

# Single Cell Transcriptomics

Newsletter February 2022

#### Paper 1

D. Lin, Y. Chen, S. Negi, et al. CellDepot: A Unified Repository for scRNA-seq Data and Visual Exploration, J Mol Biol, 2021 Dec



CellDepot is a user-friendly integrated web application with over 270 single-cell datasets from 8 species which can be found at http://celldepot.bxgenomics.com. The platform enables efficient sharing of single-cell RNA-seg datasets and communication among the community through a userfriendly interface with advanced visualization and analytic possibilities. Moreover, the platform allows

users to quickly find datasets of interest and cross-compare expression of different genes by implementing a convenient filtering tool through a MySQL database. CellDepot embeds the cellxgene VIP tool which enables fast data exploration and provides insight into gene expression profiles, cell composition, gene set enrichment analysis and differential gene expression analysis using more than 20 frequently used plotting functions. Finally, the web portal encourages scientists to contribute to the single-cell community and collaborate with each other.



### Paper 2

H. Zeng, J. Huang, H. Zhou, et al. Integrative in situ mapping of single-cell transcriptional states and tissue histopathology in an Alzheimer's disease model, bioRxiv, 2022 Jan

To investigate the poorly understood spatiotemporal cellular responses and molecular mechanisms underlying Alzheimer's disease pathophysiology, the authors of this article introduce a high-resolution method called STARmap PLUS which enables spatial transcriptomics coupled with specific protein localization in the same tissue section. They applied their method to create a transcriptomic atlas of AD at 200 nm resolution across all brain cell types during the development of tau pathology. By targeting 2766 genes, the authors identified disease-associated gene pathways in the cortical and hippocampal regions of the 8- and 13-month-old TauPS2APP-transgenic mice. Using this framework, they successfully uncovered how AD pathologies correlate with gene pathways that drive inflammation, gliosis, and neurodegeneration across different cell types. They propose a structure of glial cells which surrounds the amyloid plaques, where disease-associated microglia emerge early near the plaques as an inner reactive core, while the shell which develops later, represents a gliosis zone enriched for disease-associated astrocytes, OPCs and oligodendrocytes.



#### Paper 3

**A. J. Twigger, L. K. Engelbrecht, K. Bach., et al.** <u>Transcriptional changes in the mammary gland during lactation</u> revealed by single cell sequencing of cells from human milk, Nat Commun, 2022 Jan



Researchers from Wellcome-MRC Cambridge Stem Cell Institute and the Department of Pharmacology at the University of Cambridge discovered living epithelial and immune cells in human milk which enables them to study cell dynamics in a non-invasive way. They report an analysis of 110 744 viable single breast cells isolated from human milk and non-lactating breast tissue. They identified previously unknown two secretory luminal cell (LC) populations (LC1 and LC2) in human samples, where L2 seem to be expressing high levels of immunomodulatory and antigen-presenting cells. They hypothesize that the proteins secreted by L2 cells may play a role

in protection of the newborn and provide a mechanism for training the adaptive immune system of the offspring. The live cells are probably detaching by downregulation of adhesion genes and being transported through the lumen of alveoli or ducts to the infant. Finally, the existence of live cells from breast milk might create an opportunity to study aberrant differentiation of luminal progenitor cells which was identified during the tumorigenesis of a BRCA1 mouse model earlier by the authors.

#### Paper 4

C. Suo, E. Dann et al. Mapping the developing human immune system across organs, bioRxiv, 2022 Jan

The authors of this article present a cross-tissue single-cell atlas and spatial atlas of developing human immune cells across prenatal hematopoietic, lymphoid, and non-lymphoid peripheral organs to better characterize the tissue-specific properties of the developing immune system. Besides their inhouse single-cell data, the authors have also included publicly available datasets from the Human Developmental Cell Atlas initiative which resulted in the collection of more than 900 000 single cells. They identified exact timepoints of immune effector acquisition of specific cell types, their proliferation and migration, and they also provide the most extensive study of human B1 cells.



### New papers from Danish researchers

- → <u>Cross-tissue transcriptome-wide association studies identify susceptibility genes shared</u> <u>between schizophrenia and inflammatory bowel disease</u>. F. Uellendahl-Werth, C. Maj, O. Borisov, et al. *Commun Biol*, 2022
- → <u>Characterization of the COPD alveolar niche using single-cell RNA sequencing.</u> M. Sauler, J. E. McDonough, T. S. Adams et al. *Nat Commun*, 2022
- → <u>Genome-wide annotation of protein-coding genes in pig</u>. M. Karlsson. E. Sjöstedt, P. Oksvold et al. *BMC Biol*, 2022

## Next Single Cell Seminar

Date: 25th February 2022, location: zoom

#### 9:00 - 10:00

Jun Hee Lee, University of Michigan Medical School See Everything Quickly through SEQ-Scope -- Microscopic Examination of Spatial Transcriptome

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

Contact: katarina.dragicevic@bric.ku.dk