coffee and discussion

If you would like to announce anything single cell related, be it a job announcement, event, your published paper, technology development etc, please contact us.

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