HUBMAP Anatomy Knowledge Requirements

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CFDE Anatomy Working Group Virtual Event

April 20, 2021



WG Goals/Requirements

Anatomy Knowledge Requirements sessions will review the following questions for CFDE groups:

- 1. Search: What are your anatomical search use cases? What kind of research questions inform your targeted exploration of anatomy reference knowledge and associated resources?
- 2. Browse: How do you browse over anatomy reference knowledge in preparation for search? What functionality/experience do you seek during the untargeted browsing of anatomy reference knowledge?
- **3. Annotate:** How do you annotate/spatially register against anatomy reference knowledge in support of #1 & #2? How do you ensure FAIRness, consistency and coherence when mapping data onto anatomy reference knowledge?
- 4. **Represent:** What is your approach to anatomy reference knowledge representation in support of #1 to #3? How is this reference knowledge FAIR? Other items: Any other aspect that the cAWG should be focusing on?



Prelude: Human Reference Atlas



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 maps
- 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

An atlas is an oversized, bound book of maps.

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







An human cell **atlas** might show a landscape of all cells, or

Maps of cells per tissue type/anatomical structure.

Article | Published: 25 March 2020

Construction of a human cell landscape at single-cell level

Xiaoping Han 🗠, Ziming Zhou, [...] Guoji Guo 🖂

Nature 581, 303–309(2020) Cite this article 55k Accesses 32 Citations 409 Altmetric Metrics



A human reference **atlas** might use human anatomy as a '<u>basemap</u>,' or

an abstract space.

Weber, Griffin M, Yingnan Ju, and Katy Börner. 2020. "Considerations for Using the Vasculature as a Coordinate System to Map All the Cells in the Human Body". Frontiers in Cardiovascular Medicine 7 (29): doi: 10.3389/fcvm.2020.00029.



https://bodyworlds.com



Weber, 1978

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

Assavs/ analysis Transformative technology development (TTD) and rapid technology Data compilation implementation (RTI) **Tissue mapping** centre (TMC) HuBMAP integration, visualization and engagement (HIVE) Map generation Data Dissemination/ storage access

Tissue collection

Fig. 1 | The HubMAP consortium. The TMCs will collect tissue samples and generate spatially resolved, single-cell data. Groups involved in TTD and RTI initiatives will develop emerging and more developed technologies, respectively; in later years, these will be implemented at scale. Data from all groups will be rendered useable for the biomedical community by the HuBMAP integration, visualization and engagement (HIVE) teams. The groups will collaborate closely to iteratively refine the atlas as it is gradually realized.

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



Fig. 2 | Key tissues and organs initially analysed by the consortium.

Using innovative, production-grade ('shovel ready') technologies, HuBMAP TMCs will generate data for single-cell, three-dimensional maps of various human tissues. In parallel, TTD projects (and later RTI projects) will refine assays and analysis tools on a largely distinct set of human tissues. Samples from individuals of both sexes and different ages will be studied. The range of tissues will be expanded throughout the program.

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



Fig. 3 | Map generation and assembly across cellular and spatial

scales. HuBMAP aims to produce an atlas in which users can refer to a histological slide from a specific part of an organ and, in any given cell, understand its contents on multiple 'omic levels—genomic, epigenomic, transcriptomic, proteomic, and/or metabolomic. To achieve these ends, centres will apply a combination of imaging, 'omics and mass spectrometry

techniques to specimens collected in a reproducible manner from specific sites in the body. These data will be then be integrated to arrive at a high-resolution, high-content three-dimensional map for any given tissue. To ensure inter-individual differences will not be confounded with collection heterogeneity, a robust CCF will be developed.

CCF Requirements

Organ

Renal capsule

Renal pyramid

Renal cortex

Renal medulla

Renal calyx

Renal pelvis

The CCF must capture major **anatomical structures**, **cell types**, **and biomarkers** and their interrelations across **multiple levels of resolution**.

It should be **semantically explicit** (using existing ontologies, e.g., Uberon, CL) and **spatially explicit** (e.g., using 3D reference organs for registration and exploration).



Body

- Body
- Kidney (Left, Right)
- Aorta
- Renal artery
- Renal vein
- Ureter

Functional Tissue Unit

- Nephron
- Renal corpuscle
- Proximal convoluted tubule
- Loop of Henle
- Distal convoluted tubule
- Connecting tubule
- Collecting duct

FTU Sub-structure(s) Cellular

Bowman's capsule

Efferent arteriole

Afferent arteriole

Glomerulus

- Parietal epithelial cell
- Capillary
 - endothelial cell
- Mesangial cell
- Podocyte



CCF: ASCT+B Tables & 3D Reference Organs

ASCT+B Tables

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

Structure/Re	Substructure/Sub	Cell Type	Subset of Marker Genes
gion	region		
Renal	Bowman's Capsule	Parietal epithelial cell	CRB2*, CLDN1*
Corpuscle	Glomerulus	Podocyte	NPHS2*, PODXL*, NPHS1*
		Capillary Endothelial Cell	EHD3*, EMCN*, HECW2*,
			FLT1*, AQP1*
		Mesangial Cell	POSTN*, PIEZO2*, ROBO1*,
			ITGA8*

Partial ASCT+B Table from

• El-Achkar et al. A Multimodal and Integrated Approach to Interrogate Human Kidney Biopsies with Rigor and Reproducibility: The Kidney Precision Medicine Project. bioRxiv. 2019, Updated Aug 2020. doi:10.1101/828665

Table 3: Cell types and associated markers from KPMP Pilot 1

transcriptomic studies. Asterisk denotes genes detected by more than one technology. *Italics* genes detected by a single technology.

Structure/R egion	Sub structure/Sub region	Cell Type	Abbreviation	Subset of Marker Genes	Pertinent negatives/com ments	
	Bowman's Capsule	Parietal epithelial cell	PEC	CRB2*, CLDN1*		
Renal	Glomerulus	Podocyte	POD	NPHS2*, PODXL*, NPHS1*		
Corpuscle		Capillary Endothelial Cell	GC-EC	EHD3*, EMCN*, HECW2*, FLT1*, AQP1*		
		Mesangial Cell	MC	POSTN*, PIEZO2*, ROBO1*, ITGA8*		
	Proximal Tubule	Proximal Tubule Epithelial Cell (general)	PT	CUBN*, LRP2*, SLC13A1*, ALDOB*, GATM*		
		Proximal Convoluted Tubule Epithelial Cell Segment 1	PT-S1	SLC5A2*, SLC5A12*	The second se	
		Proximal Tubule Epithelial Cell Segment 2	PT-S2	SLC22A6*	There is overlap among the segments	
		Proximal Tubule Cell Epithelial Segment 3	PT-S3	PDZK1IP1*, MT1G*	segments	
	Loop of Henle, Thin Limb	Descending Thin Limb Cell (general)	DTL	CRYAB*, VCAM1*, AQP1*, SPP1*	CLDN10 low	
		Ascending Thin Limb Cell (general)	ATL	CRYAB*, TACSTD2*, CLDN3*	AQP1 low to none	
	Loop of Henle, Thick Limb	Thick Ascending Limb Cell (general)	TAL	SLC12A1*, UMOD*	SLC12A3 low to none	
		Cortex-TAL cell	C-TAL	SLC12A1*, UMOD*		
		Medulla-TAL cell	M-TAL	SLC12A1*, UMOD*		
		TAL-Macula Densa cell	TAL-MD	NOS1*, SLC12A1*		
	Distal Convolution	Distal Convoluted Tubule Cell (general)	DCT	SLC12A3*, TRPM6*		
Tubules		DCT type 1 cell	DCT-1	SLC12A3*, TRPM6	SLC8A1, HSD11B2 (low to none)	
		DCT type 2 cell	DCT-2	SLC12A3*, SLC8A1*, HSD11B2	Has CNT and DCT signature	
	Connecting Tubule	Connecting Tubule Cell (general)	CNT	SLC8A1*, CALB1, TRPV5		
		CNT-Principal Cell	CNT-PC	SLC8A1*, AQP2*, SCNN1G*	SLC12A3 low to	
		CNT-Intercalated Cell	CNT-IC	SLC8A1*, CA2, ATP6VOD2*	none. IC or PC without SLC8A1	
		CNT-IC-A cell	CNT-IC-A	SLC8A1*, SLC4A1*, SLC26A7*	Could be in the CNT structure	
		CNT-IC-B cell	CNT-IC-B	SLC8A1*, SLC26A4*, SLC4A9*		
	Collecting Duct	Collecting duct (general) cell	CD	GATA3*	GATA3 may be	
		CD-PC (general)	CD-PC		in subpopulation	
		C-CD-PC	C-CD-PC	AQP2*, AQP3*, FXYD4*,	of DCT, CNT	
		M-CD-PC	M-CD-PC	SCNN1G*, GATA3*	and vSMC/P.	
		Outer medulla-CD-PC	OM-CD-PC		SLC8A1,	
		Inner Medulla-CD cell	IM-CD	AQP2*, SLC14A2	CALB1, TRPV5	

		Transitional PC-IC cell	tRC,IC	FXYD4*, SLC4A9*/SLC26A7*	(low to none); Low to No
		CD-IC (general) cell	CD-IC	CA2, ATP6VOD2*	CALCA and KIT
		CD-IC-A (general) cell	CD-IC-A	SLC4A1, SLC26A7*, TMEM213*	in C-CD-IC-A. I may not be
		C-CD-IC-A cell	C-CD-IC-A	SLC26A7*, SLC4A1*	possible to
		M-CD-IC-A cell	M-CD-IC-A	SLC26A7*, SLC4A1, KIT*, CALCA	assign IC or PC to_CNT or CD
		CD-IC-B (general) cell	CD-IC-B		structures
		C-CD-IC-B cell	C-CD-IC-B	SLC4A9". SLC26A4"	without regional
		M-CD-IC-B cell	M-CD-IC-B	020110,0202011	information of their source.
		Endothelial Cell (general)	EC	EMCN*, PECAM1*, FLT1*	
		EC-Afferent/Efferent Arteriole	EC-AEA	SERPINE2*, TM4SF1*	likely PALMD
		EC-Peritubular capillaries	EC-PTC	PLVAP*	
Vessels	Endothelial Cells (non- glomerular)	EC-Descending Vasa Recta	EC-DVR	TM4SF1*, PALMD	
		EC-Ascending Vasa Recta	EC-AVR	DNASEIL3*	low to none
		EC-Lymphatics	EC-LYM	MMRN1*, PROX1	
Structure/R egion	Sub structure/Sub region	Cell Type	Abbreviation	Subset of Marker Genes	Pertinent negatives/com ments
Interstitium	Stroma (non- glomerular)	Vascular Smooth Muscle/Pericyte (general)	VSMC/P	TAGLN*, ACTA2*, MYH11*, NTRK3, MCAM	
		vSMC/P-Renin	VSMC/P-REN	REN	-
		Fibroblast	FIB	DCN*, ZEB2, C7, LUM	
	Immune	Macrophages-Resident	MAC-R	CD163*, IL7R*	
		Macrophage	MAC	S100A9	1
		Natural Killer Cell	NKC	NKG7	
		Dendritic Cell	DC	APOE	
		Monocyte	MON	C1QA, HLA-DRA	
		Monocyte T lymphocyte (general)	MON T	C1QA, HLA-DRA CD3	
		Monocyte	MON	C1QA, HLA-DRA	

El-Achkar et al. A Multimodal and Integrated Approach to Interrogate Human Kidney Biopsies with Rigor and Reproducibility: The Kidney Precision Medicine Project. bioRxiv. 2019, Updated Aug 2020. doi:10.1101/828665



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CCF ASCT+B Reporter UI



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

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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
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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.



ASCT+B Tables

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).

Ontology

ASCT Table

Structure/Region	Sub structure/Sub region	Cell Type					
	Bowman's (glomular) Capsule/parietal layer	Parietal epithelial Cell					
Renal Corpuscle	Bowman's (glomular) Capsule/visceral layer	Podocyte					
Renal Corpuscie	Glomerular Tuft	Capillary Endothelial Cell					
	Giomeratar Tare	Mesangial Cell					
	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					
	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)					
Tubules		Cortex-TAL Cell					
		Medulla-TAL Cell					
		TAL-Macula Densa Cell					
	Distal Convolution	Distal Convoluted Tubule Cell (general)					
		DCT Type 1 Cell					
		DCT Type 2 Cell					
	Connecting Tubule	Connecting Tubule Cell (general)					
		CNT-Principal Cell					

Anatomical Structures Partonomy kidney kidney capsule cortex of kidney outer cortex of kidney renal medulla Cell Types Ontology connective tissue cell pericyLe cell mesangial cell extraglomerular mesangial cell glomerular mesangial cell

3D Reference



Overview of CCF 3D Reference Models

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ASCT+B Table Working Group

Lead by Katy Börner and Jim Gee; Ellen M Quardokus serves as Knowledge Manager

Meetings take place monthly to review and approve tables, formalize and unify table design language, discuss and expand table usage, see <u>WG Charter</u>.

Upcoming meetings in **2021:** April 7, May 5, 11a-noon ET. Please <u>register</u> to receive invites and updates.



	HuBMAP	RBK	KPMP	SPARC	LungMAP	HTAN	HCA	GUDMAP	Gut Cell Atlas	BICCN	Allen Brain	TCGA	Wellcome	MRC	H2020	GTEx	Total
Kidney	1	1	1	0	0	0	1	1	0	0	0	1	1	1	0	1	9
Liver	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	1	3
Spleen	1	0	0	0	0	0	1	0	0	0	0	0	1	0	0	1	4
Heart	1	0	0	1	0	0	1	0	0	0	0	0	0	0	0	1	4
Lung	1	0	0	1	1	1	1	0	0	0	0	1	1	1	1	1	10
L intestine/Colon	1	0	0	1	0	1	1	0	1	0	0	1	0	0	0	1	7
S intestine	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	2
Bladder	1	0	0	1	0	0	0	1	0	0	0	1	0	0	0	1	5
Ureters	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	2
Thymus	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	2
Lymph nodes	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	2
mediastinal lymph node	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
Eye	1	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	3
Brain	0	0	0	0	0	0	1	0	0	1	1	1	0	0	1	1	6
Brain stem	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1
Cerebellum	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	1	3
Spinal cord	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	2
Pancreas	0	0	0	0	0	1	1	0	0	0	0	1	0	0	1	1	5
Breast	0	0	0	0	0	1	1	0	0	0	0	1	1	0	0	1	5
Skin	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	1	3
Pediatric systems	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	2
Ovaries	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	2
Testes	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	2
Cervix	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1
Uterus	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	5
Blood	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	2
Bone	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
Placenta	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
Decidua	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
Embryo	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
esophagus	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	1	3
hematopoietic system	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	2
immune system bulk	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
Stomach	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	1	3
Thyroid	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	2
Prostate	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	1	3
Adrenal gland	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	1	3
Totals	11	1	1	7	1	6	21	4	1	2	2	20	7	5	4	21	114

Table compiled for, during, and after the NIH-HCA Joint Meeting in March 2020, https://hubmapconsortium.org/nihhca2020





Organ	#AS	#CT	#B Total	#BG	#BP	#AS-AS	#AS-CT	#CT-B
Bone Marrow & Blood/Pelvis	s 3	46	327	201	126	2	70	710
Brain	187	127	254	254	0	187	127	330
Heart	52	25	48	48	0	61	164	78
Intestine, Large	65	69	94	88	6	389	1,361	197
Kidney	68	63	152	152	0	67	59	257
Lung	161	92	176	172	4	1,633	12,094	286
Lymph Node	41	49	266	108	158	62	135	544
Skin	16	42	70	0	70	17	19	105
Spleen	46	66	255	80	145	68	172	414
Thymus	25	41	511	388	123	38	180	657
Vasculature	870	2	1	1	0	869	606	2
т	otals: 1,534	622	2,154	1,492	632	3,393	14,987	3,580

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

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https://hubmapconsortium.github.io/ccf/pages/ccf-3dreference-library.html (NLM VH organs) https://community.brain-map.org/t/allen-human-referenceatlas-3d-2020-new/ (brain) https://www3.cs.stonybrook.edu/~ari/ (male colon)



DataCite Search

hubmap

Search

37 Works

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

Marda Jorgensen, Andrea J. Radtke & Rebecca T. Beuschel

Text File published via HuBMAP

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.

1 No citations were reported. No usage information was reported.

🗹 https://doi.org/10.48539/hbm625.vplj.455 🛛 💕 Cite

3D Reference Organ for Intestine, Large, Female v1.0

Kristen Browne

Digital Object published via HuBMAP

This reference organ was created using data provided by Arie Kaufman, Stony Brook University as a base for a custom model built using Pixelogic Zbrush.

https://search.datacite.org/works?query=hubmap&resource-type-id=dataset

ASCT+B Table Usage

ASCT+B tables guide **CCF Ontology** and **3D Reference Object Library** design that semantically name and spatially place tissue data from different donors into one CCF (i.e., <u>mapping</u>).

ASCT Table	2			Ontology	3D Reference Object Library
Structure/Region	Sub structure/Sub region Bowman's Capsule	Cell Type Parietal epithelial Cell		Anatomical Structures Partonomy	
Renal Corpuscle	Glomerulus	Podocyte Capillary Endothelial Cell Mesangial Cell	\rightarrow	kidney 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		cortex of kidney outer cortex of kidney renal medulla	
	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		Cell Types Ontology connective tissue cell pericyte cell	
	Distal Convolution	Distal Convoluted Tubule Cell (general) DCT Type 1 Cell DCT Type 2 Cell		mesangial cell extraglomerular mesangial cell	
	Connecting Tubule	Connecting Tubule Cell (general) CNT-Principal Cell		glomerular mesangial cell	

Tissue blocks are <u>registered</u> into the CCF using the Registration User Interface (RUI), and they can be <u>explored</u> via the Exploration User Interface (EUI).



Annotate:

How do you annotate/spatially register against anatomy reference knowledge in support of #1 & #2? How do you ensure FAIRness, consistency and coherence when mapping data onto anatomy reference knowledge?



CCF Registration User Interface (RUI)

Document the tissue extraction site by registering tissue blocks within a 3D reference organ.



Image provided by Sanjay Jain, TMC-UCSD

CCF Registration User Interface (RUI) v1.0.0

New Features:

- Organ carousel with 4 reference organs
- Support for tissue extraction sites
- Expanded ontology
- Semantic annotation via collision detection & manual annotation
- Support for non-HuBMAP usage

https://hubmap-ccf-ui.netlify.app/rui/





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Common Extraction Sites ③ Show Previous Registration Blocks

Kidney

Bisection Line

Spleen

- CC1
- CC2
- CC3

Colon

- Ascending Colon
- Descending Colon
- Transverse Colon
- Sigmoid Colon

Heart

Extraction Site Mapping

,	Left atrium, appendage	7
•	Left atrium, PV inflow	8
,	Left ventricle, apex	1
•	Left ventricle, free wall 3cm from apex	2
,	Septum, 3cm from apex including LAD	3
,	Posterior, adjacent to coronary sinus	9
,	Right atrium appendage	5
,	Right atrium, AV (atrioventricular) node	6a
,	Right atrium, SA (sinoatrial) node	6b
,	Right ventricle, free wall 3cm from apex	4



For the first HuBMAP portal release, 48 tissue blocks were registered.

ommon Extraction Sites				
 Bisection line 				
 Show Previous Registrati 	on Blocks			
natomical Structures	^			
 calyces 	20			
 capsule 	20			
) hilum				
medulla (renal columns)				-
outer cortex				
o papilla	20			
 pelvis 	20			2
o pyramids	20			
o ureter	20		6	9
Opacity				1
				K
				- 11



BACK

Heart, male

⊙ CC1

⊙ CC2

⊙ CC3

Anatomical Structures

Heart, male Common Extraction Sites Left ventricle, apex (ii) Left ventricle, free wall 3cm from apex Septum, 3cm from apex including LAD ③ Right ventricle, free wall 3cm from apex ③ Right atrium appendage Right atrium, SA node to AV node D Left atrium, appendage ③ Left atritum, PV inflow Posterior, adjacent to coronary sinus

Show Previous Registration Blocks

Anatomical Structures



CCF Registration User Interface (RUI) v1.0.0 cont.

Collision when Tissue Block hits Reference Organ



Tag Search behavior



Custom tag added to list



HuBMAP Upload Portal

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HuBMAP Display ID Generator

Generate unique identifiers which will be used consortium wide to track sample and associate data with samples.

Source HuBMAP ID • TEST0005-RK Look up HuBMAP display id: TEST0005-RK Hyperson Type: Kidney (Right) HuBMAP ID: HIBM-264-TTTJ-798 Description: Trococol 1 protocolsio DOI * https://dx.doi.org/10.17504/protocolsi.op9k/r4w Protocol document * Choose a file protocol in DOI * https://dx.doi.org/10.17504/protocolsi.op9k/r4w Protocol document * Choose a file to conserve the maximum of the sample Locations can be assigned on the next Screen After generate IDs for multiple FFFE block samples Description Metadata Image * Add Metadata				
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Generate IDs for multiple FFPE block samples G Generate IDs for multiple FFPE block samples Leb Ds and Sample Locations can be assigned on the next screen after generating the HuBMAP Ds Description Metadata		Protocol document *		
a C Lib Ds and Sample Locations can be assigned on the next Description Screen after generating the HuBMP IDs Metadata + Add Metadata			3E black complex	
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Generate ID Cancel		Generate ID	Cancel	



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HuBMAP Display ID Generator

Generate unique identifiers which will be used consortium wide to track sample and associate data with samples.

3 sample	ids were generated: TEST0005-RK-6 through TEST000	15-RK-8	
Type: FF	PE block		
	Assig	n Lab IDs and Sample Locations Return to Search	
		Assign Lab IDs and Sample Location	
	Lab Sample Id	Peoister Location SuccessView JSON	
EST0005-RK-6	TEST0005-RK-6-A	Register Location	0
EST0005-RK-7		Register Location	0
EST0005-RK-8		Register Location	Ð

Implemented by the HIVE IEC

CCF Registration User Interface (RUI)

HUBMAP CCF REGISTRATION USER INTERFACE

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



RUI in Numbers

HuBMAP Data (published) published + unpublished

15 kidney, left 11 kidney, right 15 spleen 4 intestine, large

5	Tissue Data Providers
36	Donors
153	Tissue Blocks
3763	Tissue Sections
269	Tissue Datasets

KPMP

3 kidney, left

SPARC

26 heart (13 male, 13 female)

GTEx

6 extraction sites for ca. 400 tissue blocks



15 extraction sites by Kalyanam Shivkumar, UCLA (SPARC) 10 sites by Shin Lin, UW (HuBMAP)



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

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Search:

What are your anatomical search use cases? What kind of research questions inform your targeted exploration of anatomy reference knowledge and associated resources?



Browse:

How do you browse over anatomy reference knowledge in preparation for search? What functionality/experience do you seek during the untargeted browsing of anatomy reference knowledge?



Filter:

Subset to focus on a specific subset of the data based on demographics, tissue/assay type, AS, CT, B.



CCF Exploration User Interface (EUI)

CCF Exploration User Interface (EUI)



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

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HUBMAP

body

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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.



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



Represent:

What is your approach to anatomy reference knowledge representation in support of #1 to #3? How is this reference knowledge FAIR? Other items: Any other aspect that the cAWG should be focusing on?



Visible Human MOOC (VHMOOC)

VH Massive Open Online Course (VHMOOC)

Goals

- Communicate tissue data acquisition and analysis,
- Demonstrate single-cell analysis and CCF mapping techniques, and
- Introduce major features of the HuBMAP portal.

Learning modules come with

- Videos (incl. interviews, tool demos)
- Hands-on exercises
- Self-quizzes



Meet the Instructors

Katy Börner, Victor H. Yngve

Distinguished Professor of

Engineering and Information

Network Science Center at

Indiana University

research scientist

Science. Founding Director of the Cyberinfrastructure for

Ilen M. Quardokus, staff in

the Chemistry Department and

Cyberinfrastructure for Network

Science Center, SICE with

microscopy, anatomy, and

expertise in molecular biology

interdisciplinary communication

Course Introduction

This 10h course introduces the HuBMAP project which aims to create an open, global reference attas of the human body at the cellular level. Anong others, the course describes the compliation and coverage of HuBMAP data, demonstrates new single-cell analysis and mapping techniques, and introduces major features of the HuBMAP portal. Delivered entirely online, all coursework can be completed

Delivered entirely online, all coursework can be completed asynchronously to fit busy schedules. If you have questions or experience issues during registration, please email cnscntr@indiana.edu.

Learning Outcomes

- Theoretical and practical understanding of different single-cell tissue analysis techniques.
- Expertise in single-cell data harmonization used to federate data from different individuals analyzed using different technologies in diverse labs.
- Hands-on skills in the design and usage of semantic ontologies that describe human anatomy, cell types, and biomarkers (e.g., marker genes or proteins).
- Knowledge on the design and usage of a semantically annotated three-dimensional reference system for the healthy human body.
 An understanding of how the HUBMAP reference atlas might be used to understand human health but also to diagnose and treat disease

Module Topics Include

- HuBMAP Overview: Project Goals, Setup, and Ambitions
- Tissue Data Acquisition and Analysis
 Biomolecular Data Harmonization
- Biomolecular Data Harmonization
 Ontology, 3D Reference Objects, and User Interfaces
- HuBMAP Portal Design and Usage



Audience: Biomedical students and professionals interested in singlecell tissue analysis and visualization

Andreas Bueckle, PhD Candidate in Information Science, performing research on information visualization, specifically virtual and augmented reality.

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

Acknowledgements

HuBMAP Consortium (https://hubmapconsortium.org)



Thanks go to all the **patients** that agreed to volunteer healthy tissue and open use of their data.



National Institutes of Health







Jeffrev

Spraggins







Marda

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Software Developer



Paul Hrishikesh Research Assistant

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Avinash Boppana Research Consultant Yashvardhan Jain Research Assistant

Software Developer





























Matthew Martindale

Center Assistant













Human Reference Atlas

Spatial Biology Europe: ONLINE LIVE & INTERACTIVE CONTENT SCHEDULE

Please see the full programme for the conference below. Where possible, sessions will be made available OnDemand after the scheduled time slot. Please note: Access to OnDemand sessions will only be available to delegates who purchase a full access pass

DAY TWO: 15 APRIL 2021

Panel Discussion: Human Reference Atlas

Moderator: KATY BÖRNER, Victor H. Yngve Distinguished Professor of Engineering and Information Science, Indiana University

15:30 Panellists:

JAMES GEE, Associate Professor of Radiologic Science in Radiology. Director, Penn Image Computing and Science Laboratory, Department of Radiology, Perelman School of Medicine, **University of Pennsylvania**

XUEGONG ZHANG, Professor of Pattern Recognition and Bioinformatics, Director, Bioinformatics Division, TNLIST (Tsinghua National Laboratory for Information Science & Technology), Department of Automation, Tsinghua University

AMY BERNARD, Director, Science & Technology Strategy, Allen Institute

BERNARD DE BONO, Principal Investigator, Associate Professor, University of Auckland

https://www.oxfordglobal.co.uk/spatial-biology-online

16:00

Human Reference Atlas: How to represent clinical, spatial, and semantic features of AS and CT

SPARC: Heart & colon overlap with HuBMAP organs; Heart data registered
GTEx: Well defined sampling sites (ca. 50), 100s of tissue samples.
LINCS: 130 tissues and organs, 1000 cell lines
KidsFirst: First collaboration to register tissue data
KPMP: 3 kidney samples RUI registered
HuBMAP: 25 organs. 1500 AS, 500 CT in 11 ASCT+B tables + 26 reference organs

Demographic/Clinical data: Sex, Age, Ethnicity, BMI, Disease Provenance: Author, Assay type, date