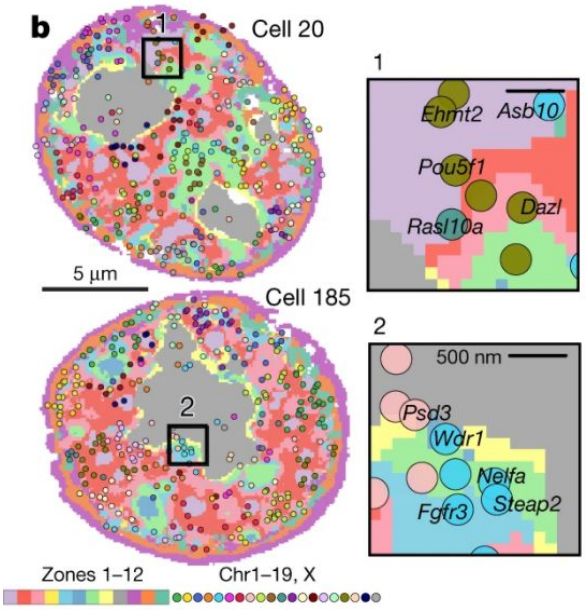
Single Cell Transcriptomics

Newsletter March 2021

Paper 1

Takei, Y *et al.* [Integrated spatial genomics reveals global architecture of single nuclei](), *Nature, 2021*

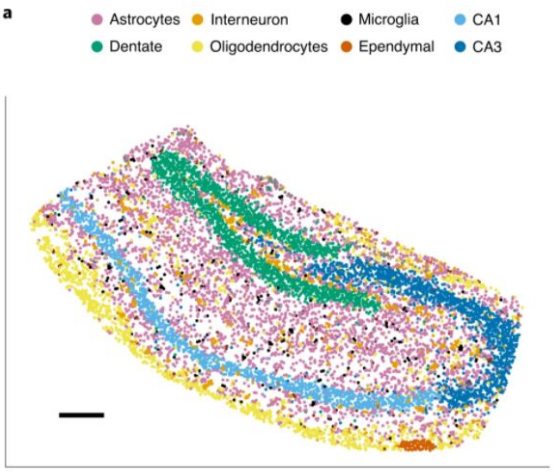
The first paper of this month focuses on the spatial organization of chromosomes as well as nuclear bodies and chromatin marks in single nuclei in an effort to map the molecular relationships of the nucleus. Here, Takei and colleagues describe their development of DNA seqFISH+, a method based on seqFISH and other multiplexed FISH methods. The method allows for examination of individual nuclei from 1-Mb resolution for the entire genome and down to 25-kb resolution for up to 20 distinct regions of at least 1.5Mb in size. By combining the genome analysis with transcripts from RNA seqFISH, histone modifications and subnuclear structures (sequential immunofluorescence), the authors define spatial relationships of nuclear zones and reveal the heterogeneity of chromatin states and that some of these states even persist across multiple generations. In essence, they present a method for unveiling the nucleosome landscape in single nuclei.



Paper 2

Cable, D *et al.* [Robust decomposition of cell type mixtures in spatial transcriptomics](), *Nature Biotechnology, 2021*

In this paper, Cable and colleagues present RCTD; **r**obust **c**ell **t**ype **d**ecomposition, a computational method that takes advantage of learned cell type profiles from single cell RNA-seq to decompose cell type mixtures observed in spatial transcriptomics. The method presents several interesting features: identification of genes in cell types that are specific to and dependent on the spatial environment; cross-platform functionality on cell type

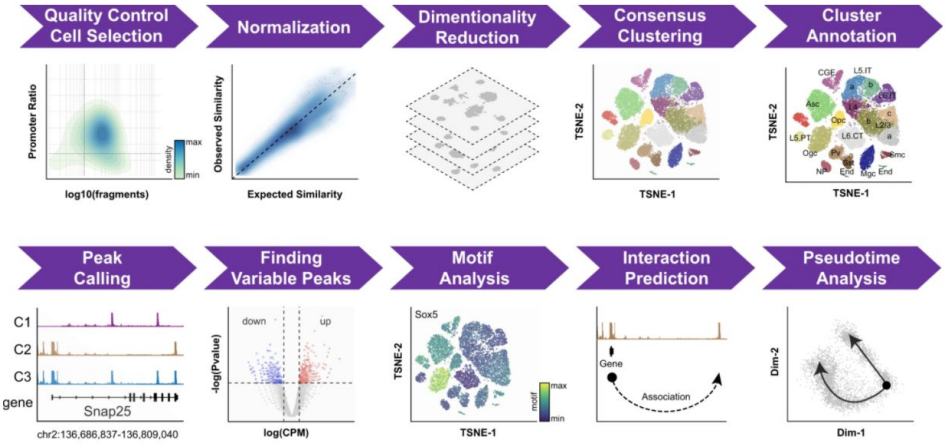


annotation and demonstrated compatibility with known spatial options such as Slide-seq and Visium datasets. This method enables increased detail levels and thus computational resolution of spatial transcriptomics.

Paper 3

Fang, R *et al.* [Comprehensive analysis of single cell ATAC-seq data with SnapATAC] , *Nature Communications, 2021*

High-level noise and large volume of data pose unique computational challenges when analyzing single cell analysis of accessible chromatin (scATAC-seq), in this paper Fang and colleagues try to address this problem. The authors developed the method **S**ingle **N**ucleus **A**nalysis **P**ipeline for ATAC-seq (SnapATAC) which dissects cellular heterogeneity in an unbiased manner and maps the trajectories of cellular states. By utilizing the Nyström method, their model can process data from up to 1.000.000 cells meanwhile incorporating existing tools to supply a comprehensive package for analyzing scATAC-seq datasets. The model was proven on 55.592 snATAC-seq profiles from the mouse secondary motor cortex and revealed approximately 370.000 candidate regulatory elements in 31 cell populations with identification of candidate cell specific transcriptional regulators.



Next Single Cell Seminar

Date: 26th March 2021, online

9:00 – 10:00

Speaker to be announced

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

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