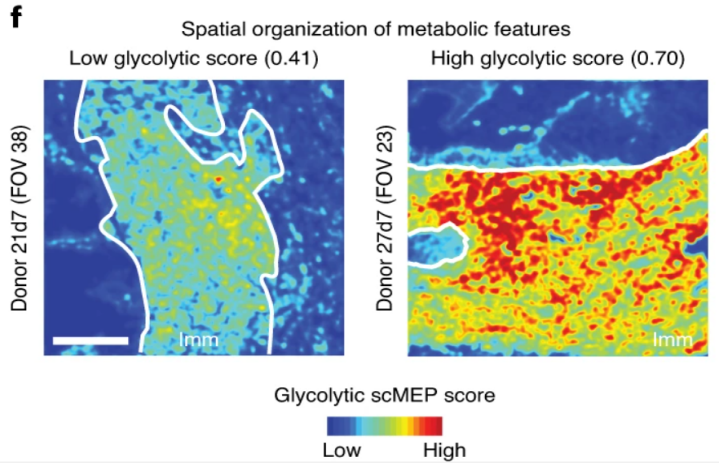
Single Cell Newsletter

September 2020

Paper 1

Hartmann, FJ *et al.* [Single-cell metabolic profiling of human cytotoxic T cells](), *Nature Biotechnology, 2020*

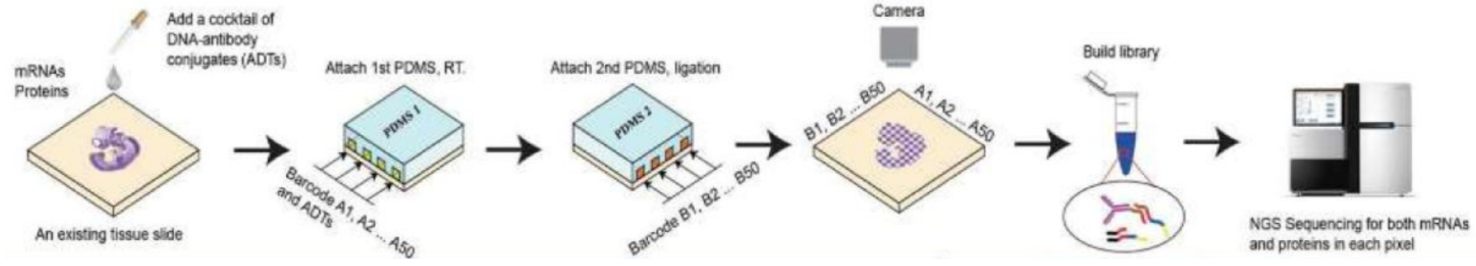
The first paper of this month focuses on the metabolome in single cells. Here, Hartmann and colleagues describe the development of single-cell metabolic regulome profiling (scMEP). The method allows for characterization of the metabolic regulome along with the phenotypic identity in single cells. ScMEP depends on metabolome-specific antibodies in combination with multiplexed mass cytometry (CyTOF). Through combination with MIBI-TOF, the authors revealed the spatial organization of metabolic states in T cells in the tumor-immune boundary. In their setup, Hartmann *et al.* showed how tissue architecture influences the metabolic regulation in tumor-immune interplay. In total, they describe how scMEP should benefit the identification of disease-associated metabolic alterations relevant for biomarker and therapeutic target discovery.



Paper 2

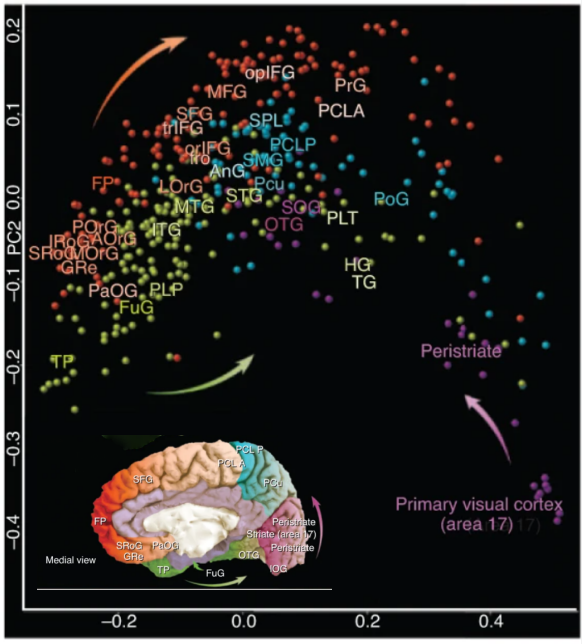
Liu, Y *et al.* [High-Spatial-Resolution Multi-Omics Atlas Sequencing of Mouse Embryos via Deterministic Barcoding in Tissue](), *bioRxiv, 2020*

In this preprint, Liu and colleagues present DBiT-Seq: Deterministic Barcoding in Tissue for spatial omics sequencing. They developed this technique to determine both mRNA and protein detection in tissue slides. Their technique presents several interesting features: They show how DBiT-Seq can be applied to formaldehyde-fixed tissue slides allowing for the use of archived tissue slides; and DBiT-Seq uses microfluidic chips directly clamped onto the tissue slides making the technique accessible for a broad range of researchers unfamiliar with microfluidic control. Proteins were determined using antibody-coupled DNA tags for subsequent sequencing, and more than 20 antibodies could be combined. In their current setup, they acquired genome-wide resolution quantifying more than 22,000 genes, with more than 2,000 genes being quantified per pixel and a pixel size of 10 µm. In comparison, the commercial Visium solution has a spot diameter of 55 µm. As an example, the authors presented data from DBiT-Seq on mouse embryos that showed good resemblance to published scRNA-seq data on similar tissue, and they were able to integrate DBiT-Seq data with scRNA-seq data to infer cell types. In summary, DBiT-Seq presents a somewhat simple way to perform high-resolution spatial transcriptomics analyses combined with limited protein quantification.



Paper 3

Yuste, R *et al.* [A community-based transcriptomics classification and nomenclature of neocortical cell types](), *Nature Neuroscience, 2020*



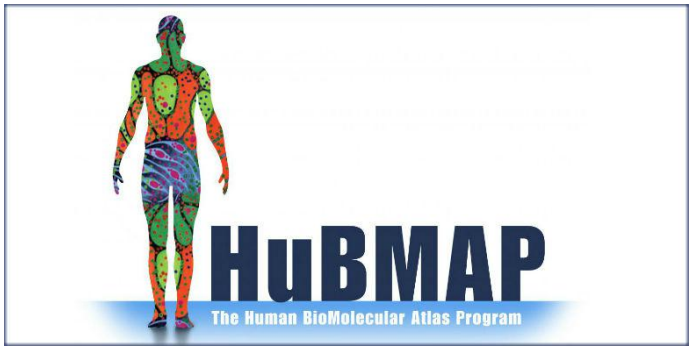
Neocortical genetic topography

This review discusses the current state of cell classification in the neocortex. Based on later years advances in single-cell transcriptomic technologies, the authors argue that the time is now for establishment of a community-based taxonomy and nomenclature of neocortical cell types. Currently, such classifications should be based on scRNA-seq data, but the authors point out that timely revisions are essential as additional datasets become available. This classification should be hierarchical and use standardized nomenclature. In order for the community to adopt the taxonomy, establishment of relevant research tools, and antibody and/or RNA probe libraries should be made available for researchers in the field. Additionally, relevant cell or mouse lines should be established. In order to avoid what the authors call the "publication graveyard", where data are stored away hardly available for researchers of the field, Yuste *et al.* suggest aggregation of data into a knowledge graph in an open platform in order to ease sharing of the data. If successful, the classification effort could be extended to other parts of the brain, or other parts of the body.

Resource

[The Human BioMolecular Atlas Program]().

HuBMAP is a novel, online resource striving to create an open, global atlas of the human body at the cellular level. At the time of release, the atlas includes samples from more than 30 donors and 7 tissues: heart, kidney, large intestine, small intestine, lymph nodes, spleen and thymus. HuBMAP seeks to embrace more data types than the Human Cell Atlas or the Human Protein Atlas by hosting data from sequencing, microscopy, and mass spectrometry studies for bulk and single-cell experiments. Single-cell or single-nuclei data are curated using Seurat. By aiming for high-spatial resolution information, HuBMAP could become a crucial resource for single-cell research.



New papers from Danish researchers

- [scVAE: Variational auto-encoders for single-cell gene expression data]() Christopher Heje Grønbech, Maximillian Fornitz Vording, Pascal Timshel, Casper Kaae Sønderby, Tune Hannes Pers, Ole Winther, ***Bioinformatics**, 2020*

Next Single Cell Seminar

Date: 25th September 2020, Location: Mærsk Tower, top floor

We will continue the mixed format (physical and virtual attendance possible) due to COVID-19 restrictions. Speakers will be announced soon in the Single Cell Group.

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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