

Why + How We Construct the Human Reference Atlas

Katy Börner (CODCC, Indiana University)

February 22, 2023

MC-IU HuBMAP+SenNet Team in Bloomington, IN

David

Ontologist

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Funded by HuBMAP and SenNet and the ATLAS efforts within KPMP, GUDMAP4, CFDE.



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HEAD





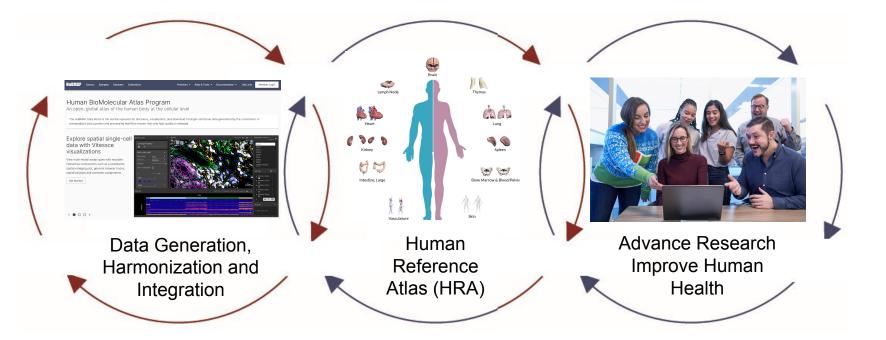








Why construct a Human Reference Atlas (HRA)?





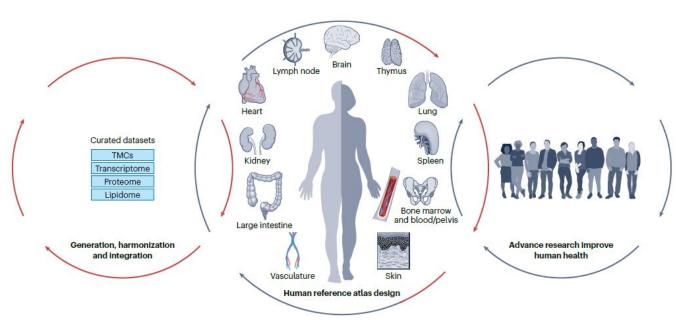


Fig. 5 | Schematic of the SenNet Consortium goals. SnC atlas building requires a framework for layering data. Data generated by the TMCs and TDA sites are input into the CODCC along with associated metadata. The datasets are organized and de-identified (curation), then analyzed and integrated. The goal is to create an atlas and public database of curated data that can be searched, analyzed and visualized as 3D images of organs using unified annotations. High-quality experimental data are needed to create a human reference atlas. The evolving reference atlas supports data standardization and federation, making it possible to integrate data from different specimens, laboratories and assay types. The atlas characterizes the healthy human–from the whole body down to the single-

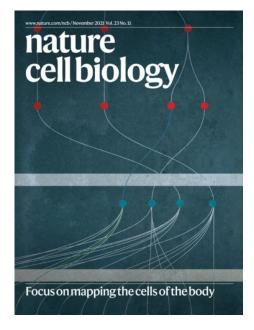
cell level; it can be compared across ages and diseases to understand differences, advance research and improve human health. Use case scenarios for different stakeholders (researchers, practitioners and students) guide atlas construction and usage but also experimental data acquisition and analysis. Of note, diversity in terms of human participant gender, race and socioeconomic status is emphasized in SenNet. However, these variables may impact SnC heterogeneity even further, meaning that, in the timeframe of the initial grants, statistically meaningful characterization of SnCs across diverse populations might not be achieved.

Defining the Human Reference Atlas (HRA)

The Human Reference Atlas (HRA)

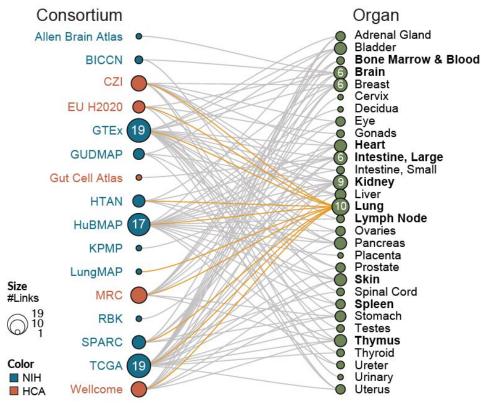
- 1. defines the 3D space and shape of anatomical structures and cell types that are of biomedical relevance plus the biomarkers used to characterize them. Anatomical structures, cell types and biomarkers are validated and represented in/added to ontologies (Uberon/FMA, CL, HGNC).
- 2. defines how new datasets can be mapped to the HRA, e.g., spatially using the Visible Human CCF or Vasculature CCF, 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).

https://www.nature.com/articles/s41556-021-00788-6



Constructing the Human Reference Atlas – Together!

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SenNet

Perspective

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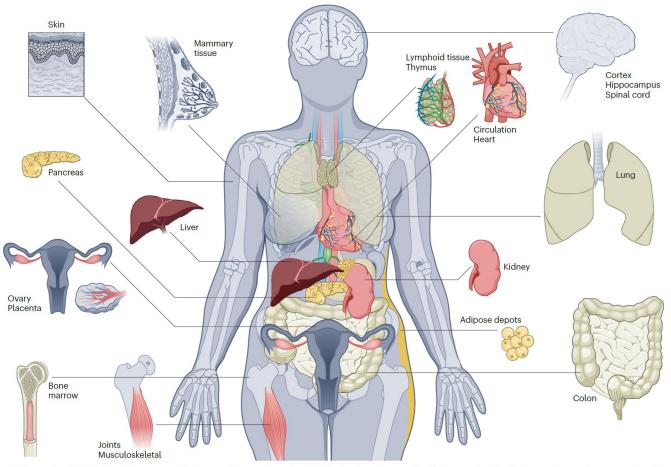


Fig. 2 | Organs in which SnCs will be mapped by SenNet. Human tissues in which SnCs will be identified and characterized by the SenNet Consortium to produce 4D atlases of senescence across the lifespan of humans.

https://doi.org/10.1038/s43587-022-00326-5

Assay Types

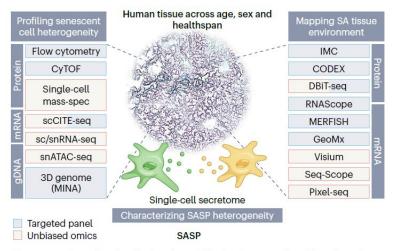
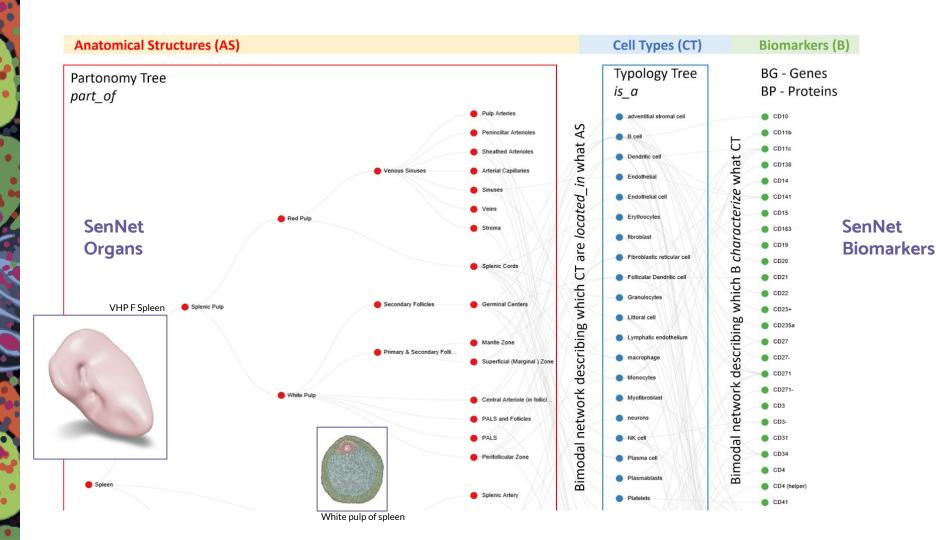


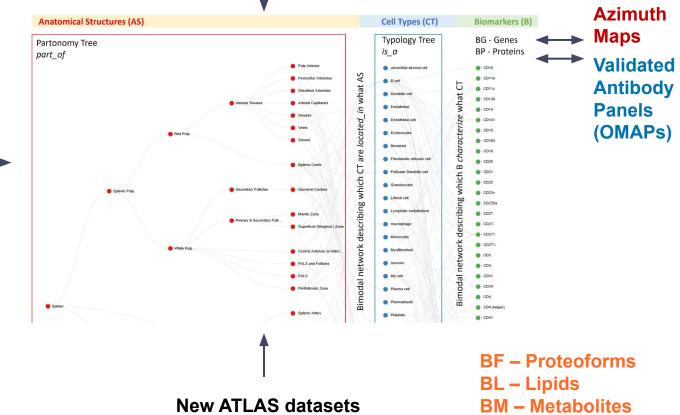
Fig. 3 | Overview of technologies that will be implemented and developed by SenNet Consortium scientists to detect, characterize and spatially map the location of SnCs. CyTOF, cytometry by time-of-flight; scCITE-seq, cellular indexing of transcriptomes and epitopes by sequencing; sc/snRNA-seq, singlecell or single-nucleus RNA sequencing; snATAC-seq, single-nucleus assay for transposase-accessible chromatin using sequencing; MINA, multiplexed imaging of nucleome architectures; IMC, imaging mass cytometry; CODEX, co-detection by indexing immunofluorescence; DBiT-seq, deterministic barcoding in tissue for spatial-omics sequencing for co-mapping mRNAs and proteins; RNAScope, RNA in situ hybridization visualization of single molecules; MERFISH, multiplexed error-robust fluorescence in situ hybridization; GeoMx, NanoString GeoMx digital spatial profiling; Visium, Visium IOx Genomics molecular profiling; Seq-Scope, a spatial barcoding technology with spatial resolution comparable to optical microscopy; Pixel-seq, polony-indexed library sequencing.



HRA Validation/ Expansion

New ATLAS publications

2D/3D Maps & Ontology Crosswalks





Requires careful data collection and processing, 100% provenance so all results can be reproduced.

Atlas of Forecasts

Modeling and Mapping Desirable Futures



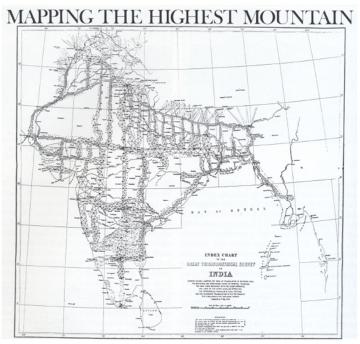
Atlas of Knowledge Anyone Can Map



https://mitpress.mit.edu/60-off-the-atlas-trilogy-from-katy-borner/

History of Map Mapmaking in Atlas of Science

For generations, a vast network of repeating sightline triangles was meticulously measured and recorded. What resembles a pattern of eyelashes on the northern border represents the sightlines to stations built above treetops. While analyzing the triangles in the calculating offices of Calcutta, the mapmakers discovered the highest peak in the world: Mount Everest.



Requires careful data collection and processing, 100% provenance so all results can be reproduced.



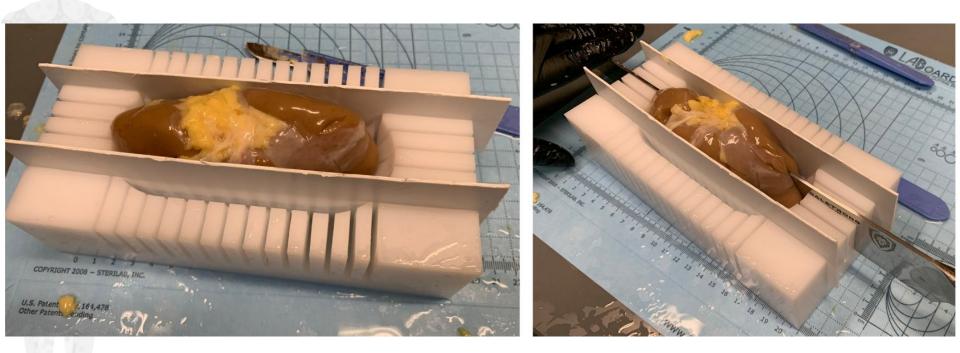
Fig 2. Millitome process for the kidney (from left to right): Digital 3D model of left male kidney, millitome for the lower half of the kidney with 7 x 14 blocks, ice cube tray holding a subset of the tissue blocks, a screenshot showing 98 blocks registered in the EUI.

https://zenodo.org/record/7382704#.Y5Zy7BzMluU





VU presented process in ASCT+B WG Meeting #22 on Jan 12, 2022, 11a ET



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Requires careful data collection and processing, 100% provenance so all results can be reproduced.

Please make sure to generate/share for each tissue block/section/suspension

- All essential donor, organ, sample, and assay metadata
- Spatial RUI registration data
- High-resolution histopathology images--used for AS and FTU segmentation
- scRNAseq data--to generate cell type annotations via Azimuth
- CODEX/CellDive/MxIF--use/contribute to OMAPs, see next slide

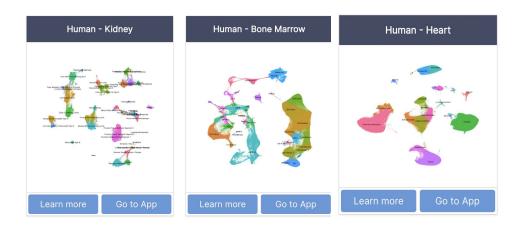
In addition, please consider

- Running the assays on the same or adjacent tissue sections
- Utilization of biomarkers mapped to ASCT+B via Azimuth references and OMAPs

Azimuth Reference Mapping

Mapping to Azimuth Single-cell References:

- Enables integration, re-use, and comparison of data across labs and consortia
- Encourages community adoption of ontologies and standards
- Projects HuBMAP data into consistent cell labels



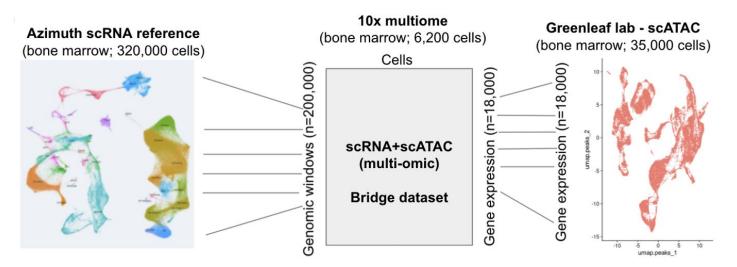
Azimuth: Bridge Integration to Annotate/Map scATAC-seq Data to HRA

scATAC-seq measures DNA accessibility per cell

• Data is sparse and difficult to annotate

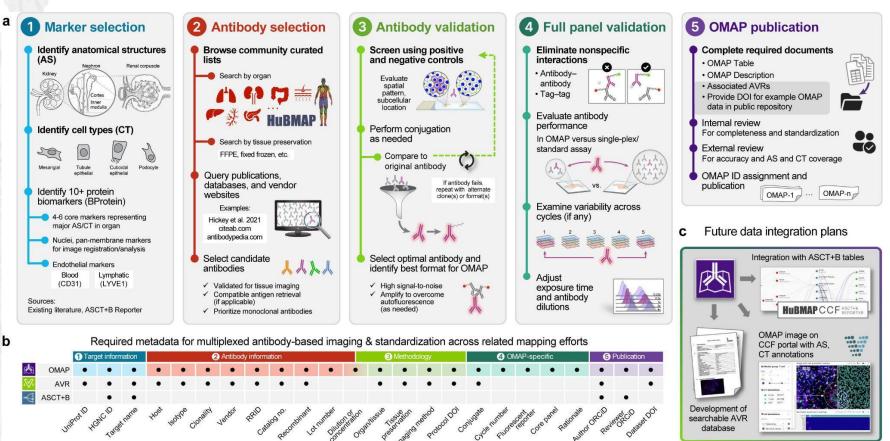
Goal: Use bridge integration (Hao et al., 2022) to map scATAC-seq query to scRNA-seq reference

Learn dictionary representation of RNA reference and ATAC query to transfer annotations



https://satijalab.org/seurat/articles/bridge integration vignette.html

Organ Mapping Antibody Panels (OMAPs)



Created by Diane Saunders, Vanderbilt University. Now accepted for Nature Methods.

OMAPs How to Contribute (Andrea Radtke, NIAID, NIH)

Goals for OMAPs:

- Offset the considerable time (6-8 months) and cost (~\$30-60,000 in 2022 USD) associated with creating such resources de novo
- Standardize data acquisition for multiplexed tissue imaging studies
- Empower construction of atlases from healthy and diseased human tissues
- Support the spatial biology community by aggregating highly cited antibody clones
- Identify essential markers for anatomical structures and cell types in diverse human organs
- SOP: Construction of Organ Mapping Antibody Panels for Multiplexed Antibody-Based Imaging of Human Tissues
- Frequently Asked Questions (FAQs) for OMAPs
- OMAP table template
- OMAP description document template

Interested in contributing to OMAPs?

Contact:

- Andrea Radtke andrea.radtke@nih.gov
- Ellen Quardokus ellenmg@indiana.edu
- Michael Caldwell michael.caldwell@northwestern.edu

Existing OMAPs

			_	ale: 187	179	197
OMAP-7	Lung	FFPE	Cell DIVE	50	42	30
OMAP-6	Pancreas	FFPE	CODEX	3	9	12
OMAP-5	Liver	Fresh Frozen	SIMS	17	16	20
OMAP-4	Skin	FFPE	Cell DIVE	16	15	18
OMAP-3	Kidney	Fresh Frozen	CODEX	30	37	26
OMAP-2	Intestines	Fresh Frozen	CODEX	42	29	51
OMAP-1	Lymph Node	Fixed Frozen	IBEX	29	31	40
OMAP ID	Organ	Tissue Preservation Method	Multiplexed antibody-based imaging method	#AS	#CT	#BP
		Choose CCF-HRA Release vers	ion: 3rd HRA Release (v1.2), June 2022			

Totals: 187 179 197

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

Human Reference Atlas Standard Operating Procedures

Table of Contents

Overview

Introduction to Standard Operating Procedures Managing SOPs Section Overview Template SOP Template Glossary Design Style Guide

3D Tissue Registration

Using the CCF Registration User Interface (RUI) Assigning RUI Data to Multiple Tissue Blocks Constructing a Millitome and Generating Virtual Tissue Blocks Using a Millitome

Anatomical Structures and Cell Type Segmentation <u>Manual Segmentation of Tissue</u> Running a Kaggle Competition

Anatomical Structures, Cell Types, Plus Biomarkers (ASCT+B) Tables

Authoring ASCT+B Tables Authoring ASCT+B Tables Using The ASCT+B Generator Python Script <u>Construction of Organ Mapping Antibody Panels (OMAPs)</u> <u>FAQ: Frequently Asked Questions (FAQ) for Organ Mapping Antibody Panels</u> <u>(OMAPs)</u> <u>Constructing Antibody Validation Reports (AVRs)</u> <u>FAQ: Frequently Asked Questions (FAQ) for Antibody Validation Report (AVR)</u> Creating Crosswalks Between ASCT+B Tables and Azimuth Reference Maps Mapping Experimental Data to the HRA Using OMAPs or Azimuth ASCT+B Table Communications <u>3D Reference Object Library</u> Creating 3D Models from Datasets Creating Crosswalks between ASCT+B Tables and 3D Reference Objects <u>3D Reference Object Approval</u> Using 3D Reference Objects

2D Functional Tissue Unit (FTU) Reference Object Library <u>Creating 2D Illustrations of Functional Tissue Units</u> <u>Style Guide: Human Reference Atlas 2D Functional Tissue Unit (FTU) Illustrations</u> <u>Creating a Crosswalk between ASCT+B Tables and 2D Functional Tissue Unit Models</u>

HRA Validation and Review

Internal Validation of ASCT+B Tables, and 2D and 3D Reference Objects External Review of ASCT+B Tables Validation Checks Performed by the DO-CMS ASCT+B Table Validation with CCF Tools ASCT+B Reporter Validation Checks HRA Editorial Process

Human Reference Atlas Tracking and Publication

Tracking Digital Object Status Maintaining the HRA Portal Designing Organ Icons Registering Digital Object Identifiers Publishing CCF.OWL on BioPortal and OLS

HRA Release Process

https://humanatlas.io

Planned Changes in <u>HRA Digital Objects</u> for 5th Release (April 1, 2023 Deadline)

Organ	Replied to email inquiry	ASCT+B Table (Authors)	2D FTU	3D Obj	OMAP	
Blood						
Blood Vasculature						
Bone Marrow						
Brain		Sector 100				
Breast						
Eye						
Fallopian Tube						
Heart						
Kidney						
Knee						
Large Intestine						
Liver						
Lung						
Lymph Node						
Lymph Vasculature						
Pancreas						
Peripheral Nervous System						
Placenta Full Term						
Prostate						
Skin						
Small Intestine						
Spinal Cord						
Spleen						
Thymus						
Uterus						
Ovary						
Tonsil						
Nasal Passage						

Azimuth

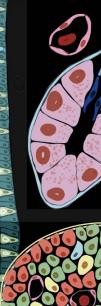
Organs in work:

- Liver
- Small and large intestine
- Skin
- Retina

HRA

29 Organs total 57 3D reference organs (L/R, M/F)







HRA Spring Release

Tasks

Tasks

Lead authors confirmed HRA digital objects submitted External review starts Reviews are shared with authors Authors submit revised DOs Release is published

HRA Fall Release

90

Lead authors confirmed HRA digital objects submitted External review starts Reviews are shared with authors Authors submit revised DOs Release is published

Deadlines July 15 October 1 October 5 October 10 October 24 December 15

Deadlines

January 15

April 1 April 5

April 10

April 24

June 15





Human Reference Atlas

Human Reference Atlas (HRA) Portal

Contect Us

HUBMAP HUMAN REFERENCE ATLAS

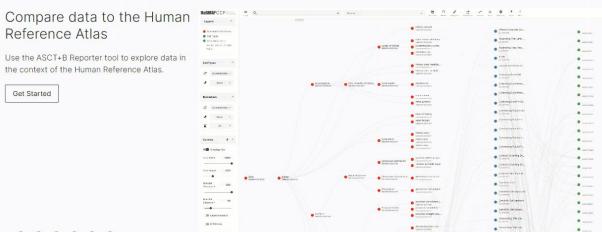
Data CCF Ontology

Tools Training & Outreach -About -

Human Reference Atlas 3D Multiscale Biomolecular Human Reference Atlas Construction, Visualization and Usage

A Common Coordinate Framework (CCF) for a human body provides a unique address for each cell in the human body. It is similar to the latitude-longtitude system used to navigate a world map.

A Human Reference Atlas (HRA) is a comprehensive, high-resolution, three-dimensional atlas of all the cells in the healthy human body. The Human Reference Atlas provides standard terminologies and data structures for describing spicimens, biological structures, and spatial positions linked to existing ontologies



HRA Use Cases: Three key use cases have been identified, discussed with experts, and help prioritize HRA construction and usage:

US#1 API to HRA, e.g, to improve CT annotation

US#2 API to HRA to predict spatial location of tissue

US#3 Exploration of CTs, Bs to understand what changes with age or during disease

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https://humanatlas.io

Human Reference Atlas data and APIs

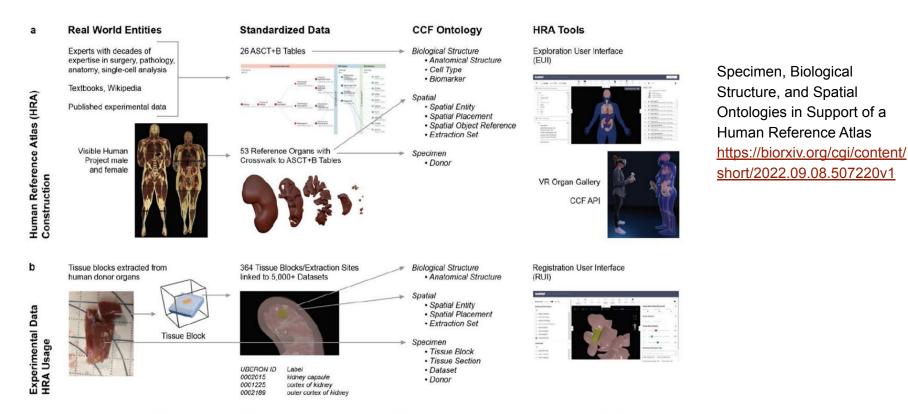


Figure 1. From real-world entities, to standardized data, to ontology. a. Human Reference Atlas construction takes real-world data and represents it in standardized data structures that are defined by the interlinked Biological Structure, Spatial, and Specimen ontologies.

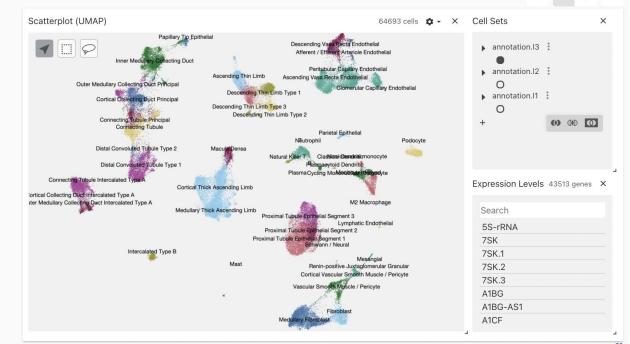
Human Reference Atlas (HRA)

Anatomical Structures, Cell Types, and Biomarkers 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). 3D and 2D reference object capture the shape, size, and spatial composition of ASCT.

ASCT Tab	le			Ontology		Reference ect Library
Structure/Region	Sub structure/Sub region Bowman's (glomular) Capsule/parietal layer	Cell Type Parietal epithelial Cell		Anatomical Structures Partonomy		•
Renal Corpuscle	Bowman's (glomular) Capsule/visceral layer	Podocyte		kidney		
Kenal Corpuscie	Glomerular Tuft	Capillary Endothelial Cell Mesangial Cell	↦	kidney capsule		
	Proximal Tubule	Proximal Tubule Epithelial Cell (general) Proximal Convoluted Tubule Epithelial Cell Segment 1 Proximal Tubule Epithelial Cell Segment 2 Proximal Tubule Epithelial Cell Segment 2	Π	cortex of kidney outer cortex of kidney renal medulla		
Tubules	Loop of Henle, Thin Limb Descending Thin Limb Cell (general) Ascending Thin Limb Cell (general)					
	Loop of Henle, Thick Limb	Thick Ascending Limb Cell (general) Cortex-TAL Cell Medulla-TAL Cell TAL-Macula Densa Cell	Ļ	Cell Types Ontology connective tissue cell pericyLe cell		936 N
	Distal Convolution	Distal Convoluted Tubule Cell (general) DCT Type 1 Cell DCT Type 2 Cell	Γ	mesangial cell extraglomerular mesangial cell		• •
	Connecting Tubule	Connecting Tubule Cell (general) CNT-Principal Cell		glomerular mesangial cell		

HuBMAP	Donors Samples Datasets Other •	Atlas & Tools ▼ Resources ▼ User Profile ▼
Sections Description	Reference-Based Analysis 🛛	Open Azimuth App 🖄
Organ info Azimuth Search	Modalities RNA Nuclei in reference 64,693 Reference dataset Lake et al, bioRxiv 2021	

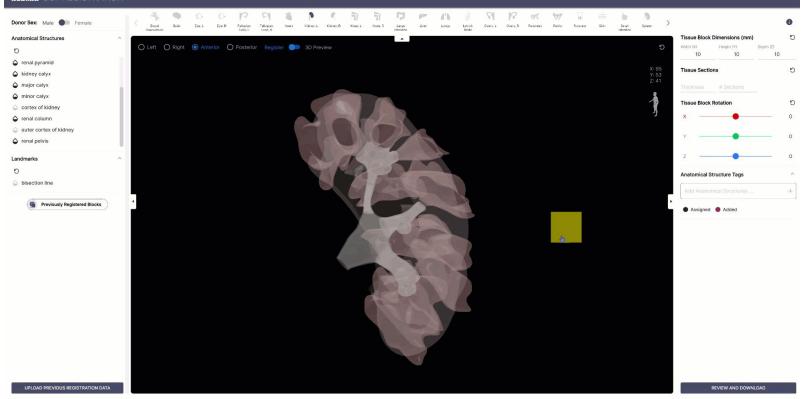
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Registration User Interface (RUI)

HUBMAP CCF REGISTRATION

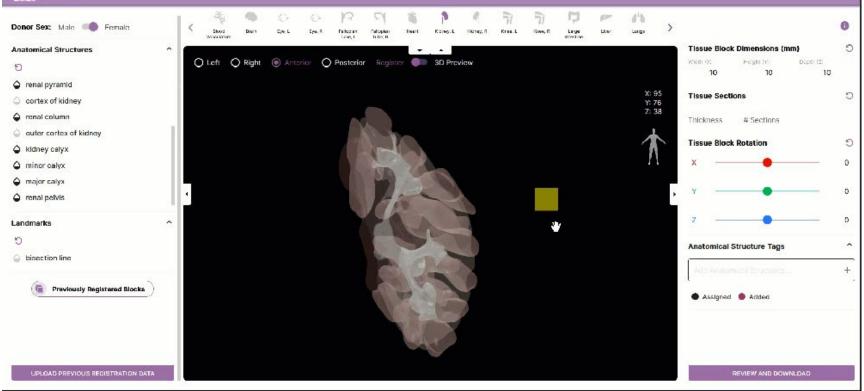


https://hubmapconsortium.github.io/ccf-ui/rui

RUI supports 57 organs (L/R, M/F) with 1,542 anatomically correct 3D anatomical structures.

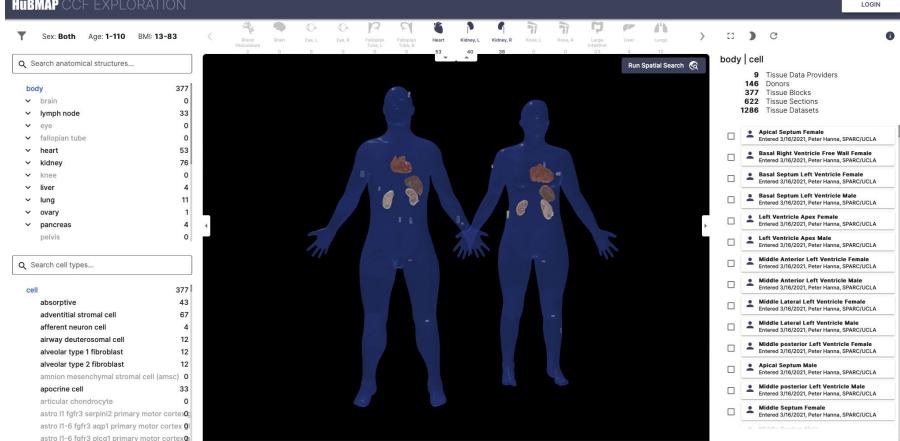
SenNet

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Exploration User Interface (EUI)

HUBMAP CCF EXPLORATION



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

EUI supports search for 1,542 AS and 953 cell types. Will soon add search for biomarkers.

SenNet

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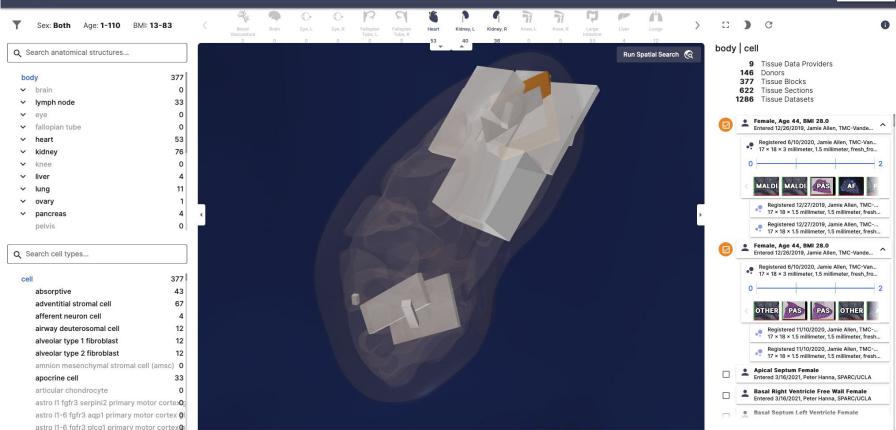


Note: The screenshot shows HuBMAP data

LOGIN

Exploration User Interface (EUI)

HUBMAP CCF EXPLORATION



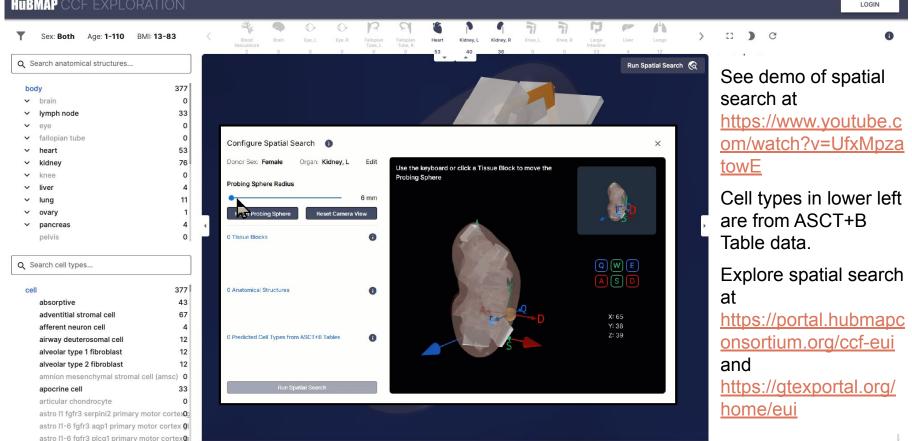
https://portal.hubmapconsortium.org/ccf-eui

More than 5,000 tissue datasets from 4 consortia have been RUI registered.

LOGIN

Exploration User Interface (EUI) - Spatial Search

HUBMAP CCF EXPLORATION

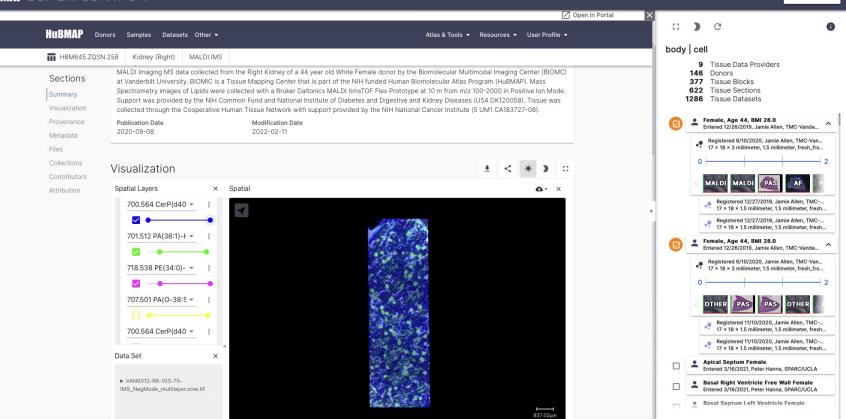


https://portal.hubmapconsortium.org/ccf-eui

Spatial search API is ready for HuBMAP portal wide usage.

Exploration User Interface (EUI) & Vitessce

HUBMAP CCF EXPLORATION



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

Works. Need to connect OMAP data to 'Spatial Layers' image channels. TMCs have this info.

LOGIN

Interactive FTUs: Explore CT x B matrices for 19 FTUs across organs--what changes as we age, change BMI?

Human Reference Atlas Functional Tissue Unit Explorer

(i) About

Expand

CLDN1

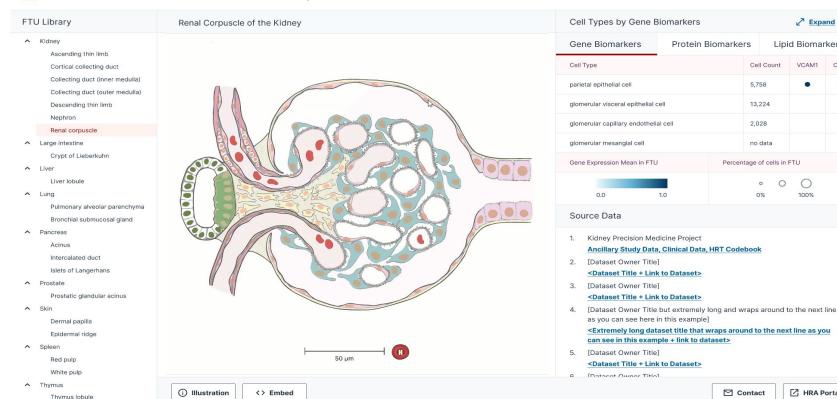
Lipid Biomarkers

VCAM1

0

100%

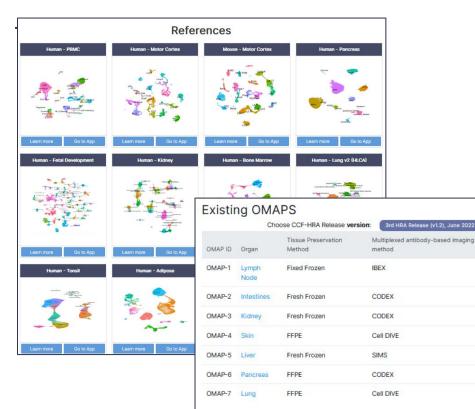
HRA Portal

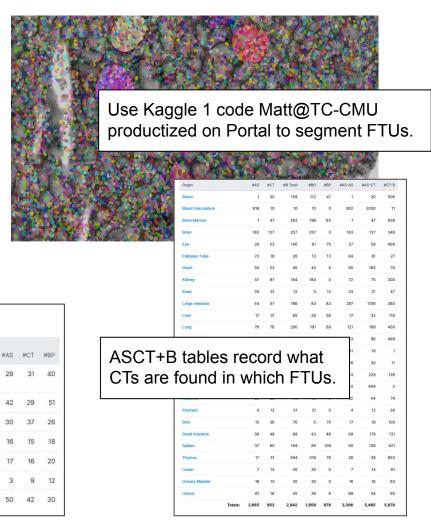


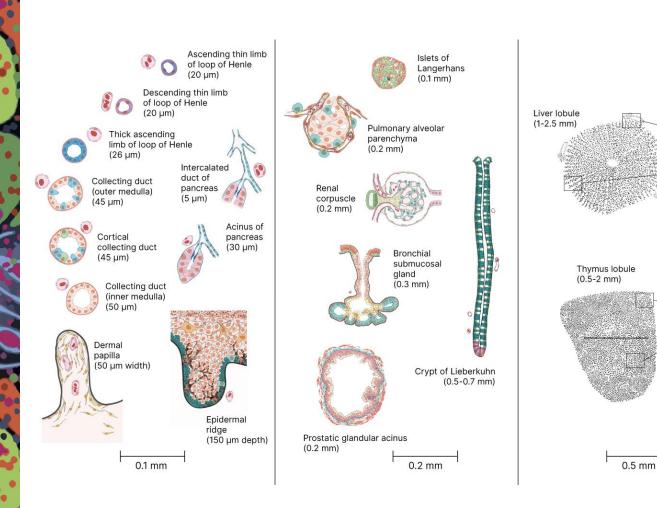
UI Specification done and tested. Will be implemented for 19 FTUs by June 2023. Need Kaggle 2 code + Azimuth/OMAP references to compile cell x gene, cell x protein data at FTU level.

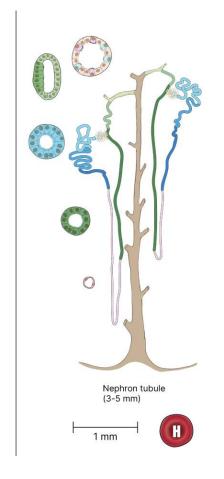
Interactive FTUs: Data

Use Azimuth references + OMAPs to assign ontology aligned CT / B names to bulk or spatially explicit experimental data.









Scientific Map/Atlas construction requires data/code that is documented/shared so others can reproduce results

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HUBMAP Donors Samples Datasets Other -Atlas & Tools
 Resources
 User Profile Human Reference Atlas (HRA) Portal ASCT+B Reporter Human BioMolecular Atlas Program Exploration User Interface (EUI) An open, global atlas of the human body at the cellular level Registration User Interface (RUI) The HuBMAP Data Portal is the central resource for discovery, visualization, and download of single-cell tissue data Azimuth: Reference-based single cell mapping standardized data curation and processing workflow ensure that only high guality is released. HRA Preview: ASCT+B Reporter Comparison HRA Preview: Vasculature CCF Visualization batial Layers Explore spatial single-cell 143673 cells 🏚 🗸 🔥 🗸 HRA Preview: HRA vs. Experimental Data data with Vitessce HRA Preview: Scrollytelling Series O req001 expr ∧ visualizations HRA Preview: Tabula Sapiens Comparison Colormap: None Domain: Min/Ma -HRA Preview: FTU Segmentation View multi-modal single-cell resolution HRA Preview: Mesh-Level Collision Detection measurements with reusable interactive components such as a scatterplot, spatial+imaging Transpare 🔲 plot, genome browser tracks, statistical plots, and controller components DAPI-02 ▶ Cell .. Get Started Cell ... Data Set Heatman 143673 cells × 29 antigens, with 143673 cells selected 🛛 🔹 🗸 Cell ... ▶ Cell ... Cells reg001 mask ► Cell ... < • 0 0 > Cell ...

105 1259 16 Organs Collections Donors

Previews explain new data, code, functionality.

https://portal.hubmapconsortium.org



SenNet Talks on HRA construction and usage:

- 2022.06.01 SenNet-Biomarkers <u>Slides</u>, <u>Recording</u> (at 35 min mark)
- 2022.04.27 Onboarding SenNet TMCs Slides, Recording

Visible Human MOOC

https://expand.iu.edu/browse/sice/cns/courses/hubmap-visible-human-mooc

3rd HuBMAP Portal Release (June 2022)



HuBMAP Halfway Point

• HuBMAP consortia members reflect on the past four years and discuss their plans and hopes for the future.



The Great VHMOOC Blooper Reel

Not everything goes according to plan when we make our VHMOOC videos. These outtakes give a humorous look behind the scenes!



Katy Börner-Atlas Construction and Usage @

Also featuring a demonstration of tissue registration with 3D models.



Introduction to the HRA-CCF

 An introduction to the three ontologies at work in the Human Reference Atlas's Common Coordinate Framework: the specimen, biological structure, and spatial ontologies.



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Mike Snyder Explains How to Map Human Intestines

A lively demonstration of the crucial role the intestines play in human health, and what we can learn by mapping them at the single-cell level.



Using the EUI on the GTEx Portal

 How to cross-compare data from GTEx and HuBMAP by using the Exploration User Interface embedded in the GTEx Portal.



Richard Conroy-How HuBMAP Works

A big-picture overview of the first four years of HuBMAP.

December 10th-11th, 2022 **Begins at 12PM EST**

24 Hour Human **Reference Atlas Event**

Let's map the human body at single cell resolution!

https://humanatlas.io/events/2022-24h/

https://humanatlas.io/events/2022-24h





1PM

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6PM in London (GMT) 3AM in Tokyo (GMT+9) Panel: What is a Human Reference Atlas?

Moderator: Todd Theriault (Co-Curator, Places & Spaces, Indiana University) with Aviv Regev (Human Cell Atlas). Sanjay Jain (Washington University in St. Louis), Kristin Ardlie (Broad Institute of MIT & Harvard), James C. Gee (University of Pennsylvania)

Desaintes (European Commission), Yong Yao (NIH/NIMH), Amy Bernard (Kavli), Jonah Cool (Chan Zuckerberg Initiative)



3PM 8PM in London (GMT), 5AM in Tokyo (GMT+9) **Creation of Homo Perfectus** With Marie Dauenheimer (Board Certified Medical Illustrator)



Conclusions

Human Reference Atlas construction requires high-quality data

We understand that all TMCs are expected to generate and submit the following for their relevant tissue:

- 1. Histopathology images
- 2. scRNAseq data
- 3. CODEX/CellDive/MxIF

In addition to basic expectations on types of data generated per tissue, there are other important considerations such as:

- 1. Running the assays above on the same or adjacent tissue sections
- 2. Including all essential donor, organ, sample, and assay metadata
- 3. RUI registration of all tissues
- 4. Utilization of biomarkers mapped to ASCT+B via Azimuth references and OMAPs

Plus, 3D data will be critically important to understand cell structure and function in their native 3D context. We would like to collaborate with teams that (will) generate 3D data.

GE Research and U. Pittsburgh RTI: 3D reconstruction of multiplexed skin samples and spatial cell analysis

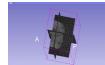


Registration of Skin Biopsy location using RUI

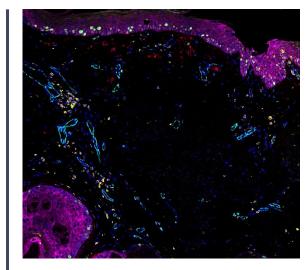
	Sebaceous glands	Ecorine cell, myoepit	 actin alpha 2, smooth. HOVE 130
	Econne (sweat) glands	Endothelial cell c. 0000115	calponin 1 Hosc 2155
Contract Contract		Fibroblast c. 6009520	CD163 molecule
	Apocrine glands	Germinative (epitheli	CD34 molecule Holic 1662
	nerve	Macrophage	CD3d molecule
	Blood vessels	Neuron CL 0008540	CD4 molecule
		Thelper C. 0009545	CD68 molecule
		T killer	CD8a molecule
	e nerve	T reg	CRCP

Registration of Skin Biomarkers in ASCT+B & OMAP

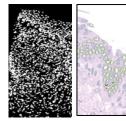




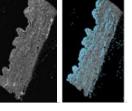
Tissue data collection: microCT imaging of skin FFPE blocks for multiplexed image 3D reconstruction



Multiplexed imaging of 18 skin biomarkers from 40 patients (Caucasian and African American)



Cell type classification (epithelial, immune, endothelial...)



3D Volume Reconstruction of 24 serial sections with micro CT as reference



3D "Digital Twin" of skin cells and quantitative interactive spatial distances (Yingnan Ju and Katy Börner, IU)



Early Maps are NOT perfect or complete

A New Map of the Whole World with the Trade Winds According to the Latest and Most Exact Observations

Makers: Herman Moll

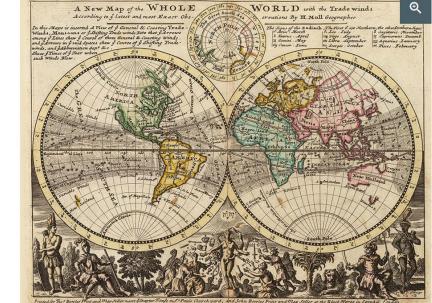
.

Languages: English | Español | 汉语 | Deutsch

At the turn of the 17th century, Herman Moll was the most famous map publisher in England. He was also the first cartographer to create an elegant map of England that correctly portrayed its shape. His style combined time-consuming embellishment with bold, clear lettering to highlight important information. Moll prided himself on his work and publicly rebuked mapmakers who republished preexisting maps under new titles without having investigated their accuracy or completion—as this could prove fatal in cases where known depths of water and sands were omitted. This map is a hand-colored, engraved double-hemisphere of the whole world, featuring California as an island, a popular misconception at the time. The continents are represented by 12 allegorical figures surrounded by plants native to these lands. The long note at the top left discusses the trade winds indicated by arrows throughout the map.

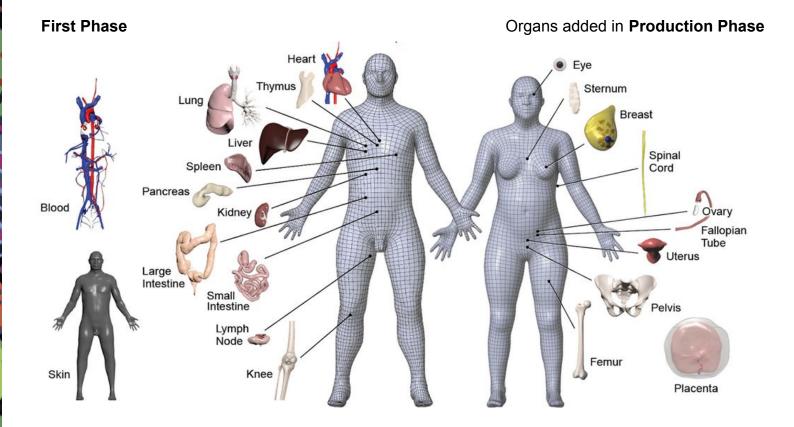
References

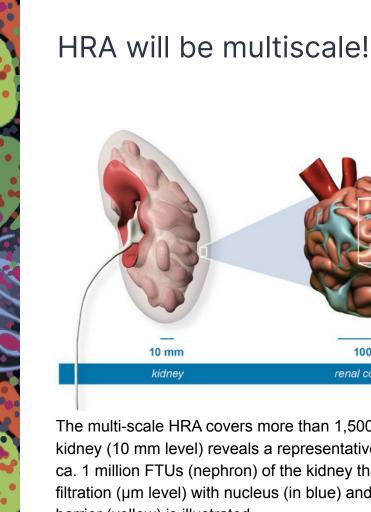
Moll, Herman. 1736. Atlas Minor. Or a New and Curious Set of Sixty-Two Maps... London: Thos. Bowles and John Bowles.



Places & Spaces: Mapping Science exhibit: https://scimaps.org/map/1/3

Early HRA will show organs that are funded. It will NOT be perfect or complete.





100 μm1 μmrenal corpusclepodocytes more than 1,500 anatomical structures in the material

The multi-scale HRA covers more than 1,500 anatomical structures in the male and female body. A zoom into the kidney (10 mm level) reveals a representative view of a renal corpuscle (200 μ m level), a subsegment of one of the ca. 1 million FTUs (nephron) of the kidney that is important in filtration. Podocytes, one of the cells important in filtration (μ m level) with nucleus (in blue) and a protein NPHS1 that maintains the structural integrity of the filtration barrier (yellow) is illustrated.

100 nm

NPHS1



Questions