FAIRifying single cell RNA-seq data from Single Cell Portal

Hackathon Report

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Broad Institute

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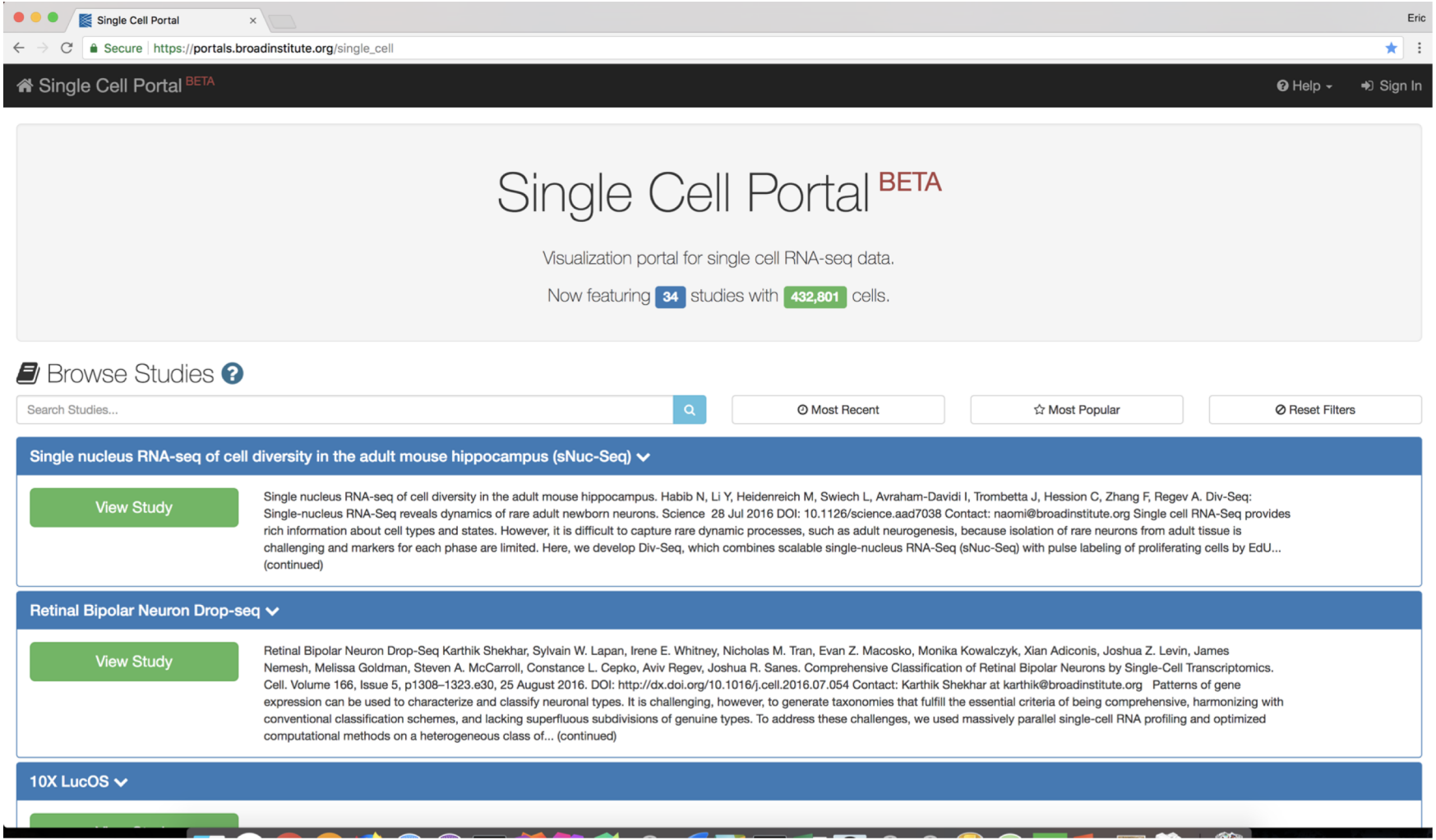
Single Cell Portal

Portal for single cell RNA-seq data

- **Summarize**: Abstracts and figures from study publications
- **Explore**: visualize gene expression with t-SNE, violin plots, heatmaps, more
- **Analyze**: Run workflows like CellRanger, leveraging a web UI and FireCloud
- **Download:** Get raw data, as individual files or in bulk

https://portals.broadinstitute.org/single_cell


Single Cell Portal
Eric
Secure https://portals.broadinstitute.org/single_cell
Single Cell Portal BETA
Help
Sign In
Single Cell Portal BETA
Visualization portal for single cell RNA-seq data.
Now featuring 34 studies with 432,801 cells.
Browse Studies
Search Studies...
Most Recent
Most Popular
Reset Filters
Single nucleus RNA-seq of cell diversity in the adult mouse hippocampus (sNuc-Seq)
View Study
Single nucleus RNA-seq of cell diversity in the adult mouse hippocampus. Habib N, Li Y, Heidenreich M, Swiech L, Avraham-Davidi 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
View Study
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

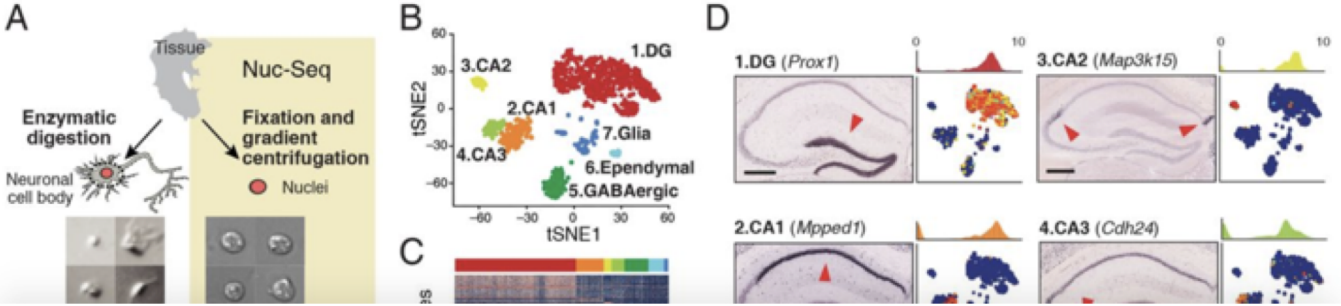
Study: Single nucleus RNA-seq of cell diversity in the adult mouse hippocampus (sNuc-Seq) 1402 cells

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

Habib N, Li Y, Heidenreich M, Swiech L, Avraham-Davidi 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 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

Advanced Gene Search

Upload gene list

Choose File No file chosen

Collapse genes by

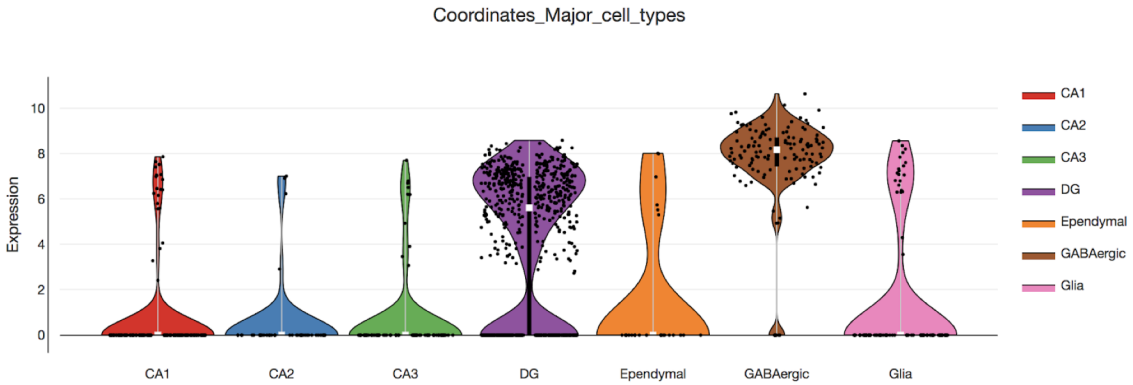
None

Back

View Gene Lists

Create Annotations

Distribution Scatter View Options



Load cluster

Coordinates_Major_cell_types

Select annotation

CLUSTER

Subsampling threshold

All Cells

Distribution

Plot Type

Violin Plot

Kernel Type

Gaussian

Bandwidth Selector

nrd0

Toggle Annotations

Scatter

Heatmap

Gene Expression for *GAD1*

Study Files 12

Bulk Download

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 Search:

Hackathon: Day 1

- Onboard team members
  - Expected 4 Broadies, 2-3 external
  - Actual 4 Broadies, ~**18** external
  - The more the merrier!
- Evaluate FAIRness of Single Cell Portal using Purple Polar Bears web survey app
- Brainstorm tasks for large number of new developers
- Get everyone integrated, unblocked, and coding productively

Hackathon: Day 2

Implement features!

Study metadata: Use cases and tasks

User story: provide FAIR metadata using Human Cell Atlas (HCA) community standards about studies

Use case: SCP has prose abstracts, needs to detect organism, tissue, etc. and map to ontology URL

NLP analysis: Soheil Danesh, Asya Lushnikova

Use case: Ontology mapping from NLP is list of key-value pairs, needs structure defined in community metadata standard

TSV-JSON transform: Tom Madden, David Managadze, Frank O

Use case: Community metadata standard uses text values, not URLs

FAIRify HCA metadata: Kenny Knecht, Adelaide Rhodes, Tom Madden

Use case: Community metadata standard uses JSON Schema, but ontologies often use OWL

JSON-OWL transform: Morgan Wahl

Use case: Tie together all these tasks in a pipeline

Pipeline: Alex Baumann, Tim Lee

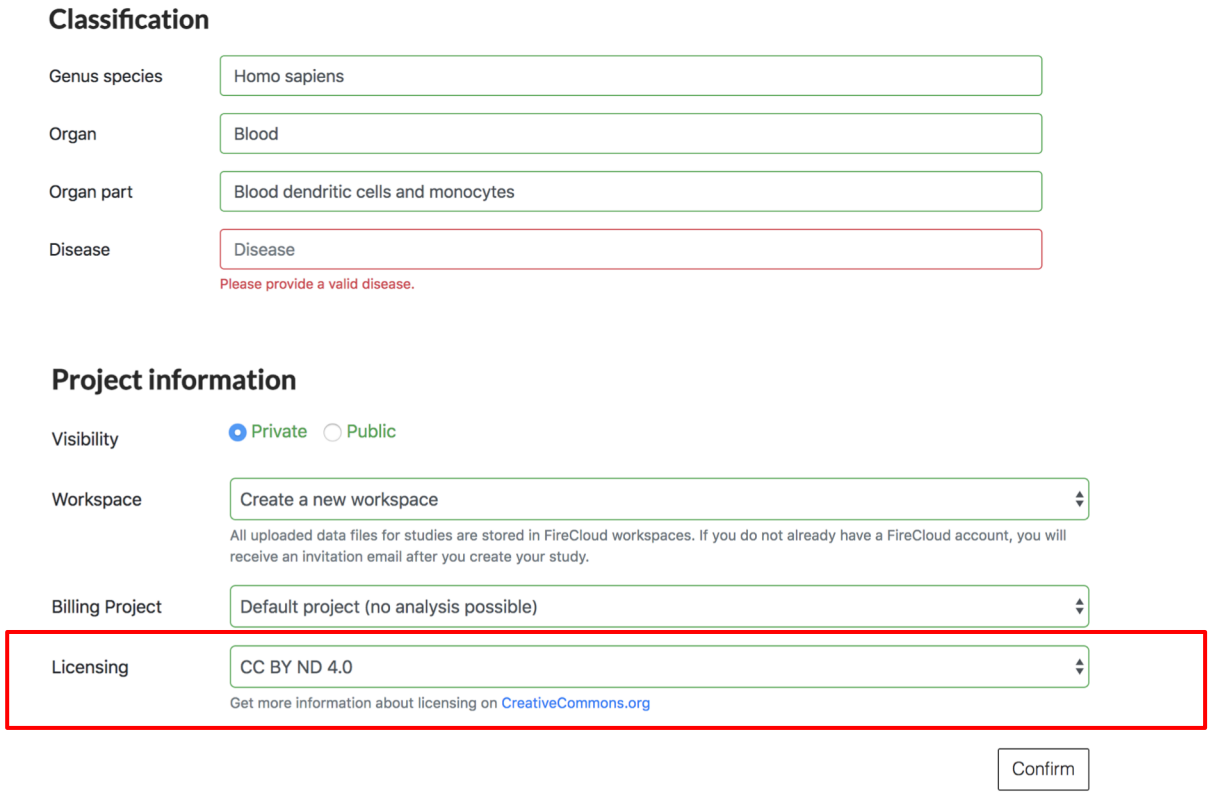
Use case: Provide adapters to convert from HCA metadata standard to GEO metadata standard

Converters: Etienne Gnimpieba, Tayler Hoekstra, Isaac Hanson

Use case: NLP can't provide all the metadata we need

Augment study creation UI/UX: Anthony Dubois, Maya Bobrovitch, Kate Voss, Morgan Wahl

Study metadata: Explicit classification and licensing



An NLP algorithm fills the form and the user can edit it using a standard dictionary (auto complete feature).

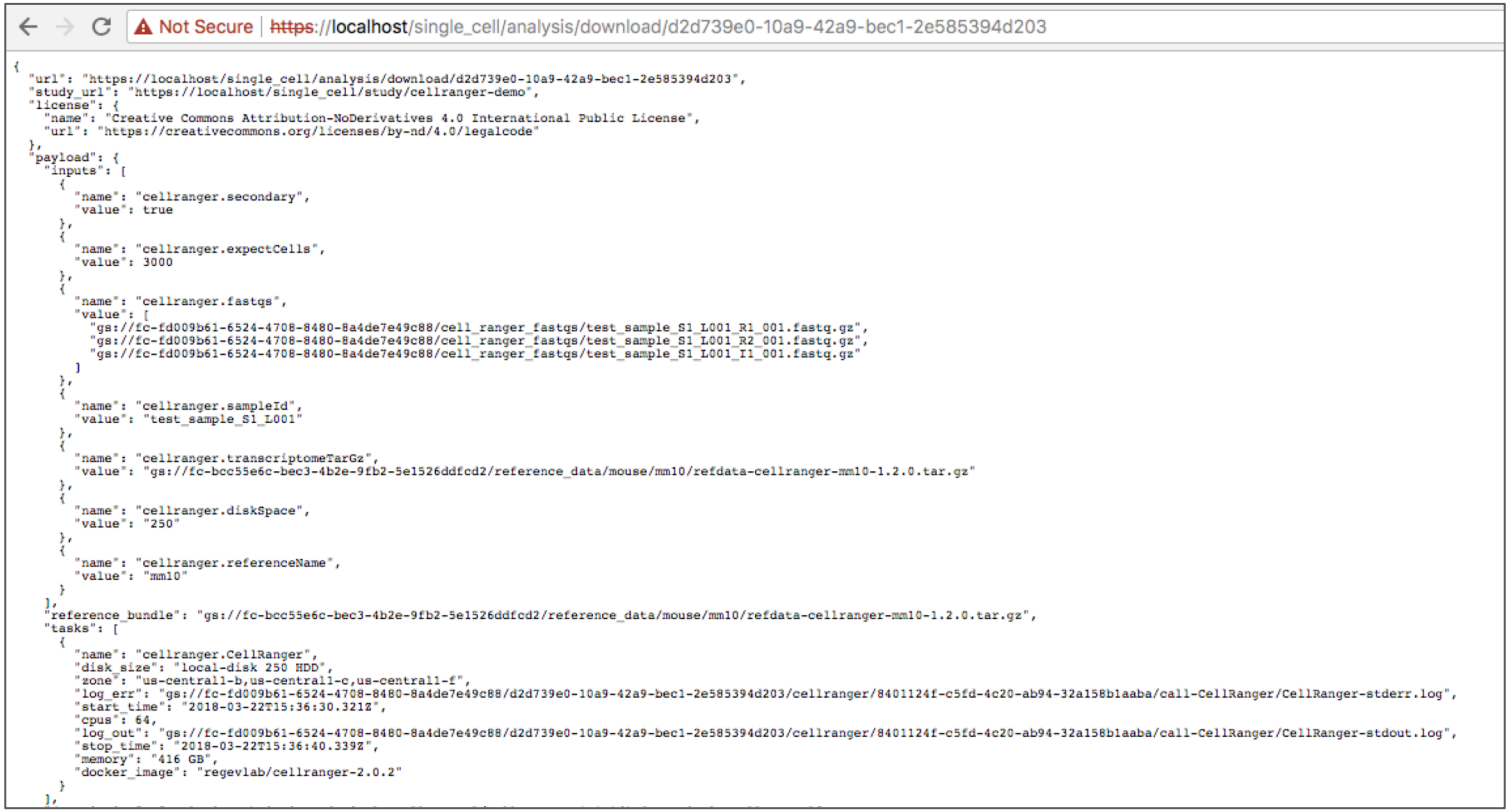
Study owner specifies an accessible usage license

Analysis metadata: Use cases and tasks

- **Use case**: Analysis metadata conforms to community standards, but audience is restricted
  - **Enable public analysis.json**: Jon Bistline

- **Use case**: Analysis metadata is not easily machine-findable
  - **Enable analysis.json search**: Jon Bistline

Analysis.json ‘FAIR’ payload




```
{
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  "study_url": "https://localhost/single_cell/study/cellranger-demo",
  "license": {
    "name": "Creative Commons Attribution-NoDerivatives 4.0 International Public License",
    "url": "https://creativecommons.org/licenses/by-nd/4.0/legalcode"
  },
  "payload": {
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        "name": "cellranger.secondary",
        "value": true
      },
      {
        "name": "cellranger.expectCells",
        "value": 3000
      },
      {
        "name": "cellranger.fastqs",
        "value": [
          "gs://fc-fd009b61-6524-4708-8480-8a4de7e49c88/cell_ranger_fastqs/test_sample_S1_L001_R1_001.fastq.gz",
          "gs://fc-fd009b61-6524-4708-8480-8a4de7e49c88/cell_ranger_fastqs/test_sample_S1_L001_R2_001.fastq.gz",
          "gs://fc-fd009b61-6524-4708-8480-8a4de7e49c88/cell_ranger_fastqs/test_sample_S1_L001_I1_001.fastq.gz"
        ]
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      },
      {
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        "value": "250"
      },
      {
        "name": "cellranger.referenceName",
        "value": "mm10"
      }
    ],
    "reference_bundle": "gs://fc-bcc55e6c-bec3-4b2e-9fb2-5e1526ddfcd2/reference_data/mouse/mm10/refdata-cellranger-mm10-1.2.0.tar.gz",
    "tasks": [
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        "log_err": "gs://fc-fd009b61-6524-4708-8480-8a4de7e49c88/d2d739e0-10a9-42a9-bec1-2e585394d203/cellranger/8401124f-c5fd-4c20-ab94-32a158b1aaba/call-CellRanger/CellRanger-stderr.log",
        "start_time": "2018-03-22T15:36:30.321Z",
        "cpus": 64,
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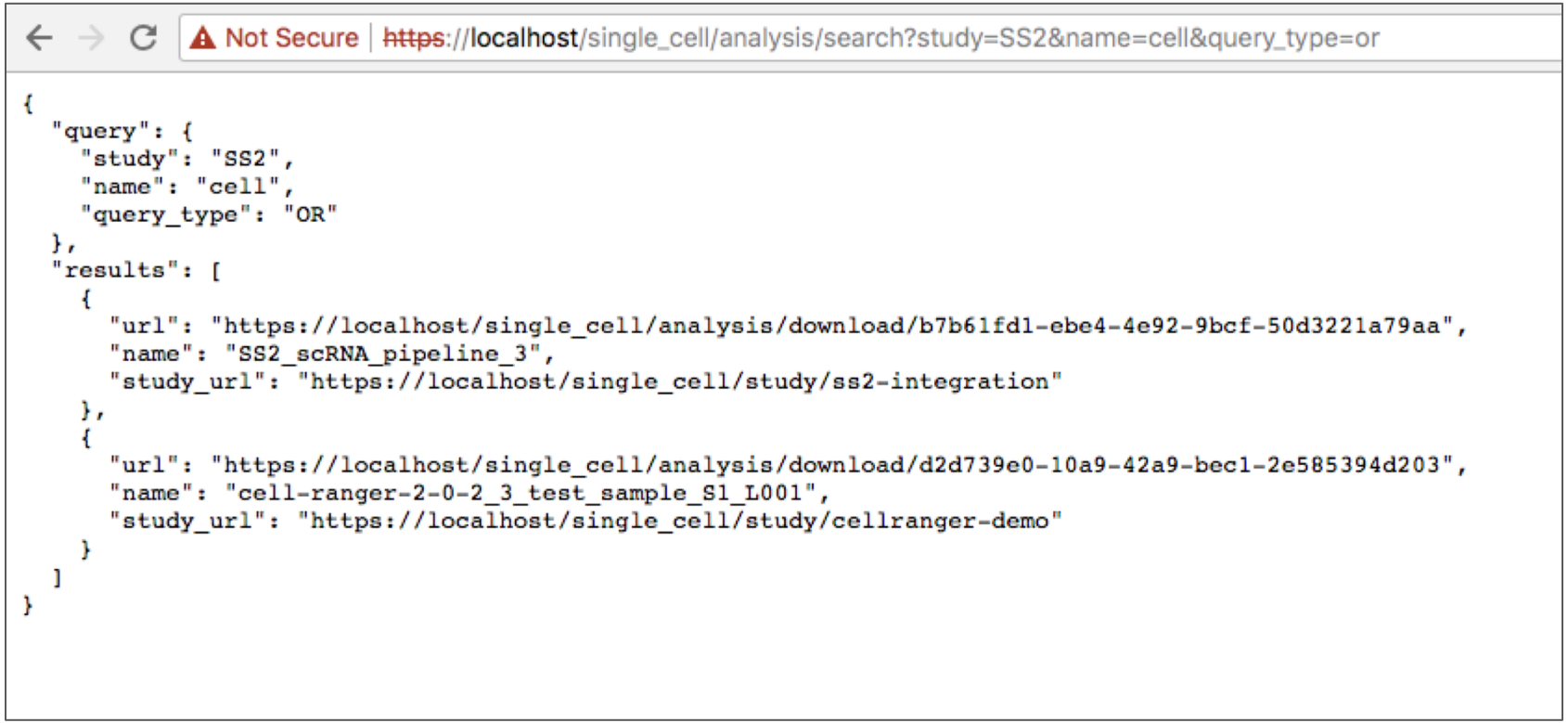
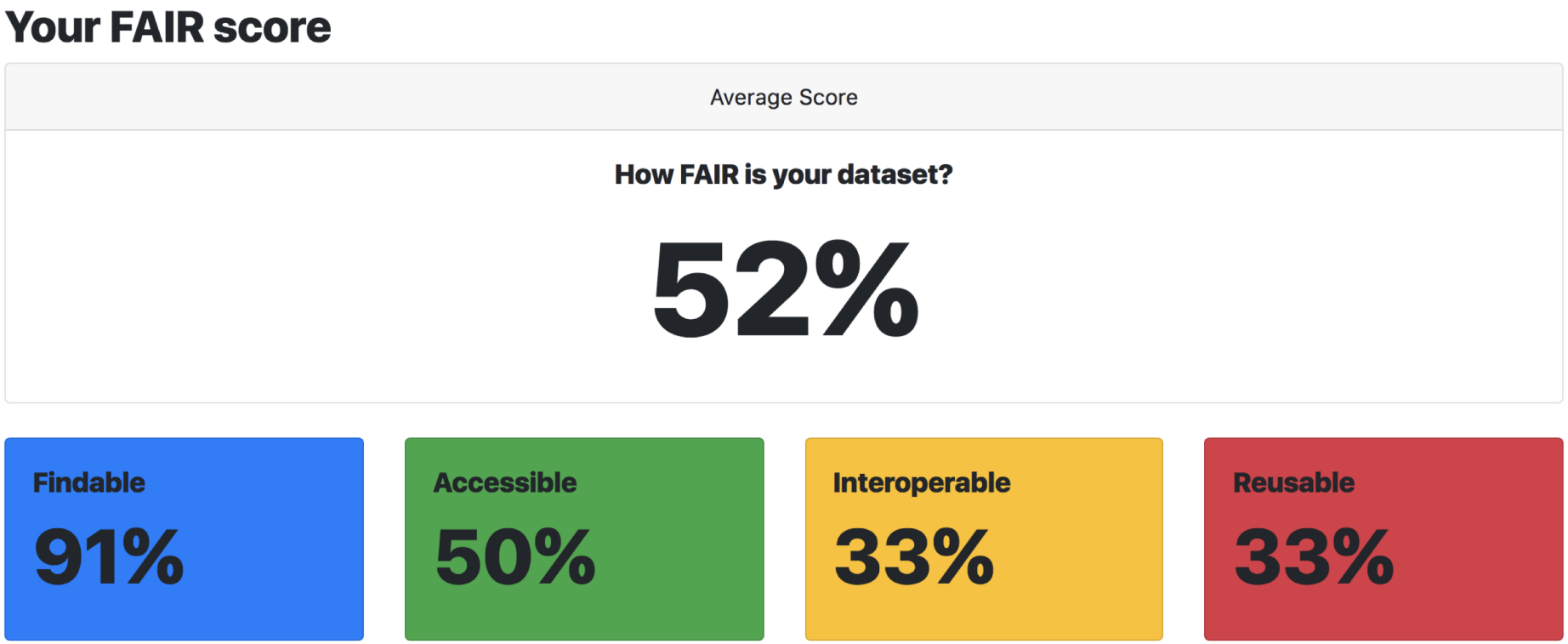
Analysis search API



Relation to FAIR Metrics

- FAIR Evaluator survey is just a start
- Single Cell Portal Resources has multiple resource types
- “Study” resource type increased in Interoperability, Reusability
- “Analysis” resource type increased in Findability, Accessibility

FAIR score: 29% -> 52%



Collaborative coding

https://github.com/BioITHackathons/single_cell_portal_core

45 commits from 12 people in < 2 days

Rapid onboarding to completely new project for 20 of 22 team members

Several people learned how to use Git and GitHub!

Broad Institute hackathon team

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Thank you!

Eric Weitz
Jon Bistline
Kate Voss
Alex Baumann
Soheil Danesh
Austin Chow
Adelaide Rhodes

Maya Bobrovitch
Tim Lee
Tom Madden
Brian Kang
Brad Nissenbaum
Frank O
Morgan Wahl

Kenny Knecht
Julia Ivashina
David Managadze
Etienne Gnimpieba
Tayler Hoekstra
Isaac Hanson
Asya Lushnikova
Anthony Dubois