

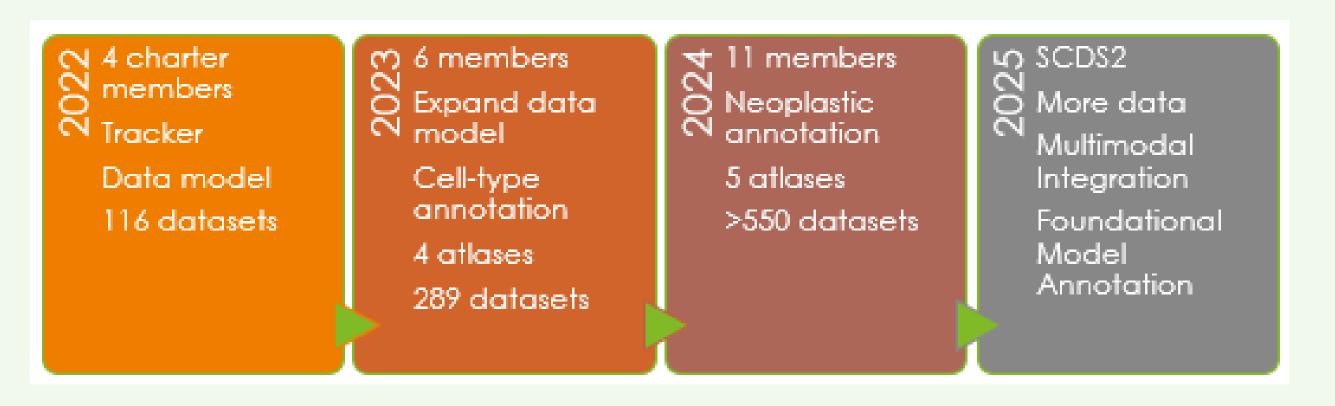
Leveraging Metadata and Sample Data Harmonization Pipelines to Ensure High-Quality Datasets in the Single-Cell Data Science Consortium Initiative

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Background

Rancho Biosciences has successfully finished the first round of its 3-year Single-Cell Data Science Consortium (SCDC). This pre-competitive effort grew from 4 charter members to 11 members over the course of 3 years. The deliverables cover more than 800 publications and 1,000 individual datasets, including recent landmark papers (e.g., Siletti et. al, 2022, Tabula Sapiens Consortium et al. 2022 and Tabula Muris Consortium et al., 2020). The ready-to-use deliverables include processed expression data and metadata harmonized across datasets at the study, donor, sample and cell levels. Our dedicated SCDS data integrity pipeline combined the best of Rancho accelerators and manual curation by subject matter experts to align metadata to attribute-specific relevant public ontologies, including DOID, UBERON, CL, MeSH, EFO and a custom vocabulary.



Data Ingestion Workflow

Members

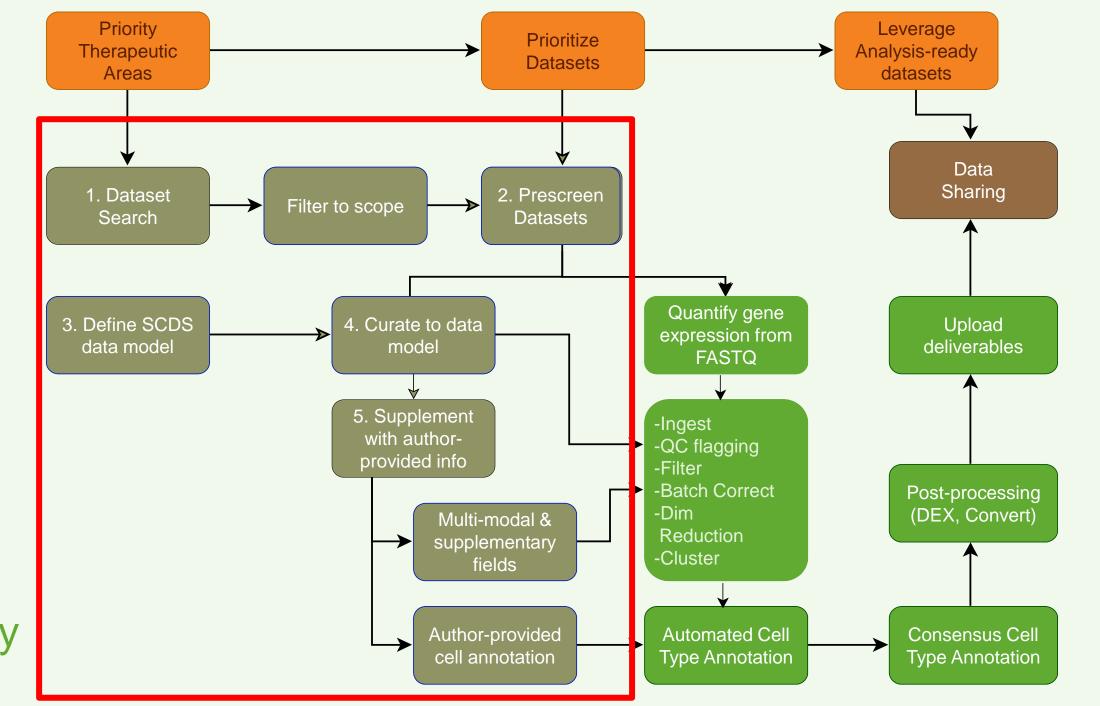
Define Priorities

Data Integrity

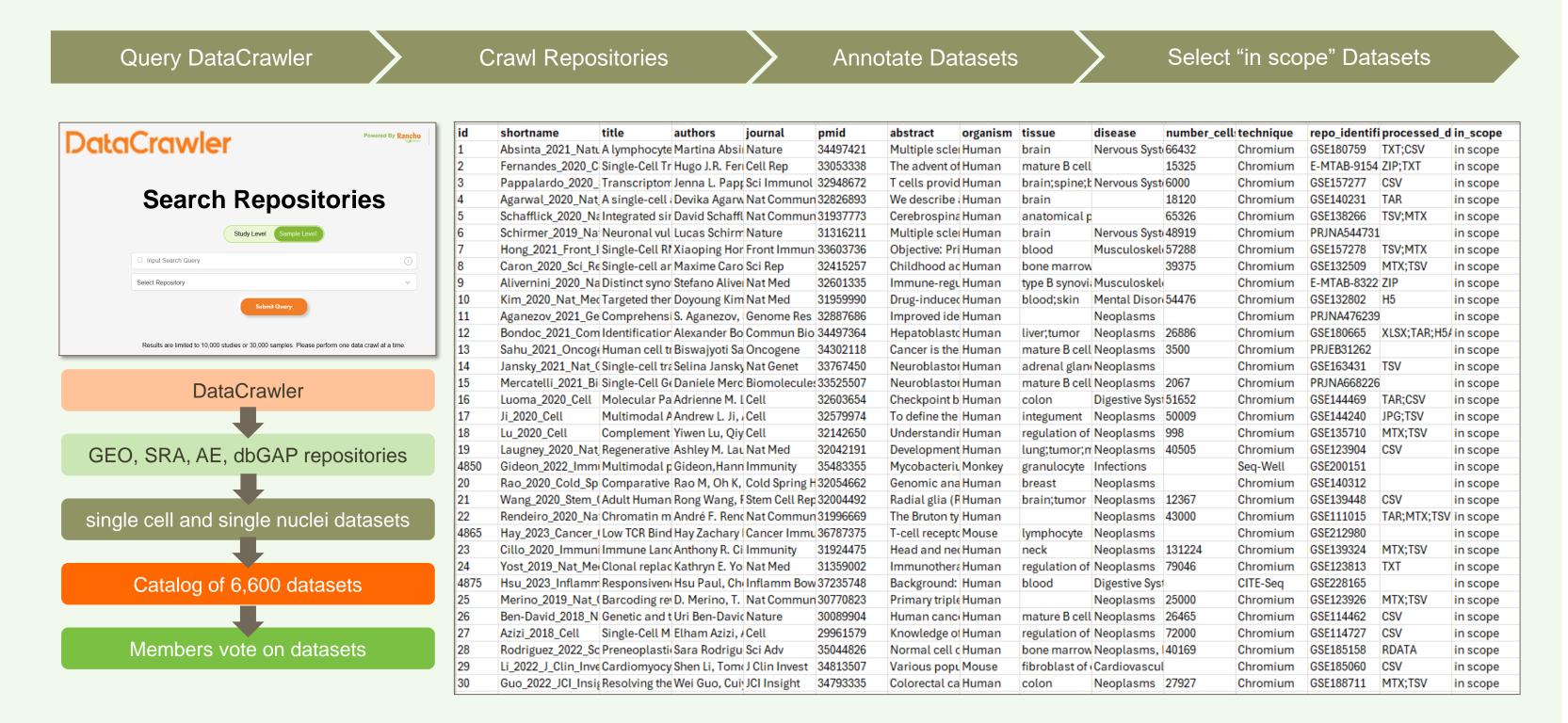
- Maintain catalog
- **Prescreen datasets**
- Harmonize samplelevel metadata

Bioinformatics

 Provide analysis-ready datasets

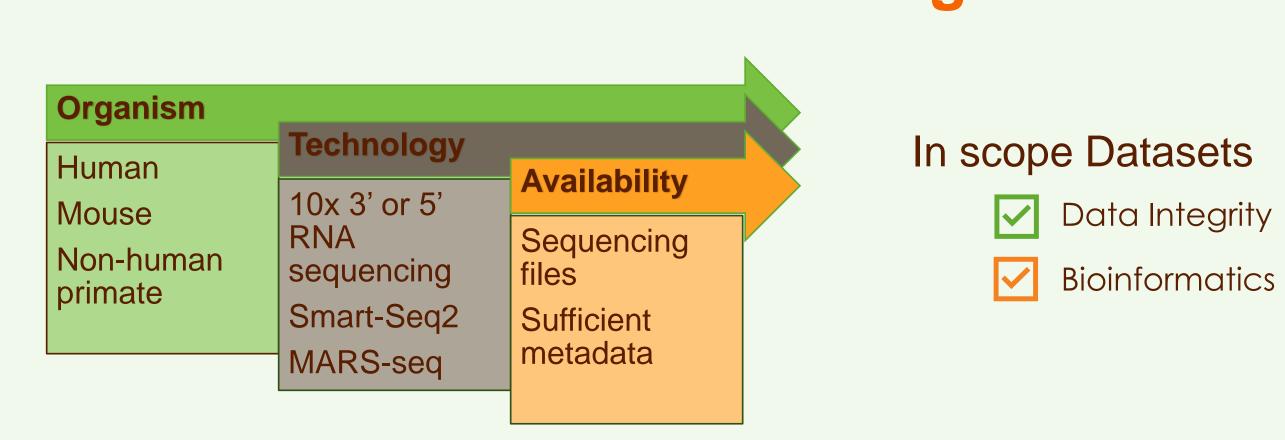


1. Building a Catalog



To assemble a catalog of relevant datasets, we surveyed several repositories, including GEO, SRA, AE, and dbGaP for single cell or single nuclei datasets. Our catalog includes over 6,600 publications or datasets published since 2013 and is annotated for disease, tissue, and assay.

2. Prescreening

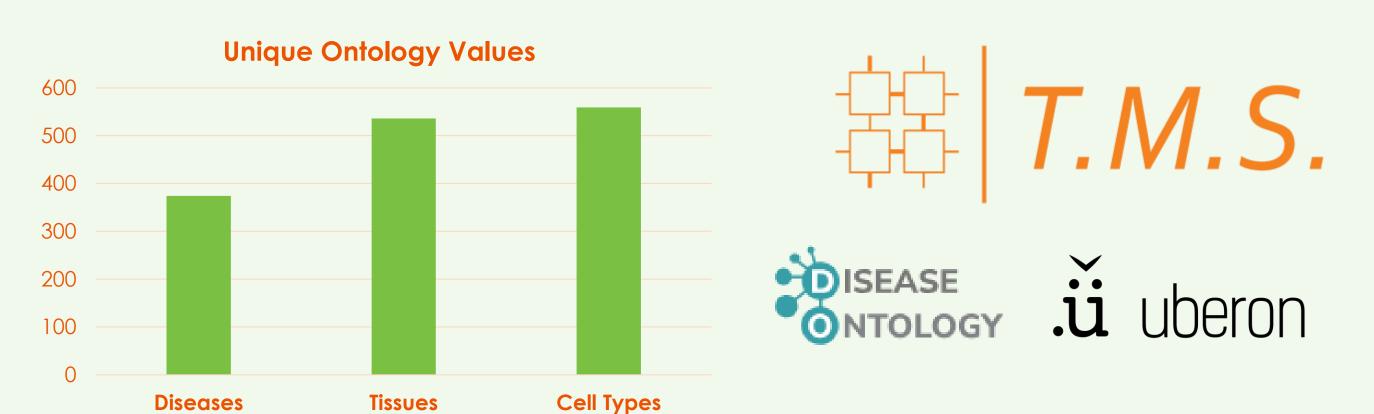


Data Integrity team members check each dataset selected by consortium members to ensure they are compatible with the bioinformatics pipeline and have sufficient metadata to provide downstream value.

3. SCDS Data Model Cell Study **Donor** Sample study and donor sample cell demographic identifiers dataset identifiers identifiers information background donor disease donor derived medical cell type characteristics treatment identifiers values history sample sample sample neoplasm tissue treatment processing characteristics information information information

We developed a custom 4 entity, 83 attribute data model that is flexible enough to be used for a wide range of experimental purposes

4. Metadata Harmonization



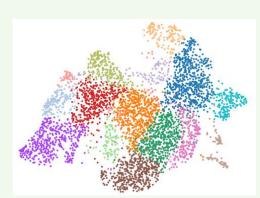


- Metadata is aligned to attribute-specific relevant public ontologies, including DOID, UBERON, CL, MeSH, EFO and a custom vocabulary using Rancho accelerator, Terminology Management Solution
- In total, 559 unique cell types, 374 unique diseases and 536 unique tissue values were harmonized to allow for intra- and inter-dataset comparisons
- Strict adherence to the data model and accompanying dictionaries reduced differences across batches and curators.

5. QC and Supplemental Information







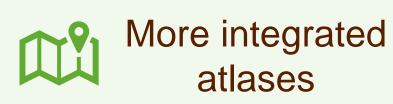
- Stringent QC tools and scripts were applied to ensure the highest quality content.
- Data integrity team members sought cell-level metadata such as cell type annotations or cluster information on alternative websites and contacted authors for additional information.
- We worked with authors to resolve discrepancies, link the donor information and sample identifiers, and otherwise enrich the metadata.

Conclusions

Curated datasets and atlases delivered as part of this consortium are valuable resources that increase the accuracy and efficiency of downstream analyses, accelerate reproducible science and facilitate joint analysis of public data.







SCDS2 kicked off in February 2025 with 6 charter members



