BDR SEMINAR(Kobe & online hybrid)

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EMBL-EBI: EMBL's European Bioinformatics Institute, Cambridge UK

Tuesday, August 9, 2022

16:00-17:00

1F Auditorium, DB Building C, Kobe / Broadcast online via Zoom

Zoom meeting URL will be announced on the event day by e-mail.

※Non-BDR members: Please register from the following link.

https://krs1.riken.jp/m/bdrseminarregistration (Registration deadline: Aug 5)

Informatics infrastructure for whole-brain cell type catalogs

Summary

Traditional, qualitative, categorical methods of classifying neurons based on location, morphology, marker expression and function have not come close to achieving a coherent, unified catalog of neuron types in all but the very simplest nervous systems. The shear number and diversity of neurons has, to date, made this impractical. The advent of whole brain single cell profiling is beginning to change this. In Drosophila, thousands of cell types have been defined based on morphological and connectomic similarity of neurons identified in connectomics data. Whole-CNS connectomes will soon be published, supporting a complete catalog of Drosophila neurons. A complete single cell transcriptomics atlas of the optic lobes already exists and while challenges remain, similar atlases of the central brain will follow. In mammals massively parallel single cell transcriptomics is being used to generate whole brain catalogs of (transcriptomically defined) cell types, with techniques such as patch-seq and MERFISH being used to map these to cell morphology function and location and to cell types in other species. Mammalian connectomics at scale will surely follow, although formidable challenges remain.

This presents major challenges for data organization. Without robust, scalable, standardized methods to organize, annotate and link the data used to define these cell types, it will not be possible to build a coherent, queryable catalog of cell types or to inspect and judge the evidence that supports it. I will present the work that my group is doing to address this problem for Drosophila (Virtual Fly Brain project) and for mammalian brains (Brain Initiative Cell Atlas Network), combining semi-automated ontology development, annotation tools, 'BLAST'-like similarity scoring and machine learning to build cell type knowledge bases as well as web-based atlas interfaces and APIs for biologists and informaticians to access them.

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