

# Human Reference Atlas Construction and Usage



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CCB Seminar Series at HMS

May 2, 2022



# HuBMAP

#### Vision

Catalyze the development of an open, global framework for comprehensively mapping the human body at cellular resolution.



### https://commonfund.nih.gov/HuBMAP

#### Goals

- 1. Accelerate the development of the next generation of tools and techniques for constructing high resolution spatial tissue maps
- 2. Generate foundational 3D tissue atlases
- 3. Establish an open data platform
- 4. Coordinate and collaborate with other funding agencies, programs, and the biomedical research community
- 5. Support projects that demonstrate the value of the resources developed by the program

**The Human Body at Cellular Resolution: The NIH Human Biomolecular Atlas Program** Snyder et al. *Nature*. 574, p. 187-192.



# HuBMAP Overview



## **Organ Specific Projects**

**The Human Body at Cellular Resolution: The NIH Human Biomolecular Atlas Program.** Snyder et al. *Nature*. 574, p. 187-192.



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Spatial Scale



















UMAP2













CD31/DAP

#### Atlas & Tools A Resources - My Lists

Common Coordinate Framework (CCF) Portal

Member Login

ASCT+B Reporter

Exploration User Interface (EUI)

Registration User Interface (RUI)

Azimuth: Reference-based single cell mapping

The HuBMAP Data Portal is the central resource for discovery, visualization, and download of singlestandardized data curation and processing workflow ensure that only high quality is released.

An open, global atlas of the human body at the cellular level

Human BioMolecular Atlas Program

# Explore spatial single-cell data with Vitessce visualizations

View multi-modal assay types with reusable interactive components such as a scatterplot, spatial+imaging plot, genome browser tracks, statistical plots and controller components.

Get Started



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#### https://portal.hubmapconsortium.org



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# HuBMAP Kaggle Competition



Google



# Deloitte.

## 

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Overview

Description	Our best estimates show there are ov
Supervised ML Evaluation	Way galaxy. By comparison, the adult relationship among these cells is a mo impacted if we better understand cell
Judges Prize	Kaggle community.
Prizes	Just as the Human Genome Project m Program (HuBMAP) is a major endeav
Timeline	working to catalyze the development
Organizers & Sponsors	functional tissue units for the first tim collaborative biological projects, HuBI
Codo Boquiromonto	This competition, "Hacking the Kidney
Code Requirements	Your challenge is to detect functional FTU is defined as a "three-dimension.

Our best estimates show there are over 7 billion people on the planet and 300 billion stars in the Milky Way galaxy. By comparison, the adult human body contains 37 *trillion* cells. To determine the function and relationship among these cells is a monumental undertaking. Many areas of human health would be impacted if we better understand cellular activity. A problem with this much data is a great match for the Kaaqle community.

Just as the Human Genome Project mapped the entirety of human DNA, the Human BioMolecular Atlas Program (HuBMAP) is a major endeavor. Sponsored by the National Institutes of Health (NIH), HuBMAP is working to catalyze the development of a framework for mapping the human body at a level of glomeruli functional tissue units for the first time in history. Hoping to become one of the world's largest collaborative biological projects, HuBMAP aims to be an open map of the human body at the cellular level.

his competition, "Hacking the Kidney," starts by mapping the human kidney at single cell resolution.

Your challenge is to detect functional tissue units (FTUs) across different tissue preparation pipelines. An FTU is defined as a "three-dimensional block of cells centered around a capillary, such that each cell in this block is within diffusion distance from any other cell in the same block" (de Bono, 2013). The goal of this competition is the implementation of a successful and robust glomeruli FTU detector.

https://www.kaggle.com/c/hubmap-kidney-segmentation https://hubmapconsortium.github.io/ccf/pages/kaggle.html <- datasets



# Human Reference Atlas (HRA)



# **Overall Vision**

An **atlas** is an oversized, bound book of maps.

It has descriptive text, an index, possibly other data visualizations.







# Define Human Reference Atlas

The NIH Human Reference Atlas (HRA)

- 1. defines the 3D space and shape of anatomical structures and cell types that are of biomedical relevance plus the biomarkers used to characterize them. Anatomical structures, cell types and biomarkers are validated and represented in/added to ontologies (Uberon/FMA, CL, HGNC).
- 2. defines how new datasets can be mapped to the HRA, e.g., spatially using the Visible Human CCF or Vasculature CCF (or both, see next slide), via ASCT+B ontology terms/IDs, or via gene expression data as in Azimuth.

3. it is

- authoritative (there exists expert agreement and it was validated by data),
- computable (supports API queries, UIs),
- published as LOD (connected to gene, disease, and other ontologies and data),
- open (anyone can use the HRA data and code), and
- continuously evolving (e.g., as new technologies become available).



## Construct a Human Reference Atlas



2&3D single cell models cell graphs

Cell type populations cell distances to vessels diverse biomarkers per cell



37T Cells

## Construct a Human Reference Atlas - Together!

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Anatomical Structures (AS), Cell Types (CT), and Biomarkers (B) or ASCT+B tables aim to capture the partonomy of anatomical structures, cell types, and major biomarkers (e.g., gene, protein, lipid or metabolic markers).

They are ESSENTIAL for developing AS partonomies, CT typologies, and 3D reference objects across scales -- from body to functional tissue unit (FTU) to cell.

Ontology

ASCT	Tabla
AJCI	Table

Structure/Region	Sub structure/Sub region	Cell Type							
Structure/Region     Sut       Bo     Bo       Renal Corpuscle     Git       Git     Pr       Lo     Lo       Tubules     D       C     C	Bowman's (glomular) Capsule/parietal layer	Parietal epithelial Cell		Anato					
Panal Corpurate	Bowman's (glomular) Capsule/visceral layer	Podocyte		kidnev					
Renal Corpuscie	Glomerular Tuft	Capillary Endothelial Cell		kid					
		Mesangial Cell		KICI					
	Proximal Tubule	Proximal Tubule Epithelial Cell (general)		cor					
P Lu Tubules		Proximal Convoluted Tubule Epithelial Cell Segment 1							
		Proximal Tubule Epithelial Cell Segment 2							
		Proximal Tubule Epithelial Cell Segment 2		ren					
	Loop of Henle, Thin Limb	Descending Thin Limb Cell (general)	ng Thin Limb Cell (general)						
	Loop of Henle, Thick Limb	Thick Ascending Limb Cell (general)		Cell Ty					
Tubules	24	Cortex-TAL Cell							
		Medulla-TAL Cell		connec					
		TAL-Macula Densa Cell		per					
	Distal Convolution	Distal Convoluted Tubule Cell (general)		1					
		DCT Type 1 Cell							
		DCT Type 2 Cell							
	Connecting Tubule	Connecting Tubule Cell (general)							
		CNT-Principal Cell							



**3D** Reference

Choose version of ASCT+B datasets: 2nd Release, December '21											
Organ	#AS	#CT	#B Total	#BG	#BP	#AS-AS	#AS-CT	#CT-B			
Blood	1	30	159	112	47	1	30	30 506			
Blood Vasculature	841	2	1	1	1 0 869 606		2				
Bone Marrow	1	47	262	198	64	1	47	838			
Brain	183	127	257	257	0	183	127	346			
Eye	26	53	136	61	75	27	58	404			
Fallopian Tube	55	22	25	13	12	72	65	32			
Heart	50	23	45	45	0	60	183	74			
Kidney	61	62	150	150	0	62	60	257			
Knee	32	19	14	0	14	32	8	17			
Large Intestine	54	57	167	84	83	287	1,156	352			
Liver	17	30	62	16	46	17	31	75			
Lung	146	83	180	174	6	909	1065	267			
Lymph Node	34	45	223	106	117	43	86	499			
Lymph Vasculature	4	1	1	1	0	4	2	1			
Ovary	71	7	13	7	6	109	12	5			
Pancreas	32	32	44	42	2	162	229	101			
Peripheral Nervous System	782	1	2	1	1	803	609	2			
Prostate	4	12	31	31	0	4	12	36			
Skin	15	36	70	0	70	17	19	101			
Small Intestine	38	48	13	13	0	69	185	13			
Spleen	37	61	194	85	109	50	129	424			
Thymus	17	52	394	318	76	28	39	620			
Ureter	7	14	30	30	0	7	14	61			
Urinary Bladder	16	15	30	30	0	16	16	63			
Uterus	58	19	45	39	6	73	28	65			
Totals:	2,582	898	2.548	1.814	734	3.905	4 816	5 161			

https://hubmapconsortium.github.io/ccf/pages/ccf-anatomi cal-structures.html



Crosswalk

https://hubmapconsortium.github.io/ccf/pages/ccf-3d-refer ence-library.html (NLM VHP organs) https://community.brain-map.org/t/allen-human-reference-a tlas-3d-2020-new/ (brain) https://www3.cs.stonybrook.edu/~ari/ (male colon)

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# Anatomical Structures, Cell Types, plus Biomarkers (ASCT+B) table for Lung v1.0

#### Description

Anatomical Structures, Cell Types, plus Biomarkers (ASCT+B) tables aim to capture the nested *part\_of* structure of anatomical human body parts, the typology of cells, and biomarkers used to identify cell types. The tables are authored and reviewed by an international team of experts.

LABEL	VALUE
Creator(s):	Gloria Pryhuber; Xin Sun
Creator ORCID:	0000-0002-9185-3994; 0000-0001-8387-4966
Project Lead:	Katy Börner
Project Lead ORCID:	0000-0002-3321-6137
Creation Date:	2021-03-12
License:	Creative Commons Attribution 4.0 International (CC BY 4.0)
Publisher:	HuBMAP
Funder:	National Institutes of Health
Award Number:	OT2OD026671
HuBMAP ID:	HBM868.DWJZ.874
Data Table:	Lung v1.0
DOI:	https://doi.org/10.48539/hbm868.dwjz.874
How to Cite This Data Table:	Gloria Pryhuber; Xin Sun. HuBMAP ASCT+B Tables. Lung v1.0 https://doi.org /10.48539/hbm868.dwjz.874
How to Cite ASCT+B Tables Overall:	Quardokus, Ellen, Hrishikesh Paul, Bruce W. Herr II, Lisel Record, Katy Börner. 2021. HuBMAP ASCT+B Tables. https://hubmapconsortium.github.io/ccf/pages/ccf- anatomical-structures.html. Accessed on March 12, 2021.

## **Construct a Human Reference Atlas**

In close collaboration with Affinity Reagents Working Group led by Andrea J. Radtke, Ellen Quardokus, Jeannie Camarillo, Neil Kelleher, and Ronald N. Germain we will publish six more OMAPs by June 15, 2022:

- 1. Skin Liz McDonough (GE; colleague Fiona Ginty) (technology: Cell Dive)
- 2. Intestines John Hickey (Nolan/Snyder labs)(technology: CODEX)
- 3. Lung Gloria Pryhuber (HuBMAP/LungMAP) (technology: Cell Dive)
- 4. Kidney Elizabeth Neumann (TMC-VU) (technology: CODEX)
- 5. Pancreas Anna Martinez Casals (SciLifeLab Sweden; colleague Emma Lundberg) (technology: CODEX)
- 6. Liver Presha Rajbhandari From Stockwell lab (technology: SIM)
- 7. Lymph node (Andrea Radtke) (revised) (technology: IBEX); Christopher Werlein (stellar reviewer!)

All OMAPs are linked to respective ASCT+B tables. Aim to submit *Nature Methods* Correspondence in May 2022.

#### HUBMAP CCF PORTAL

#### ← HOME



#### Organ Mapping Antibody Panels (OMAPs)

#### Overview

Organ Mapping Antibody Panels (OMAP) allow spatial mapping of the anatomical structures and cell types present in diverse organs (Anatomical Structures, Cell Types, plus Biomarkers (ASCT+B) tables) using multiplexed antibody-based imaging [Hickey et al, 2021]. The panels are authored and reviewed by experts in pathology, tissue biology, and multiplexed imaging. Information on antibody lots and recommended concentrations vary across experiments and, in the case of antibody dilutions, must be empirically determined.

#### Standard Operating Procedures (SOP)

SOP: Construction of Organ Mapping Antibody Panels for Multiplexed Antibody-Based Imaging of Human Tissues

#### Existing OMAPS

Organ	Tissue Preservation Method	Multiplexed antibody-based imaging method
Lymph Node	Fixed Frozen	IBEX

#### Acknowledgements

We are grateful for engaging and thoughtful discussions from the Affinity Reagent Imaging and Validation and ASCT+B working groups, HuBMAP Consortium. This work was supported, in part, by the Intramural Research Program of the NIH, National Institute of Allergy and Infectious Disease and National Cancer Institute. This work was also supported by NIH Awards UH3 CA24635 and 10T2OD026671.

#### https://hubmapconsortium.github.io/ccf/pages/omap.html

# Interlinking ASCT+B and Affinity Reagent Working Group Efforts Use Case: Skin-Specific Panel



## **Construct a Human Reference Atlas**

#### https://azimuth.hubmapconsortium.org



# Use the Human Reference Atlas for Data Harmonization

HUBMAP Donors Samples Datasets Collections Previews	• Atlas & Tools • Documentation • My Lists	Nember Login
Human BioMolecular Atlas Program An open, global atlas of the human body at the cellular leve	Common Coordinate Framework (CCF) Portal ASCT+B Reporter Exploration User Interface (EUI) Registration User Interface (RUI)	
The HuBMAP Data Portal is the central resource for discovery, visualization, and download of standardized data curation and processing workflow ensure that only high quality is released.	sin Azimuth: Reference-based single cell mapping	

#### Navigate healthy human cells with the Common Coordinate Framework

Interact with the human body data with the Anatomical Structures, Cell Types and Biomarkers (ASCT+B) Tables and CCF Ontology. Also explore two user interfaces: the Registration User Interface (RUI) for tissue data registration and Exploration User Interface (EUI) for semantic and spatial data.

Get Started

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HuBMAP

heart
 lung
 kidnes

Search ontology terms ..

left kidne



■ 38 Donors ■ 365 Samples ■ 391 Datasets ■ 13 Collections

# CCF ASCT+B Reporter UI



#### https://hubmapconsortium.github.io/ccf-asct-reporter/

## CCF Registration User Interface (RUI)



#### https://hubmapconsortium.github.io/ccf-ui/rui/

# CCF Exploration User Interface (EUI)

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#### https://portal.hubmapconsortium.org/ccf-eui

#### HUBMAP

body

heart

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ureter

> nephron

spleen

S colon

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Logout





Register your data via <u>https://hubmap-ccf-ui.netlify.app/rui/</u> so it can be spatially/semantically explored in EUI.



Register your data via <u>https://hubmap-ccf-ui.netlify.app/rui/</u> so it can be spatially/semantically explored in EUI.



http://gehlenborglab.org/research/projects/vitessce/

#### HUBMAP CCF EXPLORATION

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T	Sex	: Both	Age: <b>1-110</b>	BMI: <b>13-8</b>	3	<	Skin	Large Intestine	Heart	Kidney, L	G Kidney, R	A Spleen	Allen Brain	Lungs	Lymph Node, L	Lymph Node, R	>	C	)	C D
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#### HUBMAP CCF EXPLORATION



LOGIN

# Use the Human **Reference Atlas for Data Harmonization**

snRNA-seq assays now have ASCT+B **CT** annotations

Sections Summary /isualization Provenance /detadata files	Dataset HBM545.N snRNA-seq (SNARE-seq2	TKZ.536 [Salmon]   Kidney (L	Published   Public Access        Save Version 1							
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### Use the Human Reference Atlas



Human Digital Twin: Automated Cell Type Distance Computation and 3D Atlas Construction in Multiplexed Skin Biopsies. Soumya Ghose, Yingnan Ju, Chrystal Chadwick, Elizabeth McDonough, Anup Sood, Yousef Al-Kofahi, Katy Börner, Fiona Ginty. Submitted. https://www.biorxiv.org/content/10.1101/2022.03.30.486438v1





Human Digital Twin: Automated Cell Type Distance Computation and 3D Atlas Construction in Multiplexed Skin Biopsies. Soumya Ghose, Yingnan Ju, Chrystal Chadwick, Elizabeth McDonough, Anup Sood, Yousef Al-Kofahi, Katy Börner, Fiona Ginty. Submitted. https://www.biorxiv.org/content/10.1101/2022.03.30.486438v1

# Access the Human Reference Atlas / CCF.OWL 1.7

Indiana U, Stanford U, and EBI are collaborating closely on using Linked Open Data/Semantic Web Standards in support of ontology development and reasoning. Linked open data compatible with the Semantic Web is used as the ground truth. The CCF.OWL is published on Bioportal, <u>https://bioportal.bioontology.org/ontologies/CCF/</u>

All CCF UIs (e.g., RUI, EUI, ASCT+B Reporter) and APIs (e.g., to update Jonathan's Knowledge Graph) are using the CCF.OWL 1.7 data (2.0 coming in April). Queries can be expressed in SPARQL and exposed as standard HTTP APIs to support a whole ecosystem of collaborative and compatible APIs, libraries, UIs.

ASCT+B API Links:

- API Endpoint (includes interactive documentation): <u>https://asctb-api.herokuapp.com</u>
- API Documentation: <a href="https://hubmapconsortium.github.io/ccf-asct-reporter/docs/api">https://hubmapconsortium.github.io/ccf-asct-reporter/docs/api</a>
- OpenAPI specification: <u>https://asctb-api.herokuapp.com/asctb-api-spec.yaml</u>

CCF-API Links:

- API Endpoint (includes interactive documentation): <u>https://ccf-api.hubmapconsortium.org</u>
- API Documentation and OpenAPI specification: <u>https://ccf-api.hubmapconsortium.org</u>
- API Database backend is n3.js: <u>https://github.com/rdfjs/N3.js</u>
- Code to instantiate/use CCF Database: <u>https://github.com/hubmapconsortium/ccf-ui/tree/main/projects/ccf-database</u>
- Published Python, TypeScript, JavaScript, and Angular libraries forthcoming

# Possible/Planned Queries via CCF HRA Ontology

- 1. Query for a subset of AS, CT, B\* in the HRA or associated experimental datasets; filtered by demographics. [EAS for AS+CT, S for B]
- 2. Find cell types are present in a certain AS (body to organ to FTU). [S]
- 3. What Bs characterize a certain CT in a specific AS. [S]
- 4. What kind of biomarker is a given marker (e.g., gene, protein). [S]
- 5. What extraction sites exist for the heart? [S] How many tissue blocks exist for what extraction site? [EAS]
- 6. Given a 3D spatial location, retrieve all tissue blocks in this location. [EA\* (by end of June)]
- 7. Given the location of an image/tissue registered in the CCF RUI, get the cell types present and any associated biomarkers. [EAS roughly via collisions, S to get biomarkers]
- 8. Given one or more anatomical structure IDs, retrieve cell type population information (#cells per cell type) for each. [EAS\*]
- 9. Given cell type population information for a tissue block, compute the likely spatial location of the block based on similarity in CT population with RUI-registered tissue blocks. [EAS\*]
- 10. Given cell type population information for a tissue block, retrieve all other tissue blocks that have similar cell type populations and show the spatial location of RIU-registered tissue blocks in the EUI. [EAS\*]
- 11. What cells are co-expressed (access different Bs) or co-located (in 2D or 3D)? [EAS\*]
- 12. Given a 3D spatial location OR cell type population, retrieve all experimental data (DOIs) and publication citation evidence (DOIs if available). [EAS\*]
- E = Exploration User Interface; A = CCF-API; S = SPARQL; \* = planned support;

# HRA Validation/ Expansion

#### **New ATLAS publications**

2D/3D Maps & Ontology Crosswalks





## Constructing a Meta-HRA

There is interest to add the atlas data/work reported in major papers to the Human Reference Atlas (HRA). They make wonderful high-resolution inserts! GE Skin paper is DONE and serves as a good example.

If you

- used the kidney Azimuth reference, your CxG data is already part of the HRA.
- used OMAPs, your CxP data is covered.
- registered all tissue blocks, spatial search in EUI is soon possible.

In general, we need for each paper:

- (HuBMAP) IDs for all healthy adult tissue blocks so we can API-retrieve sex, age, BMI, etc.
- RUI register ALL these tissue blocks so we have spatial size, location, rotation (the RUI now supports 50+ organs at <a href="https://hubmapconsortium.github.io/ccf-ui/rui">https://hubmapconsortium.github.io/ccf-ui/rui</a>) and
- Compile an ASCT+B table with all AS, CT, Bs used in the study (should be a matter or deleting rows in the relevant master tables, see

https://hubmapconsortium.github.io/ccf/pages/ccf-anatomical-structures.html).

# Questions for the (Bioconductor) Experts

- How might you use ASCT+B tables to advance research/practice? Please share sample queries, e.g., "retrieve AS/location of my favorite CT/B\* across 30 organs."
- Are you interested to run spatial queries? If yes, which, e.g., "retrieve all CTs/B\*s in a 3D volume."

• What other datasets could be used to extend the ASCT+B tables or provide experimental evidence for existing AS, CT, B?

- How comfortable are you with ontologies and semantic web technologies?
- Would you prefer direct access to technologies like SPARQL, RDF, and JSON-LD or would you prefer APIs to be higher level?



