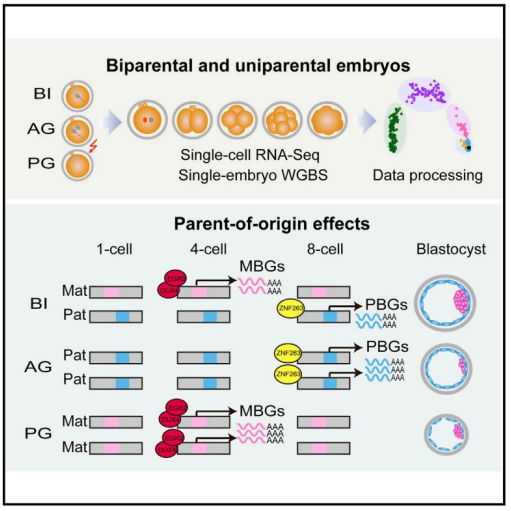
Single Cell Transcriptomics

Newsletter October 2019

Paper 1

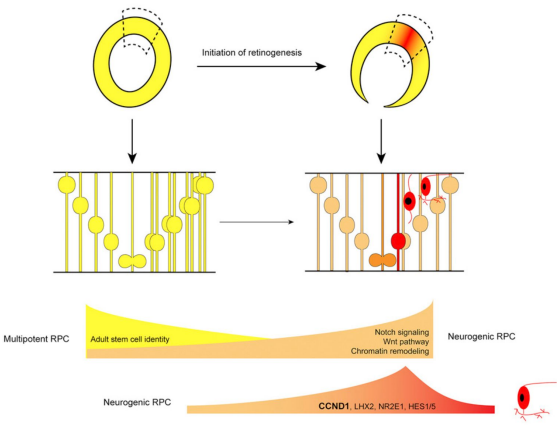
Leng et al. [Single-Cell Transcriptome Analysis of Uniparental Embryos Reveals Parent-of-Origin Effects on Human Preimplantation Development] *Cell Stem Cell*, 2019.

Leng et al. performed a comparative analysis of transcriptional activities between human biparental and uniparental embryos from the 1-cell to the morula stage by single-cell RNA sequencing. They identified 807 maternally biased expressed genes (MBGs) and 581 paternally biased expressed genes (PBGs) in the preimplantation stages. MBGs became apparent at the 4-cell stage and contributed to the initiation of the embryonic
genome activation, whereas PBGs preferentially appeared at the 8-cell stage and might affect embryo compaction and trophectoderm specification. The findings of this investigation suggest critical functions of MBGs and PBGs in early embryos, providing a valuable resource for understanding parent-of-origin gene expression patterns in human preimplantation embryos and could help to dissect gamete-related development abnormalities in routine in vitro fertilization practices.



Paper 2

Mao et al. [Single-Cell RNA Sequencing of hESC-Derived 3D Retinal Organoids Reveals Novel Genes Regulating RPC Commitment in Early Human Retinogenesis] *Stem Cell Reports*, 2019.

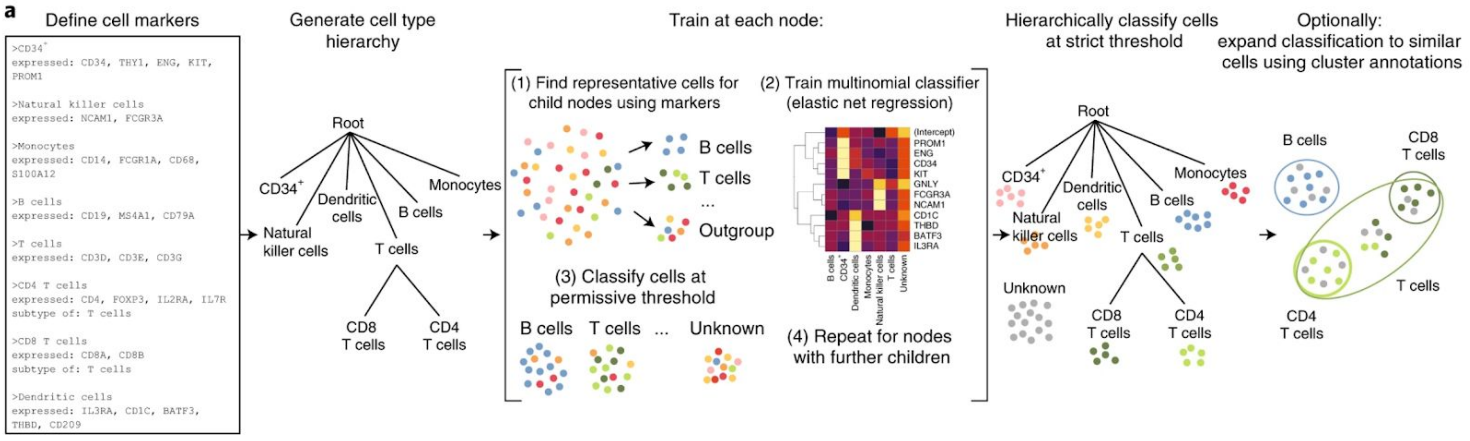


By performing single-cell RNA sequencing of cells isolated from human ESC (hESC)-derived 3D retinal organoids, the authors successfully deconstructed the temporal progression of retinal progenitor cells during early human retinogenesis. Two distinctive subtypes of RPCs with unique molecular profiles were identified, namely multipotent RPCs and neurogenic RPCs. Single-cell analysis has revealed also the involvement of the Wnt pathway in the regulation of this transition being was negatively regulated via the upregulation of DKK3 along RPC progression. they also identified the cell-cycle gene CCND1 as necessary for the progenitor maintenance and for promoting neurogenesis, which is consistent with the finding in developing mouse spinal cord.

Paper 3

Pilner et al. [Supervised classification enables rapid annotation of cell atlases.](#) *Nature Methods,* 2019.

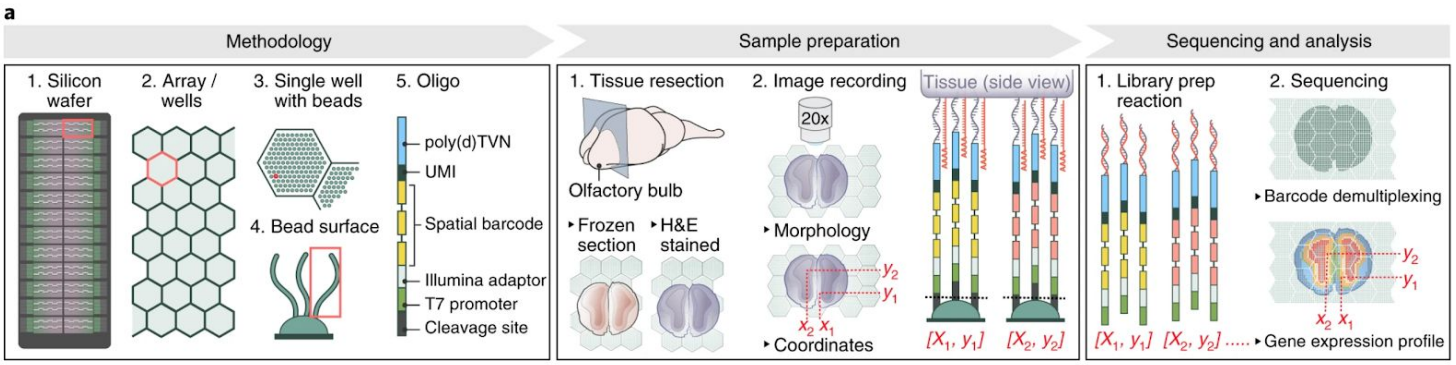
In order to address the challenges behind the manual annotation of different cell types among the resulting clusters, the Trapnell lab developed Garnett (https://cole-trapnell-lab.github.io/garnett). Garnett is an algorithm and accompanying software system for rapidly annotating cell types in scRNA-seq and scATAC-seq datasets, based on an interpretable, hierarchical markup language of cell type-specific genes. The software trains classifiers and apply them across platforms to automatically assign cell type from scRNA-seq. they applied Garnett into different single-cell datasets demonstrating that Garnett has the potential to operate across related species, and is not necessarily confounded by the presence of pathological cell states when trained on normal healthy tissue.



Paper 4

Vickovic et al. [High-definition spatial transcriptomics for in situ tissue profiling.](#) *Nature Methods*, 2019.

The positional context of gene expression is of key importance to understanding tissue functionality and pathological changes. In the article, the authors developed a dense, spatially barcoded bead array which captures RNA from histological tissue sections for spatially resolved gene expression analysis. Each experiment recovers several hundred thousand transcript-coupled spatial barcodes at 2-μm resolution. The technology relies on robust and commoditized tissue, molecular, bead-array and imaging modular tasks, which can be readily deployed across the scientific community. This high definition spatial transcriptomics uses standard histological stains, providing the means to relate morphology, extracellular features and gene expression.



Conferences

- 7th Annual Single Cell Analysis Congress, November 7-8 2019, London, UK
- The Conceptual Power of Single-Cell Biology, April 19-21 2020, San Francisco, CA, USA
- Single Cell Biology: Pushing New Frontiers in the Life Sciences, May 4-8 2020, Florence, Italy

Next Single Cell Seminar

Date: 25th October 2019, Location: Mærsk Tower, Top Floor, 7.15.152

9:00 – 9:40
Rasmus Rydbirk, Bispebjerg Hospital, Copenhagen
snRNA-seq investigation of the putamen in Multiple system atrophy patients

10:00 – 10:40
Grzegorz Maciag, BRIC, Copenhagen
Deciphering cellular heterogeneity in the colon

10:40 – 11:00 Coffee and Discussion

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