

FAIRifying single cell RNA-seq data from Single Cell Portal

Bio-IT FAIR Data Hackthon
Monday, May 14, 2018

Single Cell Portal BETA

Visualization portal for single cell RNA-seq data.

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Single nucleus RNA-seq of cell diversity in the adult mouse hippocampus (sNuc-Seq) ▾

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Single nucleus RNA-seq of cell diversity in the adult mouse hippocampus. Habib N, Li Y, Heidenreich M, Swiech L, Avraham-David I, Trombetta J, Hession C, Zhang F, Regev A. *Div-Seq: Single-nucleus RNA-Seq reveals dynamics of rare adult newborn neurons*. *Science* 28 Jul 2016 DOI: 10.1126/science.aad7038 Contact: naomi@broadinstitute.org Single cell RNA-Seq provides rich information about cell types and states. However, it is difficult to capture rare dynamic processes, such as adult neurogenesis, because isolation of rare neurons from adult tissue is challenging and markers for each phase are limited. Here, we develop Div-Seq, which combines scalable single-nucleus RNA-Seq (sNuc-Seq) with pulse labeling of proliferating cells by EdU... (continued)

Retinal Bipolar Neuron Drop-seq ▾

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Retinal Bipolar Neuron Drop-Seq Karthik Shekhar, Sylvain W. Lapan, Irene E. Whitney, Nicholas M. Tran, Evan Z. Macosko, Monika Kowalczyk, Xian Adiconis, Joshua Z. Levin, James Nemesh, Melissa Goldman, Steven A. McCarroll, Constance L. Cepko, Aviv Regev, Joshua R. Sanes. *Comprehensive Classification of Retinal Bipolar Neurons by Single-Cell Transcriptomics*. *Cell*. Volume 166, Issue 5, p1308–1323.e30, 25 August 2016. DOI: <http://dx.doi.org/10.1016/j.cell.2016.07.054> Contact: Karthik Shekhar at karthik@broadinstitute.org Patterns of gene expression can be used to characterize and classify neuronal types. It is challenging, however, to generate taxonomies that fulfill the essential criteria of being comprehensive, harmonizing with conventional classification schemes, and lacking superfluous subdivisions of genuine types. To address these challenges, we used massively parallel single-cell RNA profiling and optimized computational methods on a heterogeneous class of... (continued)

10X LucOS ▾



Study: Single nucleus RNA-seq of cell diversity in the adult mouse hippocampus (sNuc-Seq) 1402 cells

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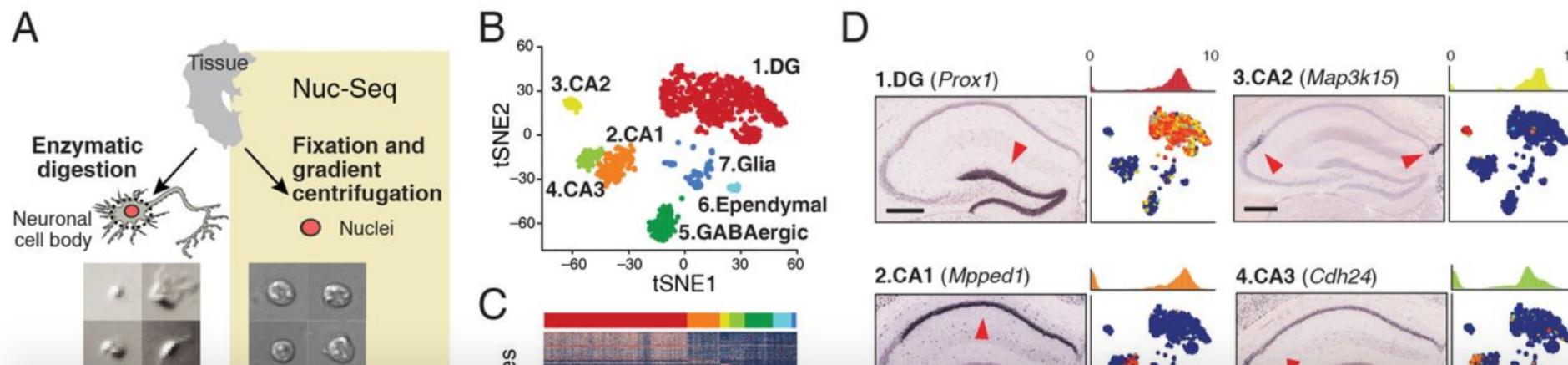
Single nucleus RNA-seq of cell diversity in the adult mouse hippocampus.

Habib N, Li Y, Heidenreich M, Swiech L, Avraham-David I, Trombetta J, Hession C, Zhang F, Regev A. **Div-Seq: Single-nucleus RNA-Seq reveals dynamics of rare adult newborn neurons.** *Science* 28 Jul 2016 DOI: [10.1126/science.aad7038](https://doi.org/10.1126/science.aad7038)

Contact: naomi@broadinstitute.org

Single cell RNA-Seq provides rich information about cell types and states. However, it is difficult to capture rare dynamic processes, such as adult neurogenesis, because isolation of rare neurons from adult tissue is challenging and markers for each phase are limited. Here, we develop Div-Seq, which combines scalable single-nucleus RNA-Seq (sNuc-Seq) with pulse labeling of proliferating cells by EdU to profile individual dividing cells. sNuc-Seq and Div-Seq can sensitively identify closely related hippocampal cell types and track transcriptional dynamics of newborn neurons within the adult hippocampal neurogenic niche, respectively. This study contains the sNuc-Seq analysis performed as a part of the Div-Seq method development.

Using sNuc-Seq, we analyzed 1,367 single nuclei from hippocampal anatomical sub-regions (DG, CA1, CA2, and CA3) from adult mice, including enrichment of genetically-tagged lowly abundant GABAergic neurons (9). sNuc-Seq robustly generated high quality data across animal age groups (including 2 years old mice), detecting 5,100 expressed genes per nucleus on average, with comparable complexity to single neuron RNA-Seq from young mice (1, 2, 3). Analysis of sNuc-Seq data revealed distinct nuclei clusters (Fig. 1B-D shown below) corresponding to known cell types and anatomical distinctions in the hippocampus.



Gene Expression for *GAD1*[Summary](#)[Explore](#)[Download](#)[Settings](#)

GAD1

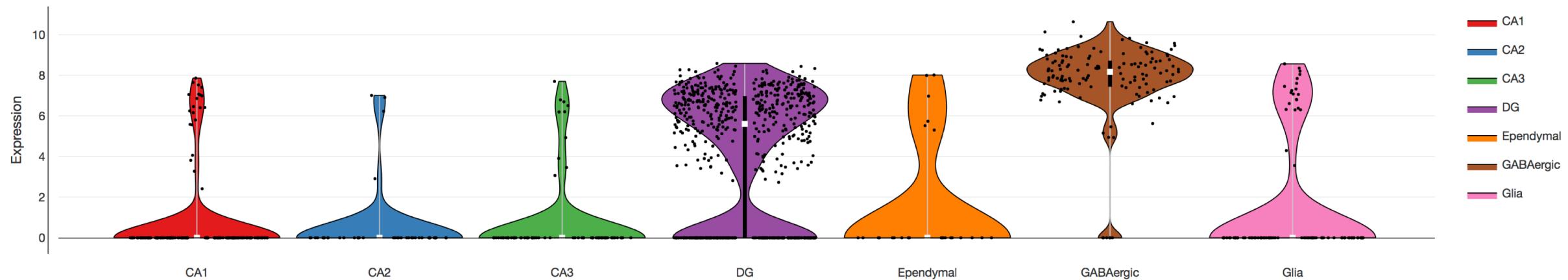


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Coordinates_Major_cell_types



Gene Expression for **GAD1**[Summary](#)[Explore](#)[Download](#)[Settings](#)[Bulk Download](#)**Study Files** 12

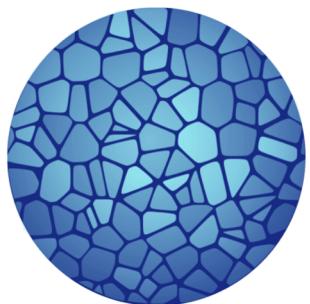
| Filename | Description | Download |
|---|--|-----------|
| CLUSTER_AND_SUBCLUSTER_INDEX.txt | Cluster and sub-cluster assignments for all single cells | 52.9 KB |
| Coordinates_CA1.txt (Coordinates_CA1.txt) | Cluster coordinates for sub clusters in CA1 | 6.46 KB |
| Coordinates_CA3.txt (Coordinates_CA3.txt) | Cluster coordinates for sub-clusters in CA3 | 3 KB |
| Coordinates_DG.txt (Coordinates_DG.txt) | Cluster coordinates for sub-clusters in DG | 27.6 KB |
| Coordinates_GABAergic.txt (Coordinates_GABAergic.txt) | Cluster coordinates for sub-clusters in GABAergic | 5.67 KB |
| Coordinates_Glia.txt (Coordinates_Glia.txt) | Cluster coordinates for sub-clusters in Glia | 4.53 KB |
| Coordinates_Major_cell_types.txt (Coordinates_Major_cell_types.txt) | Major cell types coordinates (top-level clusters) | 49.2 KB |
| DATA_MATRIX_LOG TPM.txt | Expression Matrix, log(TPM) cells X genes | 214 MB |
| GABAergic_edit_subcluster_marker_gene.txt | GABAergic cluster marker genes | 26 KB |
| Glia_subcluster_marker_genes.txt | Glia cluster marker genes | 20.7 KB |
| Major_cell_types_marker_genes.txt | Major cell types marker gene list | 32.5 KB |
| README.txt | Experimental design & file format information | 861 Bytes |

Primary Data 1

Show 10 entries

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```
ubuntu@ip-172-31-36-197:~/single-nucleus-rna-seq-data$ ls -latr
total 209084
-rw-rw-r-- 1 ubuntu ubuntu      4549 May 14 13:39 Coordinates_Glia.txt
-rw-rw-r-- 1 ubuntu ubuntu    25976 May 14 13:39 GABAergic_edit_subcluster_marker_gene.txt
-rw-rw-r-- 1 ubuntu ubuntu     3017 May 14 13:39 Coordinates_CA3.txt
-rw-rw-r-- 1 ubuntu ubuntu    27569 May 14 13:39 Coordinates_DG.txt
-rw-rw-r-- 1 ubuntu ubuntu     5685 May 14 13:39 Coordinates_GABAergic.txt
-rw-rw-r-- 1 ubuntu ubuntu     6474 May 14 13:39 Coordinates_CA1.txt
-rw-rw-r-- 1 ubuntu ubuntu    20670 May 14 13:39 Glia_subcluster_marker_genes.txt
-rw-rw-r-- 1 ubuntu ubuntu    49219 May 14 13:39 Coordinates_Major_cell_types.txt
-rw-rw-r-- 1 ubuntu ubuntu       861 May 14 13:39 README.txt
-rw-rw-r-- 1 ubuntu ubuntu    32452 May 14 13:39 Major_cell_types_marker_genes.txt
-rw-rw-r-- 1 ubuntu ubuntu    52947 May 14 13:39 CLUSTER_AND_SUBCLUSTER_INDEX.txt
-rw-rw-r-- 1 ubuntu ubuntu  213832299 May 14 13:39 DATA_MATRIX_LOG TPM.txt
drwxrwxr-x 2 ubuntu ubuntu      4096 May 14 14:35 .
drwxr-xr-x 12 ubuntu ubuntu     4096 May 14 15:17 ..
```



HUMAN CELL ATLAS

HumanCellAtlas/metadata-schema

GitHub, Inc. [US] | https://github.com/HumanCellAtlas/metadata-schema

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HumanCellAtlas / metadata-schema

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This repo is for the metadata schemas associated with the HCA

958 commits 9 branches 10 releases 17 contributors

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daniwelter Merge pull request #272 from HumanCellAtlas/develop ... Latest commit 03a1be7 11 days ago

docs Merge pull request #271 from HumanCellAtlas/mf-update-readme-docs 11 days ago

examples Add files via upload 2 months ago

json_schema Updated README markdown files. 2 months ago

json_schema_extensions Renamed dir containing schema extensions. 4 months ago

schema_test_files Added analysis_process.json example for testing. 2 months ago

src jsonBrowser now has additional required_fields doc. describedBy and s... 21 days ago

.gitignore Added failing bundle to automatic testing. 4 months ago

.travis.yml Release v5.0.0 HCA metadata schema. 3 months ago

README.md Updated intro for contributing. a month ago

changelog.md Updated changelog 2 months ago

issue_template.md Added a PR template file. Updated issue template file. 2 months ago

pull_request_template.md Added a PR template file. Updated issue template file. 2 months ago

requirements.txt Initial commit 3 months ago

README.md

https://github.com/BioITHackathons/single_cell_portal_core/tree/master/hackathon