



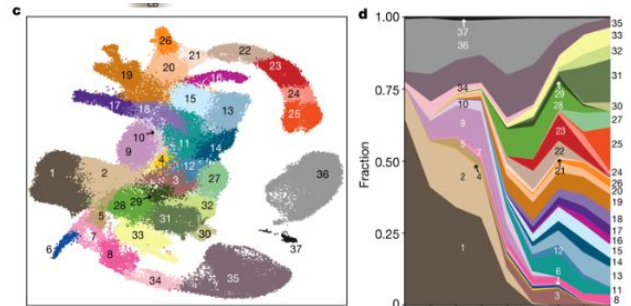
Single Cell Transcriptomics

Newsletter March 2019

Paper 1

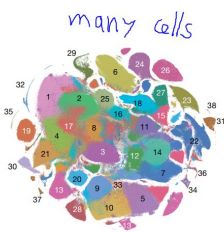
Pijuan-Sala et al. [A single-cell molecular map of mouse gastrulation and early organogenesis](#) *Nature*, 2019.

In this work Pijuan-Sala et al. lay out a map of cellular differentiation from pluripotency towards all major embryonic lineages. They combine temporal and transcriptional information (9 time-points) and use it to understand the effects of a gene mutation during development using a chimaera mouse. They infer cellular transitions along sequential collection time points using a computational tool called transport maps (a cell can be transported between time points if it meets certain criteria).



Paper 2

Cao et al. [The single-cell transcriptional landscape of mammalian organogenesis](#) *Nature*, 2019.

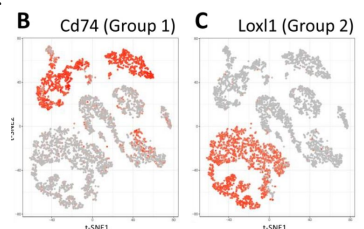


Cao et al. introduce sci-RNA-seq3. Single-cell combinatorial indexing is a methodological framework involving split-pool barcoding of cells or nuclei. A conceptually identical method was recently termed SPLiT-seq. Even without automation, sci-RNA-seq3 library preparation can be completed through the intensive effort of a single researcher in one week at a cost of less than \$0.01 per cell. This allows for a coverage of up to 80% of the cellular content of an individual mouse embryo (2mio nuclei, 519 genes per nuclei). Lesson: Cell types are readily distinguishable despite having hundreds rather than thousands of UMIs per cell.

Paper 3

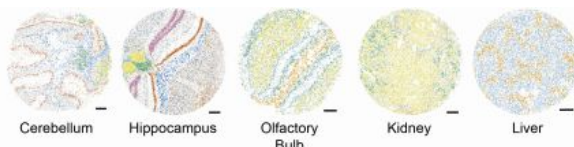
Vandenbon et al. [singleCellHaystack: Finding surprising genes in 2-dimensional representations](#) *bioRxiv*, 2019.

Scientists from Japan developed an alternative "cluster-free" approach for the detection of marker genes. The method called singleCellHaystack finds genes, which drive the main patterns on a t-SNE embedding. To do that, it ranks genes based on their divergence in 2D density. In contrast to classical DE methods, it doesn't depend on cell clustering, but just gives a list of most "influential" genes. With all its simplicity, it looks like an interesting alternative to conventional algorithms.



Paper 4

Rodrigues et al. [Slide-seq: Genome-Wide Expression at High Spatial Resolution](#) *bioRxiv*, 2019.



The developers of dropseq have been at it again. This time they have come up with a labour and cost-efficient approach for high-throughput spatial transcriptomics. They demonstrate their method on various brain regions, liver and kidney.

Next Single Cell Seminar - 29th March, Mærsk Tower, Top Floor

9:00 – 9:40 Prof Kyoung Jae Won, BRIC - We all say something: modelling population from individuals

10:00 – 10:40 Mike Krogh Terkelsen, BMB, SDU - Mesenchymal plasticity during hepatic fibrogenesis

Other:

The Identity and Evolution of Cell Types, [EMBL Symposium](#)
Single-Cell Computational Workshop - 10th May, Apply [here](#)