

Breakout Session 6:

The NHBLI LungMAP Cloud Ecosystem: Connecting Diverse Digital and Lung Biology Resources

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The NHBLI LungMAP Cloud Ecosystem: Connecting Diverse Digital and Biology Resources

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Cincinnati Children's Hospital



- Regeneration and repair
- Role of stem cells
- Developmental hierarchies
- Mechanisms of disease
- Genetics and infection

Addressing these questions challenges require:

- Team science approaches with diverse experts
- New tools and techniques to construct systems models
- Integrated atlas level initiatives

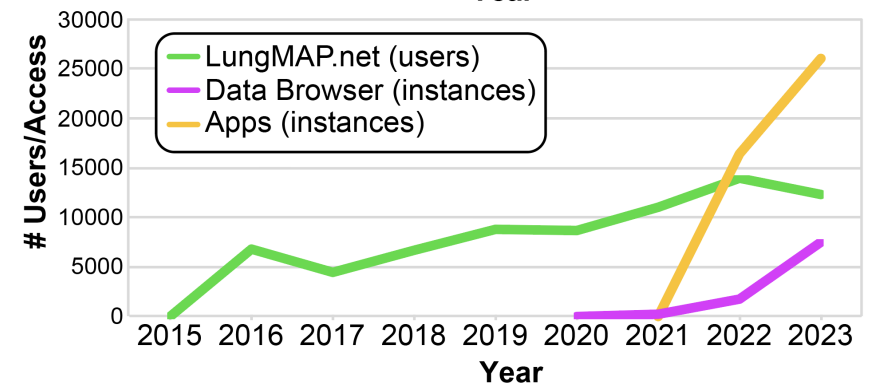
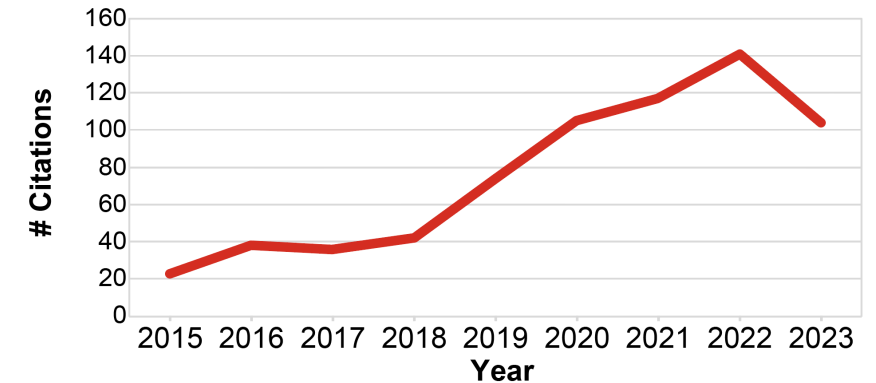
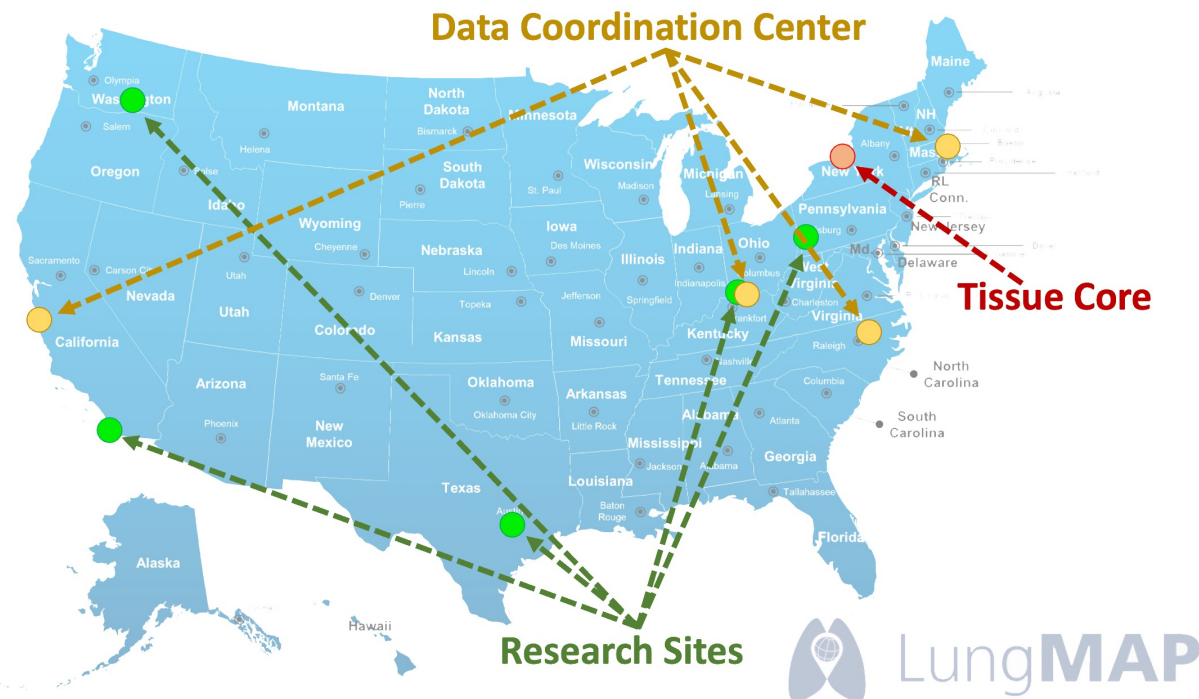
The LungMAP Consortium



LungMAP
Molecular Atlas of Lung
Development Program

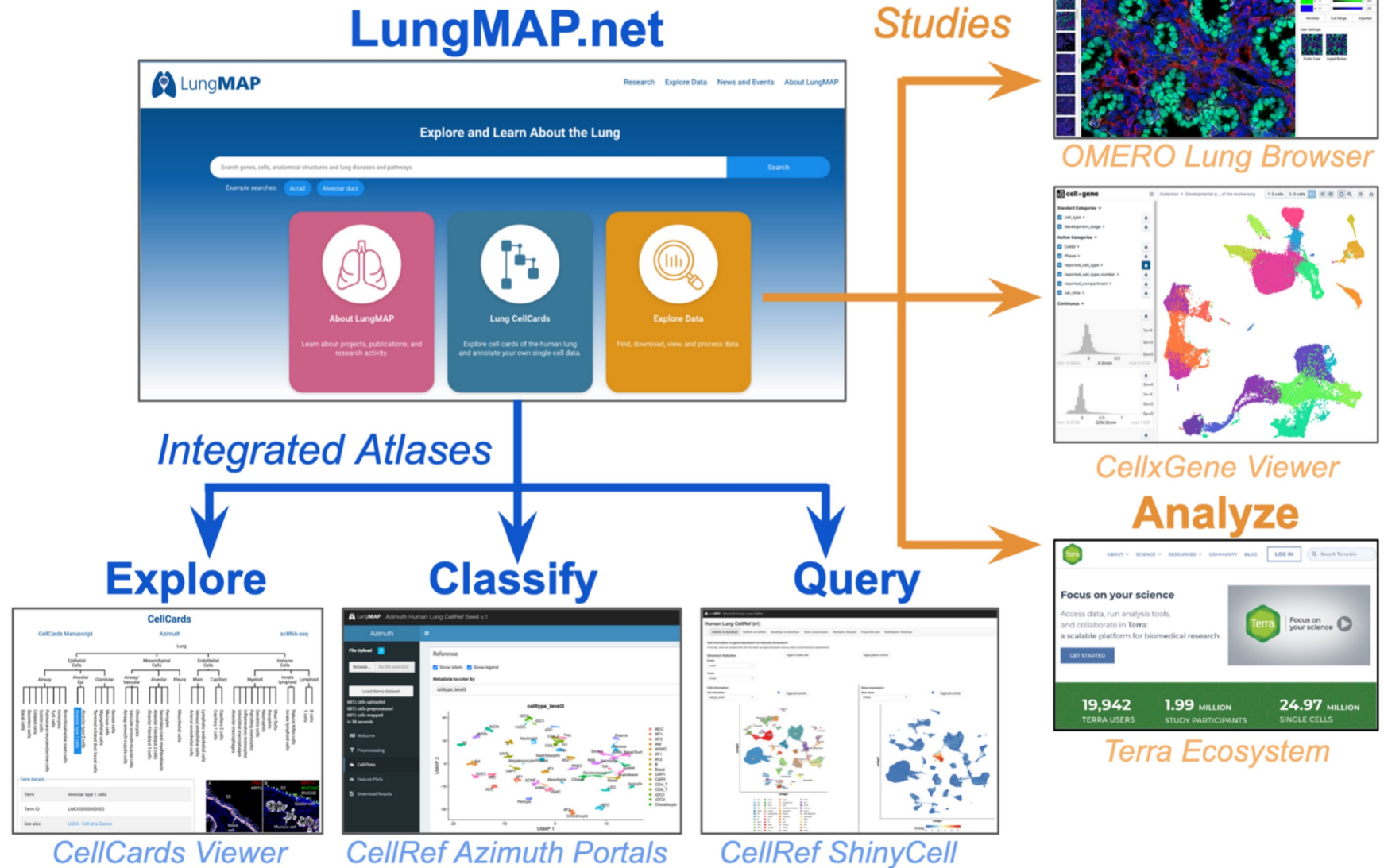


- NHBLI consortia spanning 6 research centers over the last 10 years
- Human Tissue Core at the University of Rochester (Gloria Pryhuber)
- Data Coordination Center: CCHMC, Broad, UCSC, RTI
- *Entering Phase 3 in 2023 to create accessible atlases of lung disease*



LungMAP Knowledgebase

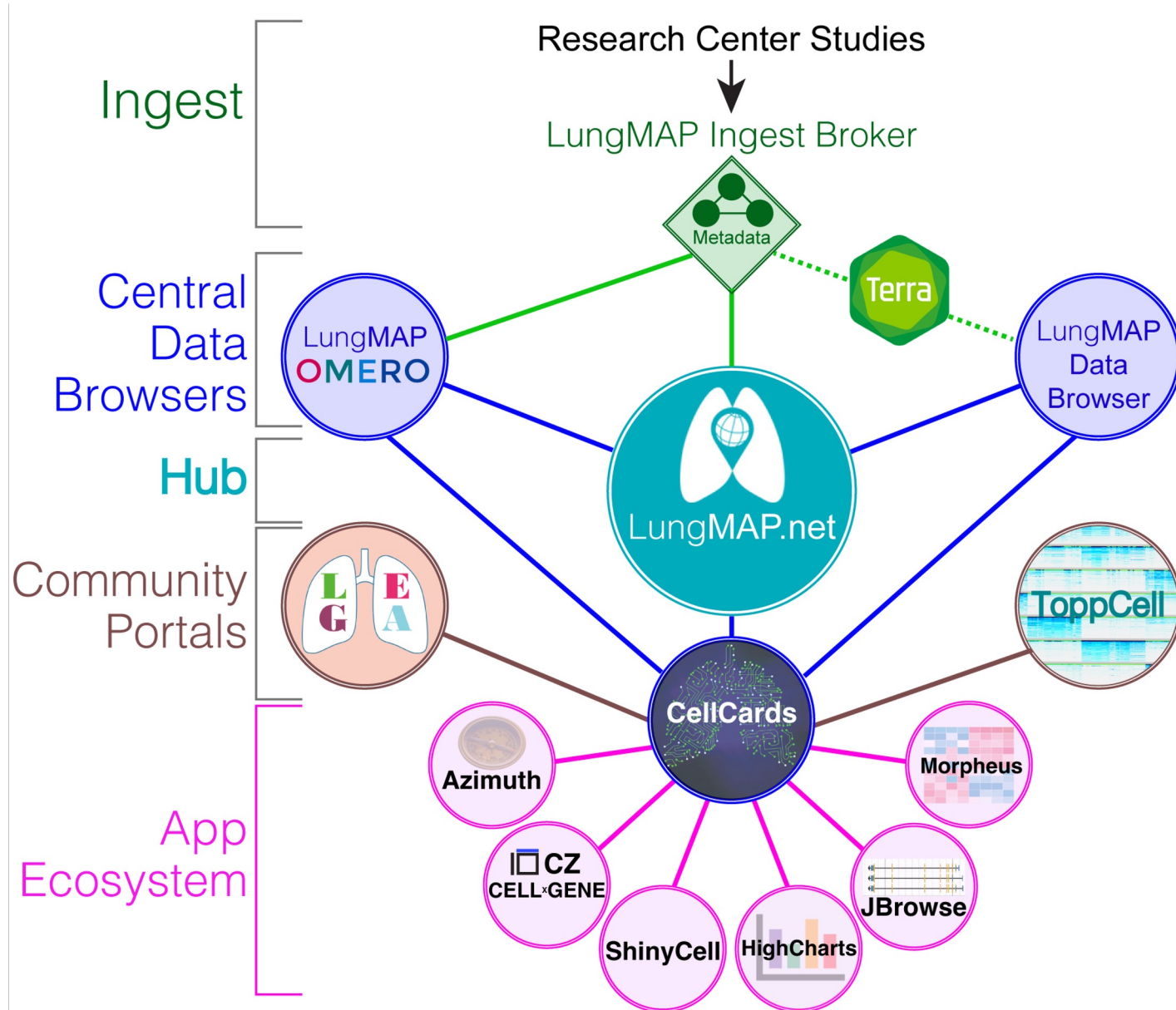
Gaddis et al. *Am J Respir Cell Mol Biol.* 2022



LungMAP.net Ecosystem



LungMAP
Molecular Atlas of Lung
Development Program



- Redesigned website
- CellCards and App focused
- Driving towards maximal interactivity (within/between)
- Pushing data and analysis to the cloud.

What are the Products of LungMAP?



LungMAP
Molecular Atlas of Lung
Development Program



- **Insights:** New cell-states, regulatory models
- **Tissues:** Biopsies, whole lung
- **Data:** Omics, imaging
- **Protocols:** Experimental, analytical
- **Tools:** Organoids, omics, informatics

LungMAP Data Flow

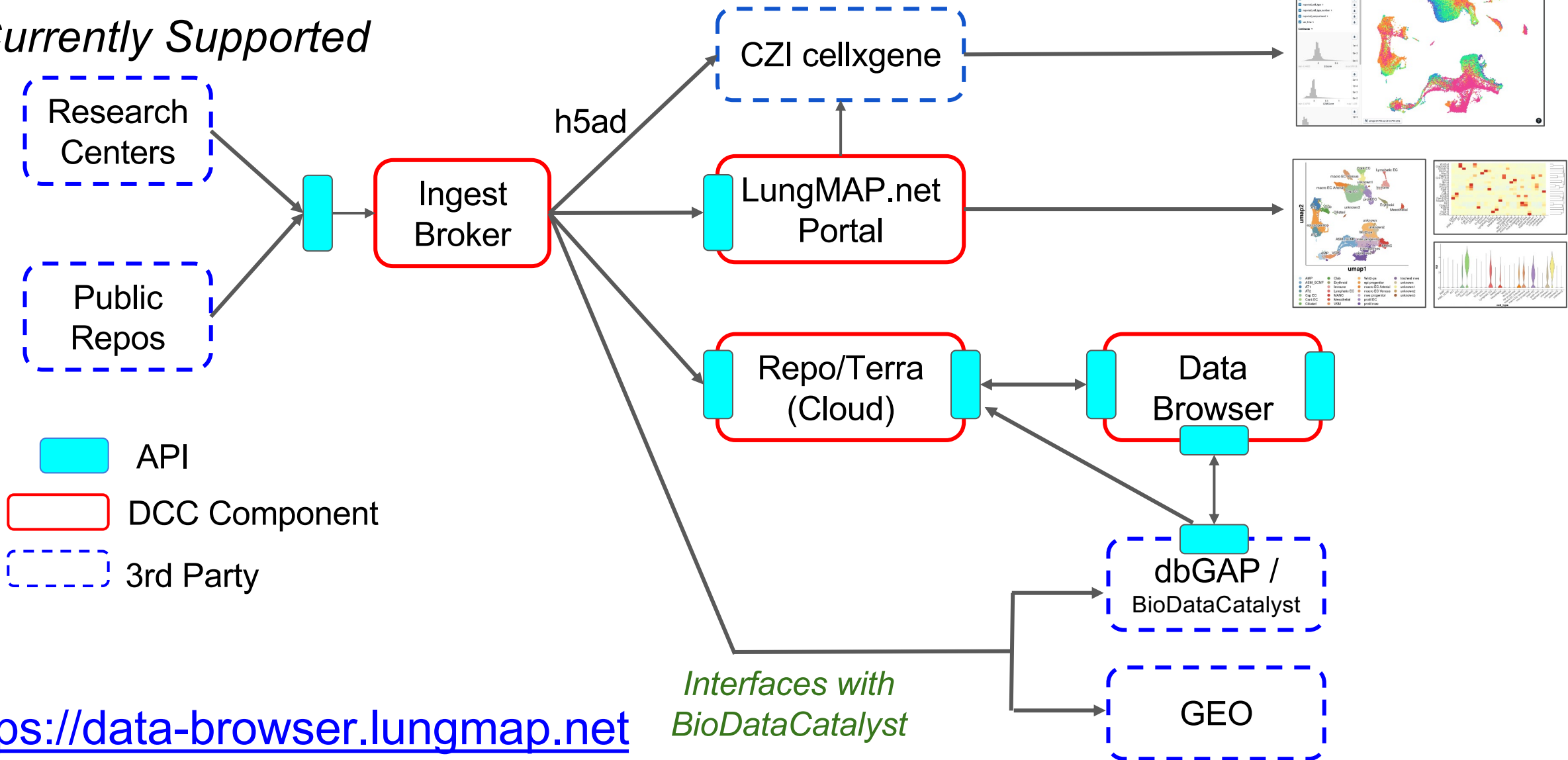


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Development Program



Data Flow

Currently Supported



<https://data-browser.lungmap.net>



Explore and Learn About the Lung

Search genes, cells, anatomical structures and lung diseases and pathways

Search

Example searches:

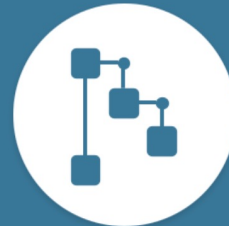
Acta2

Alveolar duct



About LungMAP

Learn about projects, publications, and research activity.



Lung CellCards

Explore cell cards of the human lung and annotate your own single-cell data.

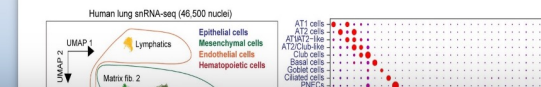


Explore Data

Find, download, view, and process data.

Highlights

Developmental Cell



Cross-Consortia Cell-Type Curation



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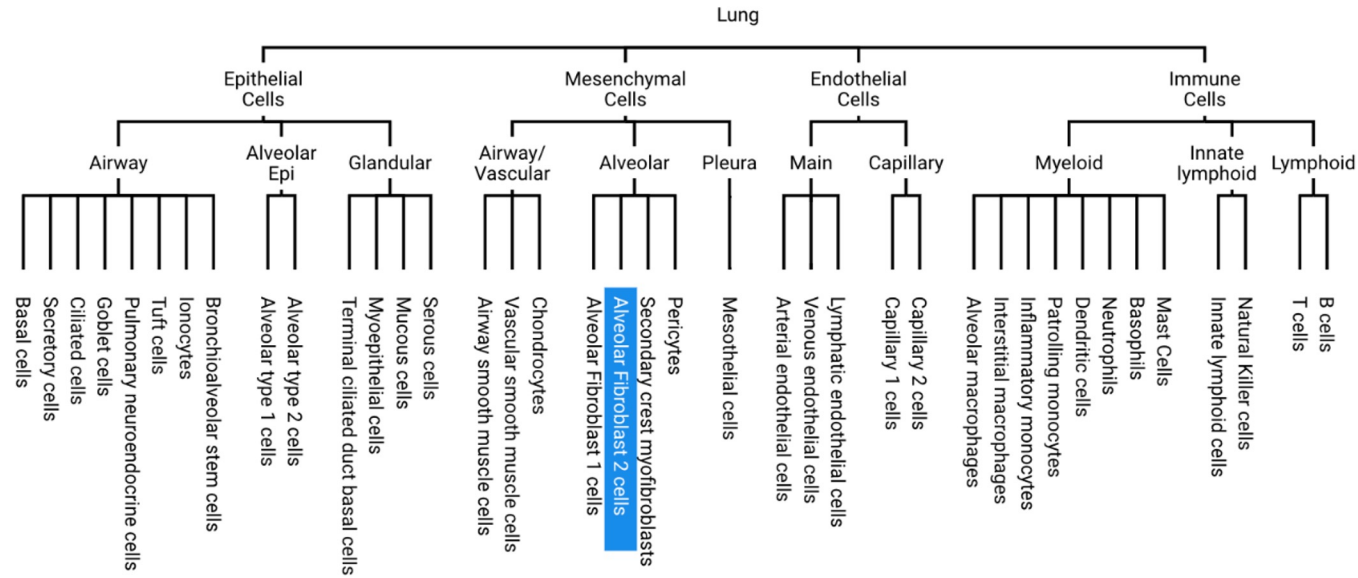
CellCards

CellCards Reference

CellRef scRNA-seq

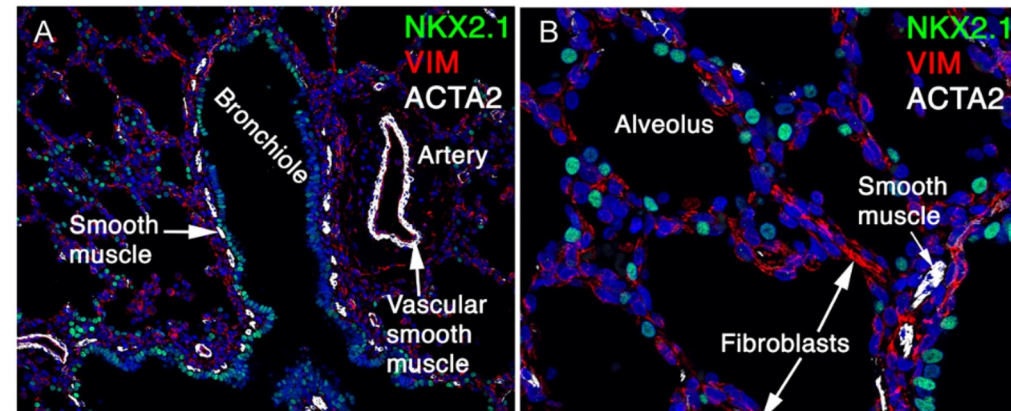
CellRef ATAC-seq

CellRef Azimuth



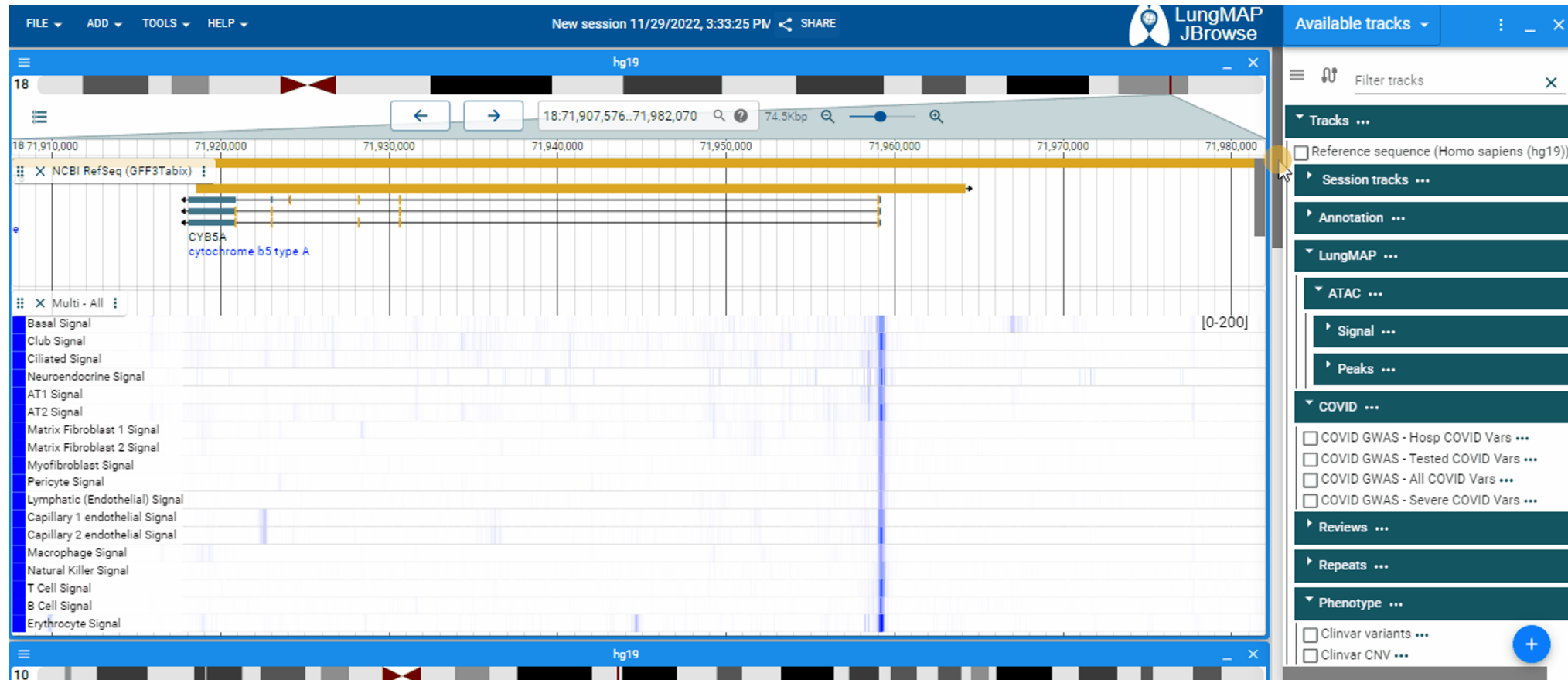
Term Details

Term	Alveolar Fibroblast 2 cells
Term ID	LMCC0000000026
See also	LGEA - Cell at a Glance
Related synonyms	Type-2 associated stromal cell (TASC)(Chung, et al., 2018) Type-2 associated stromal cell (TASC)(Chung, et al., 2018) Adventitial fibroblast (Travaglini, et al., 2020) Adventitial fibroblast (Travaglini, et al., 2020) Matrix fibroblast 2 MANC (Zepp, et al., 2017) (Park, et al., 2019) (Torday, et al., 2016) MANC (Zepp, et al., 2017) (Park, et al., 2019) (Torday, et al., 2016) Mesenchymal alveolar niche cell





- View pre-loaded, UCSC Track Hub, or bring-your-own-track
- View and compare multiple loci (including species*)





Human CellCards Multi-Study CellRef 1.0 Atlas

Minzhe Guo (CCHMC) | Jeremy Clair (PNNL) | Joshua N. Adkins (PNNL) | Gloria Pryhuber (HTC/URMC) | Ravi Misra (HTC/URMC) | Bruce Aronow (CCHMC) | Timothy L. Tickle (Broad) | Nathan Salomonis (CCHMC) | Xin Sun (UCSD) | Edward E. Morrissey (UPenn) | Jeffrey A. Whitsett (CCHMC) | Yan Xu (CCHMC)

How to explore data (tutorial)

Description

The "LungMAP Human Lung CellRef" atlas incorporates 48 well-defined lung cell types (CellCards) catalogued from diverse anatomic locations and stages of lung maturation. This atlas spans sc/snRNA-seq of 505,256 lung cells from 148 normal human lung samples from 104 donors from parenchyma, trachea, bronchi, bronchus SMG and small airway. This study includes 21 new lung samples. An accompanying R-shiny app (Azimuth) enables fast supervised annotation of user-provided single-cell RNA-Seq datasets (see below).

LungMAP ID: LMEX0000004396

Stages: Adult | Child | Adolescent

Technology: 10x Genomics

Organism: Human

Assay type: Single-cell RNA-seq

Reference: Guo, et al. (2022)

Exploratory Tools

Samples

Downloads



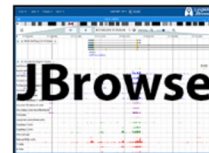
(Tutorial)



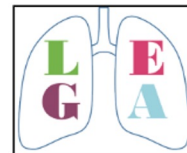
(Tutorial)



(Tutorial)



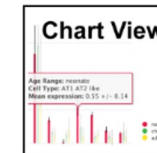
(Tutorial)



(Tutorial)



(Tutorial)



(Tutorial)



(Tutorial)

Interactive Visualization & Analysis



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LungMAP Apps

Human Lung CellRef (v1)

CellInfo vs GeneExpr | CellInfo vs CellInfo | GeneExpr vs GeneExpr | Gene coexpression | Violinplot / Boxplot | Pro

Cell information vs gene expression on reduced dimensions
In this tab, users can visualise both cell information and gene expression side-by-side on low-dimensional representations.

Dimension Reduction Toggle to subset cells

X-axis: umap1

Y-axis: umap2

Cell information

Cell information: celltype_level3 Toggle plot controls

Legend:

- AEC, AF1, AF2, AM, ASMC, AT1, AT2, Basal, Basophil, CAP1, CAP2, CD4_T, CD8_T, cDC1, cDC2, Chondrocyte, Ciliated, Deuterosomal, EPC, ILC, IM, iMON, LEC, Mast, Mesothelial, Mucous, Neutrophil, PNEC, Pericyte, PMP, RAS, SCMF, Secretory, Sox9_Epi, Treg, VEC, VSMC

LungMAP Apps

Azimuth

File Upload ?

Browse... No file selected

Load Adult Human Demo

Load e15.5 Mouse Demo

Gene expression

In this tab, users can visualise gene expression on low-dimensional representations. The normalised expression values are shown as a heatmap.

List of gene names (Max 50 genes, separated by , or ; or new line)

8567 cells uploaded
8567 cells preprocessed
8567 cells mapped in 38 seconds

Welcome

Preprocessing

Cell Plots

Feature Plots

Download Results

Group by: celltype_level3

Plot type: Bubbleplot

Scale gene expression

Cluster rows

Cluster columns

Toggle to subset cells

Toggle graphics

Colour scheme: Blue-Yellow-Red

Plot size: Small

Font size:

debug ID: 1ef08560e2f4
Azimuth version: 0.4.3
Seurat version: 4.0.3
Reference version: 0.0.0

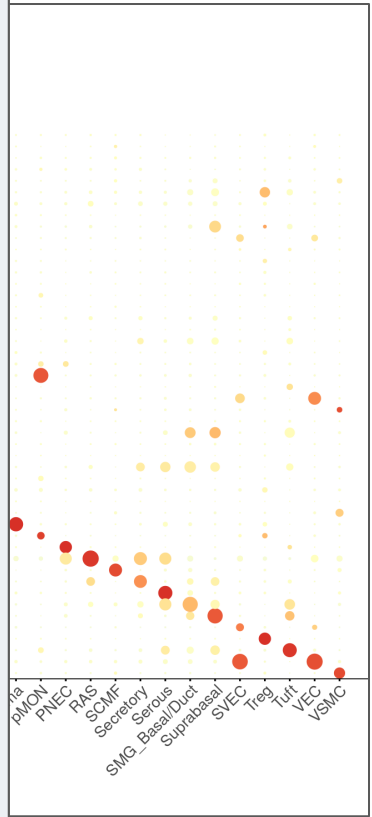
Reference

Show labels Show legend

Metadata to color by: celltype_level3

Query

Metadata to color by: predicted.celltype_level3





#3 – LungMAP-HCA Data/Metadata Explorer

Explore Metadata APIs

Explore Data

556.0k Estimated Cells 206 Specimens 160 Donors 600 Files 1.57 TB File Size
Export Selected Data

Projects
Samples
Files

↑ Sample Id	Project Title	Species	Sample Type	Anatomical Entity	Organ Part	Model Organ	Selected Cell Types	Library Construction Method	Nucleic Acid Source	Paired End	Analysis Protocol	Age	Sex	Disease Status (Specimen)
(206)	(6)	(3)	(1)	(3)	(4)	(1)	(1)	(6)	(2)	(3)	(20)		(4)	(2)
022006ad-1...	Human Lung Reference Cell Atlas version 1.0	Hom...	specimens	Lung	Unspecified	–	Unspe...	10X 3' v2 sequencing	single cell	false	004d1c80-5b66-46f3-b01a-63757d4807ab, d818ffdf-fcdb-45f3-946a-fd725c32e6c3	29 y	male	normal
0257bc98-...	Genomic, epigenomic, and biophysical cues controlling the emergence of the lung alveolus	Mus ...	specimens	Lung	Unspecified	–	Unspe...	10X 3' v2 sequencing	single cell	Unspecified	1c145725-c287-45c8-b0d7-6b5ed78674fc, 823cb2ce-79ff-4737-82d8-c50c286ede54	Unspecified	female	normal
02a139f0-a...	Human Lung Reference Cell Atlas version 1.0	Hom...	specimens	Lung	Unspecified	–	Unspe...	10X 3' v2 sequencing	single cell	false	004d1c80-5b66-46f3-b01a-63757d4807ab, d818ffdf-fcdb-45f3-946a-fd725c32e6c3	33 y	male	normal
0458fcb6-f...	Human Lung Reference Cell Atlas version 1.0	Hom...	specimens	Lung	Unspecified	–	Unspe...	10X 3' v2 sequencing	single cell	false	004d1c80-5b66-46f3-b01a-63757d4807ab, d818ffdf-fcdb-45f3-946a-fd725c32e6c3	26 y	female	normal



Open-access data repository facilitating integration with NHLBI ecosystem



HCA schema



Streamlined
integration



BioData
CATALYST

Cloud workspace for scalable analysis

The screenshot shows the Terra workspace interface. The top navigation bar includes 'WORKSPACES' and 'Dashboard'. The main content area is titled 'Explore LungMAP single-cell data' and contains a list of steps for using the workspace. On the right, there is a sidebar with 'WORKSPACE INFORMATION' and 'CLOUD INFORMATION' sections.

ABOUT THE WORKSPACE

Explore LungMAP single-cell data

This tutorial workspace is a step-by-step guide to importing, accessing, and analyzing single-cell RNA sequencing data from the LungMAP [Data Browser](#) using community-supported single-cell analysis tools.

Using this workspace, you will:

1. Import 10x sequencing reads in FASTQ format from the LungMAP [Data Browser](#)
2. Use a Jupyter Notebook to create new data tables to organize data for downstream alignment and preprocessing with the Optimus workflow
3. Preprocess 10x FASTQs with the Optimus workflow
4. Convert the Optimus raw cell-by-gene matrix output to mtx format for downstream Seurat analysis
5. Import mtx files and visualize the count matrix in an example **Seurat** Jupyter Notebook

WORKSPACE INFORMATION

Last Updated	10/26/2022
Creation Date	10/18/2022
Workflow Submissions	2
Access Level	Reader

CLOUD INFORMATION

OWNERS

TAGS

Tutorials: <https://lungmap.net/resources-2/tutorials/>
→ Tutorial 5: Cloud-based omics data analysis with Terra
→ Video 2: Exploring and Analyzing LungMAP Data in Terra





- **Exponential Growth:** Dozens of new atlases & interfaces
- **Creating atlases in the cloud:** Public + consortia + user
- **Leveraging AI:** User facing language models and disease gene regulatory network models.
- **Cost management:** Balancing growth, community needs and cloud versus on prem compute.

Thank you!



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DCC Leadership



Bruce
Aronow



Nathan
Salomonis



Bing-Xing
Huo



Timothy
Tickle



Benedict
Patten



Eric
Bardes



Scott
Tabar



Joshua
Fortriede



Kevin
Burns



Liam
Dolan

DCC CCHMC



Surya Prasath



Michal
Kouril



Yan Xu



Jeff Whitsett



Benjamin
Crooks



Kang
Jin



Minzhe
Guo



Dan
Schnell

DCC Broad Institute



Nate
Calvanese



Kat
Thayer

ACC CCHMC



Stephanie
Loos



Chelsea
Yeary

DCC UCSC



Trevor
Heathorn



Hannes
Schmidt

RTI



Nathan
Gaddis

with assistance from CZI and the NIH Strides & dbGAP team