Single Cell Transcriptomics

Newsletter January 2020

In the January issue of Nature Methods, single-cell multimodal omics was selected as method of the year 2019!

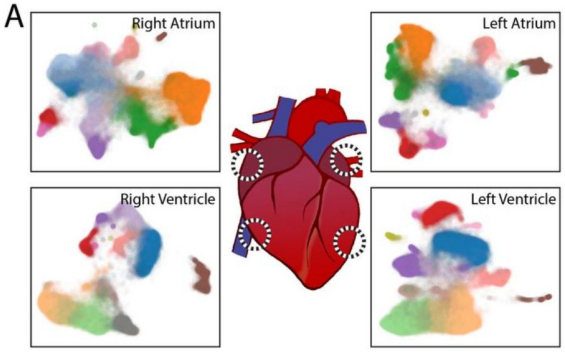
Following single-cell RNAseq technology and with the expansion of sequencing techniques, that allowes the improvement of profiling different aspects of a cell, including its genome, transcriptome and epigenome, as well as the spatial organization of these -omes.

Therefore, multimodal omics measurement offers opportunities for gaining holistic views of cells one by one, showing a great potential in answering biological questions.

Paper 1

Tucker. N et al. Transcriptional and Cellular Diversity of the Human Heart. *bioRxiv, 2020.*

In this paper, Tucket et al. have developed the largest collection of single nuclear transcriptomes from the human heart to date. They analyzed 287,269 nuclei derived from the four chambers of the normal human heart from 7 potential transplant donors. They could identify 9 major cell types and more than 20 cell subtypes. They observed distinct transcriptional profile of atrial and ventricular cardiomyocytes and they identified activated and non-activated cardiac fibroblasts and also a complex cardiac immune cell component.



Through differentially expression analysis they described marked differences in cell subtype transcription by chamber, laterality, and gender. Interestingly cardiomyocytes are the most distinct cell type between chambers, although there was no difference between the left versus the right side of the heart.

Lately, they intersected the snRNAseq data with the results from genome wide association studies (GWAS) and found out that genes implicated in cardiomyopathies and arrhythmia syndromes are enriched in cardiomyocytes subtypes, linking specific cell types to common and rare genetic variants underlying cardiovascular diseases.

Paper 2

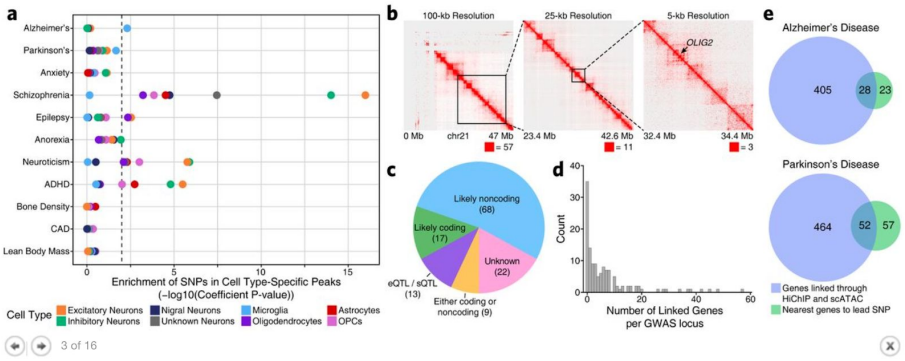
Corces, M. et al. [Single-cell epigenomic identification of inherited risk loci in Alzheimer's and Parkinson's disease.](#) *bioRxiv*, *2020*.

The authors present a multi-omic epigenetic atlas of the adult human brain through profiling of the chromatin accessibility landscapes and three-dimensional chromatin interactions (ATAC-seq, scATAC-seq, and HiChIP enhancer connectome) in seven brain regions across 39 cognitively healthy individuals.

ATAC-seq revealed brain regional epigenomic heterogeneity. Single-cell chromatin accessibility profiling of 70,631 cells from six of these brain regions identifies 24 distinct cell clusters and 359,022 cell type-specific regulatory elements, capturing the regulatory diversity of the adult brain for both neuronal and glial cells.

They then developed a machine learning classifier to integrate this multi-omic analysis together with GWAS and predict putative functional SNPs driving association with neurodegenerative diseases, specifically for Alzheimer's disease (AD) and Parkinson's disease (PD).

These predictions both inform well-studied disease-relevant genes, such as BIN1 in microglia and reveal novel gene-disease associations, such as STAB1 in microglia and MAL in oligodendrocytes for PD.

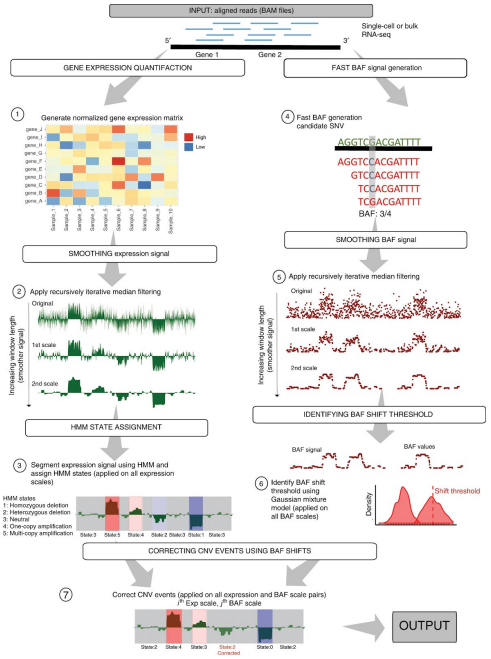


This study expands the understanding of inherited variation in AD and PD and provides a roadmap for the epigenomic dissection of noncoding variation in neurodegenerative and other complex genetic diseases.

Paper 3

Harmanci, AS. et al. [CaSpER identifies and visualizes CNV events by integrative analysis of single-cell or bulk RNA-sequencing data.](#) *Nature Communications, 2020*.

Here, researchers from the University of Texas present CaSpER, a signal processing approach for identification, visualization, and integrative analysis of focal and large-scale CNV events in multiscale resolution using either bulk or single-cell RNA sequencing data. CaSpER integrates the multiscale smoothing of expression signal and allelic shift signals for CNV calling. Unlike most other tools, CaSpER does not require a high-quality heterozygous variant call set to generate the allelic shift profile. Thus, CaSpER does not require an SNV variant call set as an input. CaSpER utilizes the multiscale decomposition to smooth the expression and allelic shift signals in multiple length scales. This processing removes much of the noise and enhances the copy number information within the expression and allelic shift signals.



Conferences

- **The Conceptual Power of Single-Cell biology**
  19-21 April, 2020, San Francisco, CA, USA
  Abstract submission deadline: January 17, 2020

- **Single Cell Biology: Pushing New Frontiers in the Life Sciences**
  4-8 May 2020, Florence, Italy
  Abstract submission deadline:5 February, 2020

- **Single cell profiling and analysis in neuroscience**
  15 June - 3 July 2020, Bordeaux, France
  Application deadline: March 2, 2020.

Next Single Cell Seminar

Date: 15th January 2020, Location: Holst Auditorium, Mærsk Tower.

9:00 – 10:00
Nikolai Slavov, Department of Bioengineering, Northeastern University, Boston, USA
Joint protein and RNA analysis across thousands of genes and single cells

10:00 – 10:30 Coffee and Discussion

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

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