



Human Reference Atlas: ASCT+B Tables, 3D Reference Library & CCF User Interfaces

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CFDE April Cross-Pollination Event
Virtual Event

April 6, 2021

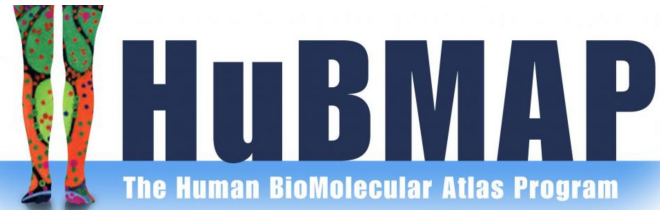
HuBMAP

Vision

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

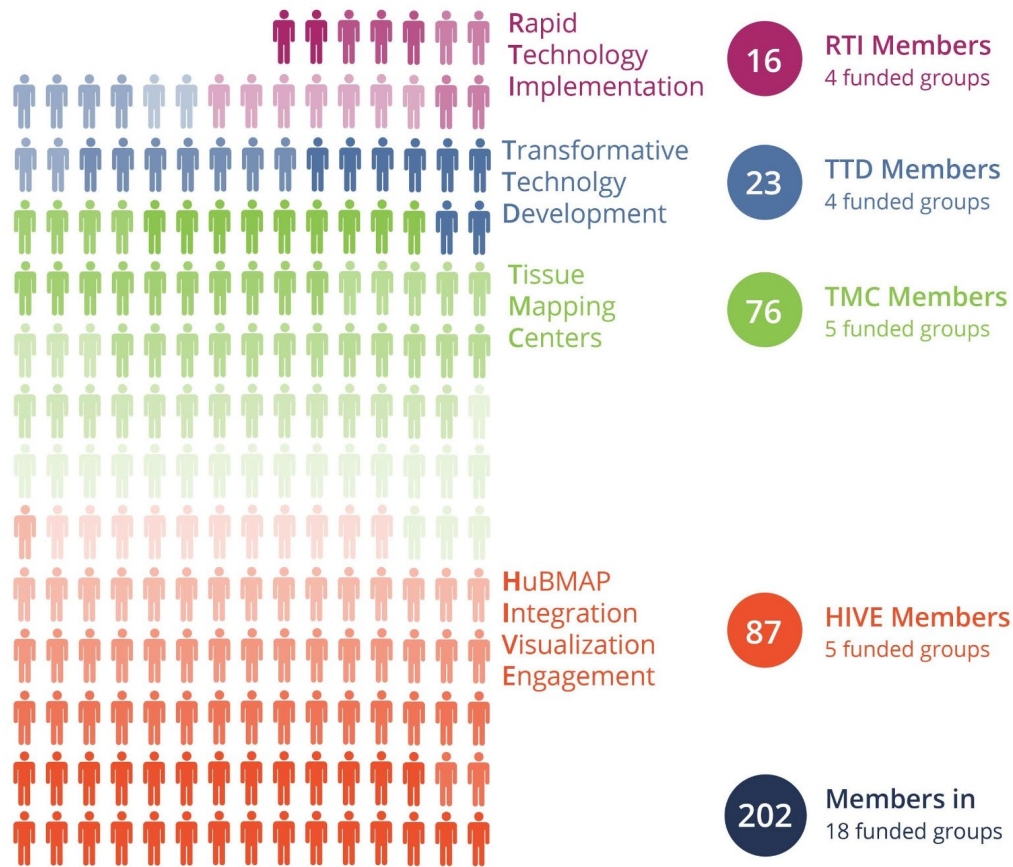
Goals

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



<https://commonfund.nih.gov/HuBMAP>

HuBMAP Funded Groups



HuBMAP Contributing Sites

TMC

University of Washington
Pacific Northwest National Lab

RTI, TTD

Northwestern University
Washington University, St. Louis
Washington University School of Medicine

TMC

University of Iowa

TTD

Marquette University

HIVE - Mapping, RTI

New York Genome Center
GE Global Research
University of Rochester

TMC

Washington University, St. Louis
Washington University School of Medicine

HIVE - Mapping, TTD

Indiana University
Purdue University

HIVE - Tools, TTD, RTI, TMC

Harvard University, Medical School
Broad Institute
Dana Farber Institute
Columbia University
Children's Hospital of Boston



SWITZERLAND

TMC

University of Zurich



NETHERLANDS

TMC

Delft University of Technology

TMC, TTD

University of Connecticut
Yale University

HIVE - IEC, HIVE - Tools, RTI, TMC

Carnegie Mellon University
Pittsburgh Supercomputing Center
University of Pittsburgh
National Disease Research Interchange
Children's Hospital of Philadelphia
University of Pennsylvania
Pennsylvania State University



UNITED KINGDOM

TMC, TTD, HIVE - TC

Stanford University,
University of California, Santa Cruz
University of California San Diego
California Institute of Technology
City of Hope National Medical Center

TMC

University of Alabama, Birmingham

NIH

Common Fund

TMC

Vanderbilt University

TMC

University of North Carolina, Chapel Hill

TMC

Texas Advanced Computing Center

TMC

University of Florida

HIVE - Tools, TMC

European Bioinformatics Institute
Wellcome Sanger Institute

The Human Body at Cellular Resolution: The NIH Human Biomolecular Atlas Program.

Snyder et al. *Nature*. 574, p. 187-192.

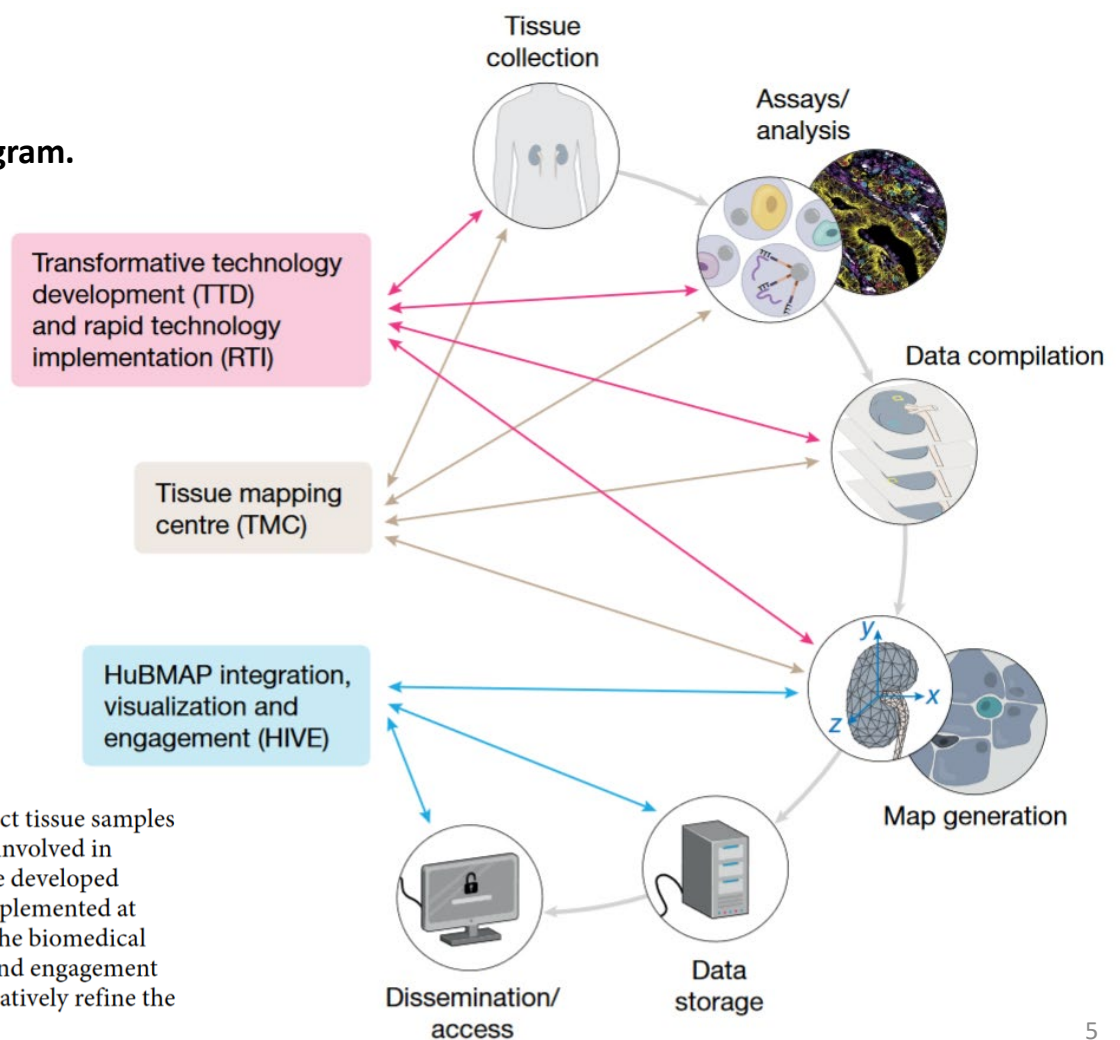


Fig. 1 | The HubMAP consortium. The TMCs will collect tissue samples and generate spatially resolved, single-cell data. Groups involved in TTD and RTI initiatives will develop emerging and more developed technologies, respectively; in later years, these will be implemented at scale. Data from all groups 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.

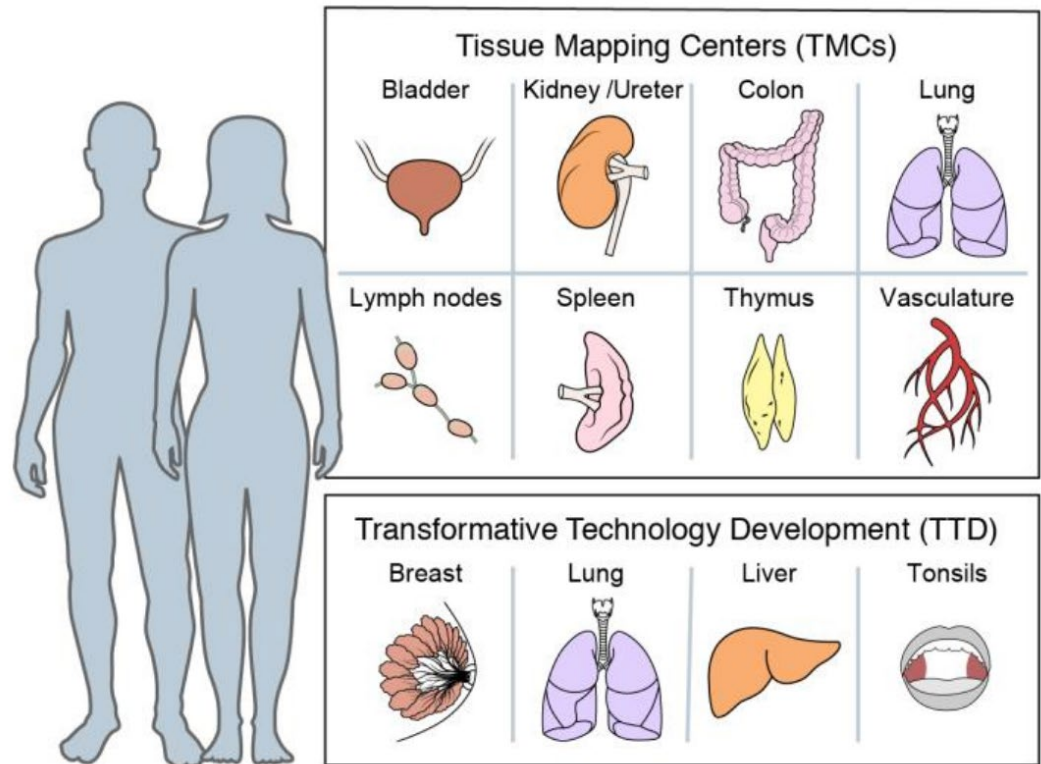


Fig. 2 | Key tissues and organs initially analysed by the consortium.

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.

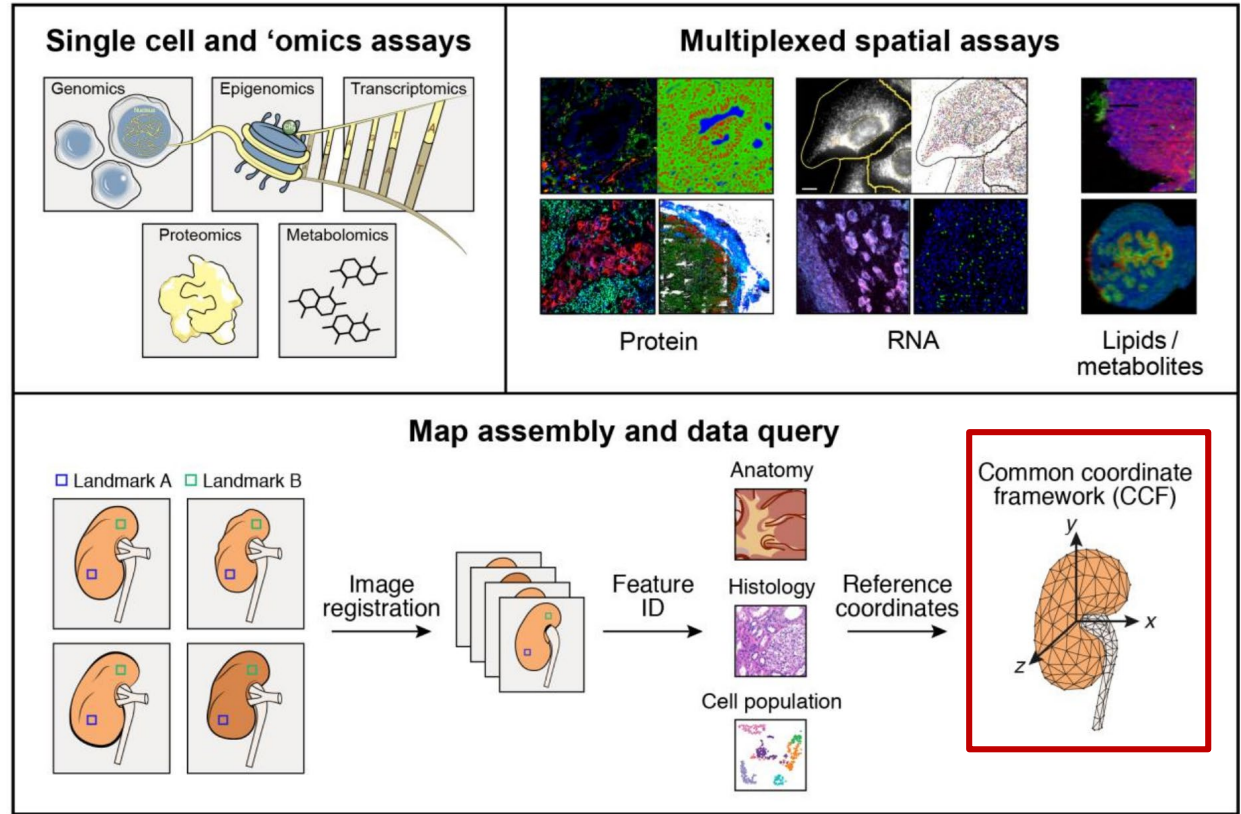


Fig. 3 | Map generation and assembly across cellular and spatial scales. HuBMAP aims to produce an atlas in which users can refer to a histological slide from a specific part of an organ and, in any given cell, understand its contents on multiple 'omic levels—genomic, epigenomic, transcriptomic, proteomic, 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.

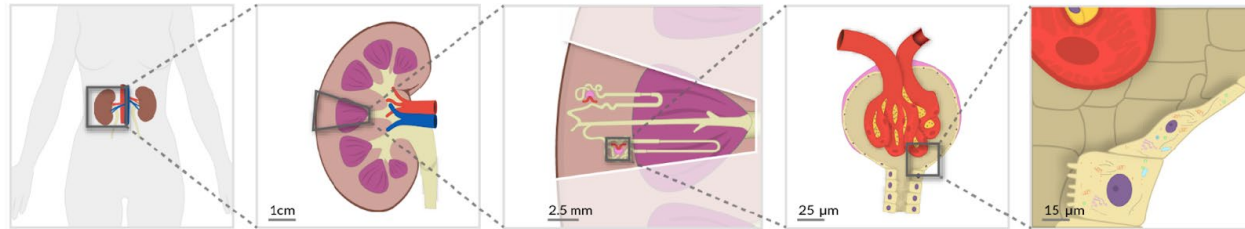


CCF ASCT+B Tables

CCF Requirements

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

Organ

- Renal capsule
- Renal pyramid
- Renal cortex
- Renal medulla
- Renal calyx
- Renal pelvis

Functional Tissue Unit

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

FTU Sub-structure(s)

- Bowman's capsule
- Glomerulus
- Efferent arteriole
- Afferent arteriole

Cellular

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

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

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 region	Sub structure/Sub region	Cell Type	Abbreviation	Subset of Marker Genes	Pertinent negatives/comments
Renal Corpuscle	Bowman's Capsule	Parietal epithelial cell	PEC	<i>CRB2*</i> , <i>CLDN1*</i>	
	Glomerulus	Podocyte	POD	<i>NPHS2*</i> , <i>PODXL*</i> , <i>NPHS1*</i>	
		Capillary Endothelial Cell	GC-EC	<i>EHD3*</i> , <i>EMCN*</i> , <i>HECW2*</i> , <i>FLT1*</i> , <i>AQP1*</i>	
		Mesangial Cell	MC	<i>POSTN*</i> , <i>PIEZO2*</i> , <i>ROBO1*</i> , <i>ITGA8*</i>	
Tubules	Proximal Tubule	Proximal Tubule Epithelial Cell (general)	PT	<i>CUBN*</i> , <i>LRF2*</i> , <i>SLC13A1*</i> , <i>ALDOB*</i> , <i>GATM*</i>	There is overlap among the segments
		Proximal Convoluted Tubule Epithelial Cell Segment 1	PT-S1	<i>SLC5A2*</i> , <i>SLC5A12*</i>	
		Proximal Tubule Epithelial Cell Segment 2	PT-S2	<i>SLC22A6*</i>	
		Proximal Tubule Cell Epithelial Segment 3	PT-S3	<i>PDZK1IP1*</i> , <i>MT1G*</i>	
	Loop of Henle, Thin Limb	Descending Thin Limb Cell (general)	DTL	<i>CRYAB*</i> , <i>VCAM1*</i> , <i>AQP1*</i> , <i>SPP1*</i>	<i>CLDN10</i> low
		Ascending Thin Limb Cell (general)	ATL	<i>CRYAB*</i> , <i>TACSTD2*</i> , <i>CLDN3*</i>	<i>AQP1</i> low to none
	Loop of Henle, Thick Limb	Thick Ascending Limb Cell (general)	TAL	<i>SLC12A1*</i> , <i>UMOD*</i>	<i>SLC12A3</i> low to none
		Cortex-TAL cell	C-TAL	<i>SLC12A1*</i> , <i>UMOD*</i>	
		Medulla-TAL cell	M-TAL	<i>SLC12A1*</i> , <i>UMOD*</i>	
		TAL-Macula <i>Densa</i> cell	TAL_MD	<i>NOS1*</i> , <i>SLC12A1*</i>	
Distal Convolution	Distal Convoluted Tubule Cell (general)	DCT	<i>SLC12A3*</i> , <i>TRPM6*</i>		
	DCT type 1 cell	DCT-1	<i>SLC12A3*</i> , <i>TRPM6</i>	<i>SLC8A1</i> , <i>HSD11B2</i> (low to none)	
	DCT type 2 cell	DCT-2	<i>SLC12A3*</i> , <i>SLC8A1*</i> , <i>HSD11B2</i>	Has CNT and DCT signature	
	Connecting Tubule	Connecting Tubule Cell (general)	CNT	<i>SLC8A1*</i> , <i>CALB1</i> , <i>TRPV5</i>	<i>SLC12A3</i> low to none. IC or PC without <i>SLC8A1</i> could be in the CNT structure
		CNT-Principal Cell	CNT-PC	<i>SLC8A1*</i> , <i>AQP2*</i> , <i>SCNN1G*</i>	
		CNT-Intercalated Cell	CNT-IC	<i>SLC8A1*</i> , <i>CA2</i> , <i>ATP6VOD2*</i>	
CNT-IC-A cell		CNT-IC-A	<i>SLC8A1*</i> , <i>SLC4A1*</i> , <i>SLC26A7*</i>		
	CNT-IC-B cell	CNT-IC-B	<i>SLC8A1*</i> , <i>SLC26A4*</i> , <i>SLC4A9*</i>		
Collecting Duct	Collecting duct (general) cell	CD	<i>GATA3*</i>	<i>GATA3</i> may be in subpopulation of DCT, CNT and <i>vSMC/P</i> . <i>SLC8A1</i> , <i>CALB1</i> , <i>TRPV5</i>	
	CD-PC (general)	CD-PC			
	C-CD-PC	C-CD-PC	<i>AQP2*</i> , <i>AQP3*</i> , <i>FXYP4*</i>		
	M-CD-PC	M-CD-PC	<i>SCNN1G*</i> , <i>GATA3*</i>		
	Outer medulla-CD-PC	OM-CD-PC			
	Inner Medulla-CD cell	IM-CD	<i>AQP2*</i> , <i>SLC14A2</i>		

Vessels	Endothelial Cells (non-glomerular)	Transitional PC-IC cell	<i>IRC</i> , <i>IC</i>	<i>FXYP4*</i> , <i>SLC4A9*</i> , <i>SLC26A7*</i>	(low to none); Low to No
		CD-IC (general) cell	CD-IC	<i>CA2</i> , <i>ATP6VOD2*</i>	<i>CALCA</i> and <i>KIT</i> in C-CD-IC-A. It may not be possible to assign IC or PC to <i>CNT</i> or CD structures without regional information of their source.
		CD-IC-A (general) cell	CD-IC-A	<i>SLC4A1</i> , <i>SLC26A7*</i> , <i>TMEM213*</i>	
		C-CD-IC-A cell	C-CD-IC-A	<i>SLC26A7*</i> , <i>SLC4A1*</i>	
		M-CD-IC-A cell	M-CD-IC-A	<i>SLC26A7*</i> , <i>SLC4A1*</i> , <i>KIT*</i> , <i>CALCA</i>	
		CD-IC-B (general) cell	CD-IC-B		
		C-CD-IC-B cell	C-CD-IC-B	<i>SLC4A9*</i> , <i>SLC26A4*</i>	
		M-CD-IC-B cell	M-CD-IC-B		
		EC-IC-B cell	EC-IC-B		
		EC-IC-B cell	EC-IC-B		
Vessels	Endothelial Cells (non-glomerular)	Endothelial Cell (general)	EC	<i>EMCN*</i> , <i>PECAM1*</i> , <i>FLT1*</i>	
		EC-Afferent/Effluent Arteriole	EC-AEA	<i>SERPINE2*</i> , <i>TM6SF1*</i>	likely <i>PALMD</i>
		EC-Peritubular capillaries	EC-PTC	<i>PLVAP*</i>	
		EC-Descending Vasa Recta	EC-DVR	<i>TM6SF1*</i> , <i>PALMD</i>	
		EC-Ascending Vasa Recta	EC-AVR	<i>DNASEIL3*</i>	low to none
		EC-Lymphatics	EC-LYM	<i>MMRN1*</i> , <i>PROX1</i>	
Structure/R region	Sub structure/Sub region	Cell Type	Abbreviation	Subset of Marker Genes	Pertinent negatives/comments
Interstitium	Stroma (non-glomerular)	Vascular Smooth Muscle/Pericyte (general)	<i>vSMC/P</i>	<i>TAGLN*</i> , <i>ACTA2*</i> , <i>MYH11*</i> , <i>NTRK3</i> , <i>MCAM</i>	
		<i>vSMC/P</i> -Renin	<i>vSMC/P</i> -REN	<i>REN</i>	
		Fibroblast	FIB	<i>DCN*</i> , <i>ZEB2</i> , <i>C7</i> , <i>LUM</i>	
	Immune	Macrophages-Resident	MAC-R	<i>CD163*</i> , <i>IL7R*</i>	
		Macrophage	MAC	<i>ST00A9</i>	
		Natural Killer Cell	NKG7		
		Dendritic Cell	DC	<i>APOE</i>	
		Monocyte	MON	<i>CTQA</i> , <i>HLA-DRA</i>	
		T lymphocyte (general)	T	<i>CD3</i>	
		T Cytotoxic	T-CYT	<i>GZMA</i>	
		B lymphocyte	B	<i>IGJ</i>	

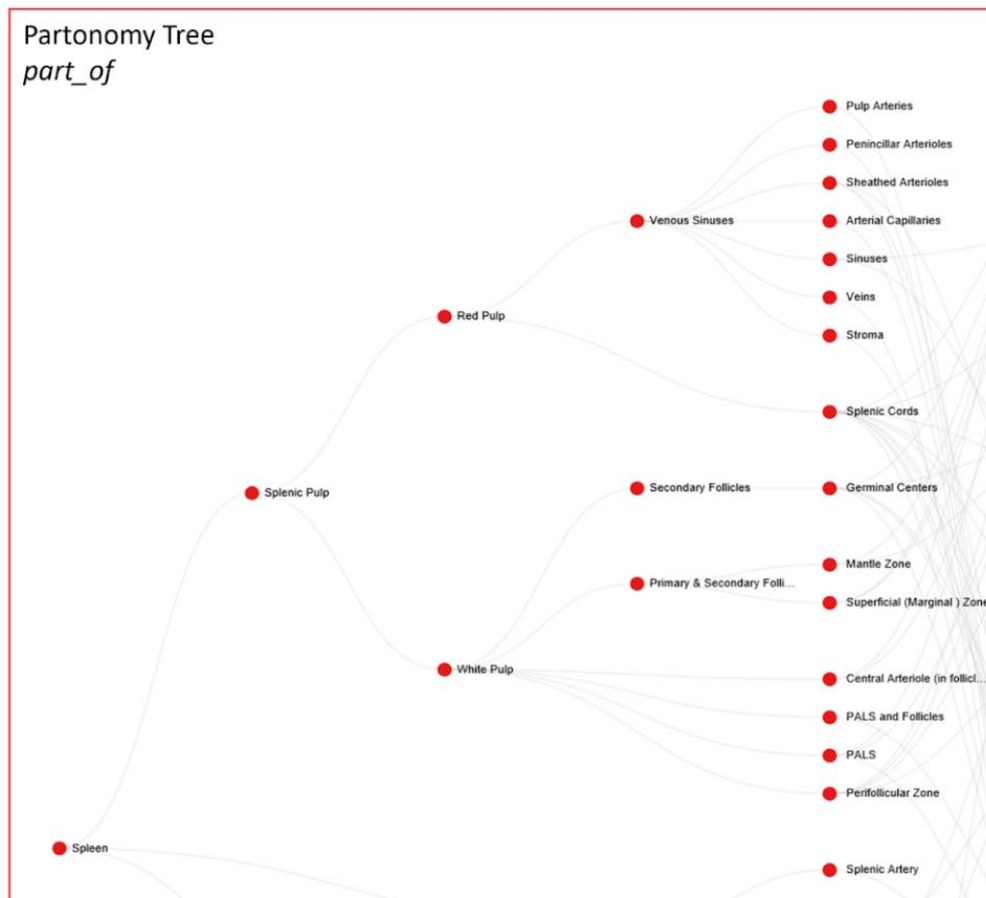
El-Achkar et al. A Multimodal and Integrated Approach to Interrogate Human Kidney Biopsies with Rigor and Reproducibility: The Kidney Precision Medicine Project. bioRxiv. 2019, Updated Aug 2020. doi:10.1101/828665

Anatomical Structures (AS)

Cell Types (CT)

Biomarkers (B)

Partonomy Tree
part_of



Bimodal network describing which CT are located_in what AS

Typology Tree
is_a

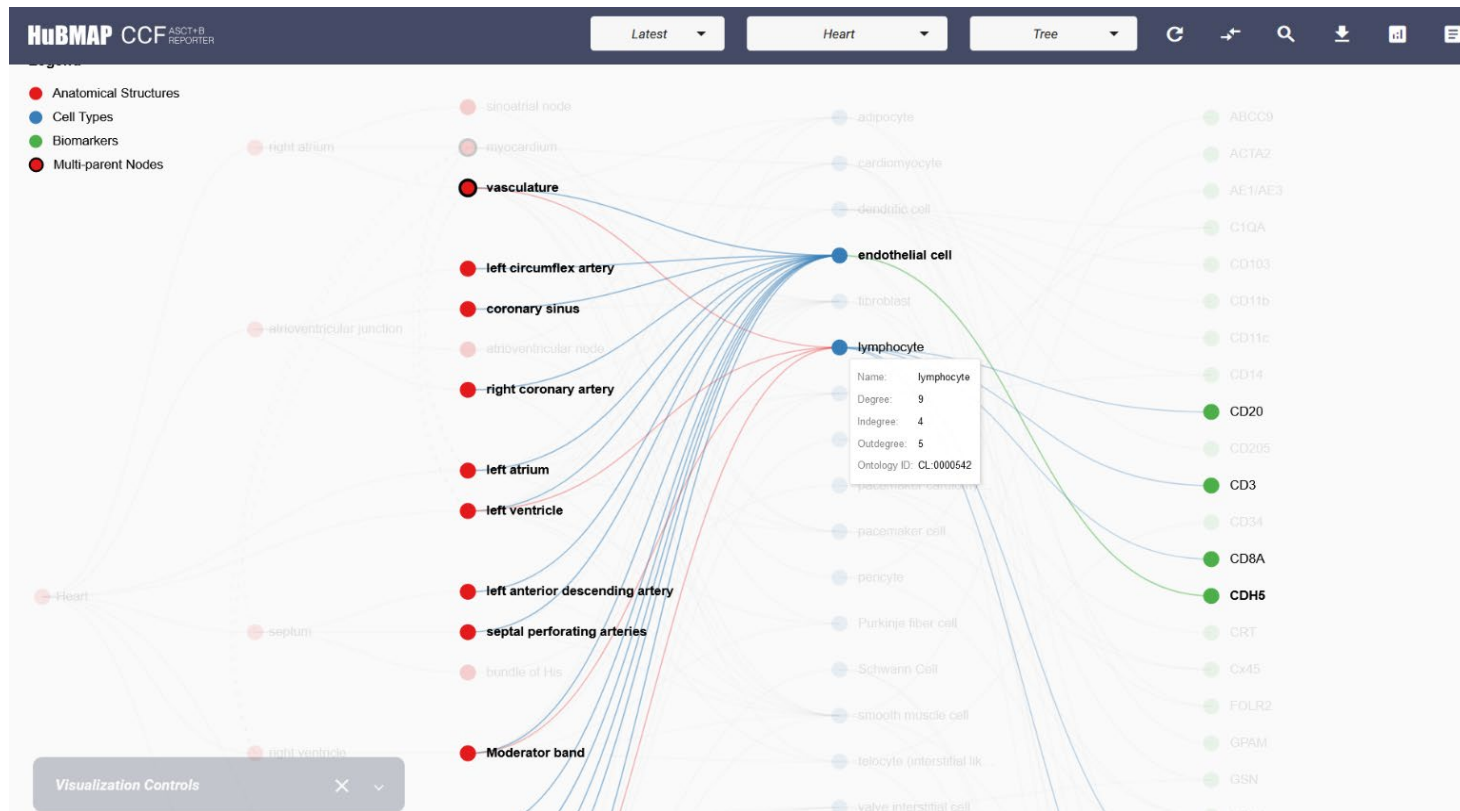
- adventitial stromal cell
- B cell
- Dendritic cell
- Endothelial
- Endothelial cell
- Erythrocytes
- fibroblast
- Fibroblastic reticular cell
- Follicular Dendritic cell
- Granulocytes
- Littoral cell
- Lymphatic endothelium
- macrophage
- Monocytes
- Myofibroblast
- neurons
- NK cell
- Plasma cell
- Plasmablasts
- Platelets

Bimodal network describing which B characterize what CT

BG - Genes
BP - Proteins

- CD10
- CD11b
- CD11c
- CD138
- CD14
- CD141
- CD15
- CD163
- CD19
- CD20
- CD21
- CD22
- CD23+
- CD235a
- CD27
- CD27-
- CD271
- CD271-
- CD3
- CD3-
- CD31
- CD34
- CD4
- CD4 (helper)
- CD41

CCF ASCT+B Reporter UI



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

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).

ASCT Table

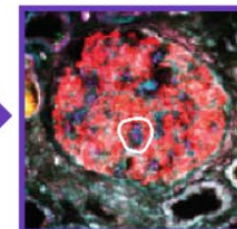
Structure/Region	Sub structure/Sub region	Cell Type
Renal Corpuscle	Bowman's (glomerular) Capsule/parietal layer	Parietal epithelial Cell
	Bowman's (glomerular) Capsule/visceral layer	Podocyte
	Glomerular Tuft	Capillary Endothelial Cell
Tubules	Proximal Tubule	Proximal Tubule Epithelial Cell (general)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

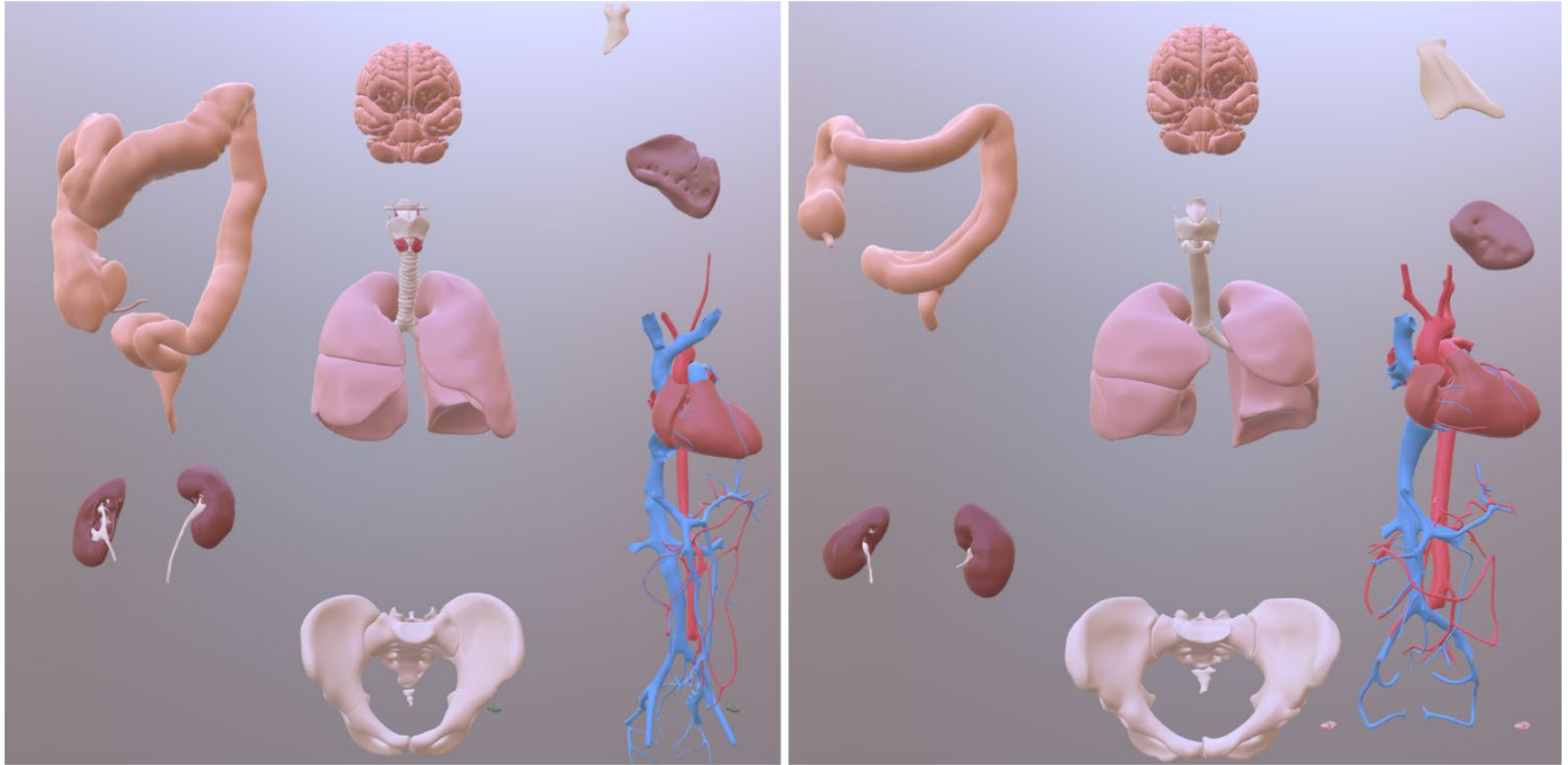
Ontology

Anatomical Structures Partonomy
 kidney
 kidney capsule
 cortex of kidney
 outer cortex of kidney
 renal medulla

Cell Types Ontology
 connective tissue cell
 pericyte cell
 mesangial cell
 extraglomerular mesangial cell
 glomerular mesangial cell

3D Reference Object Library





Overview of CCF 3D Reference Models

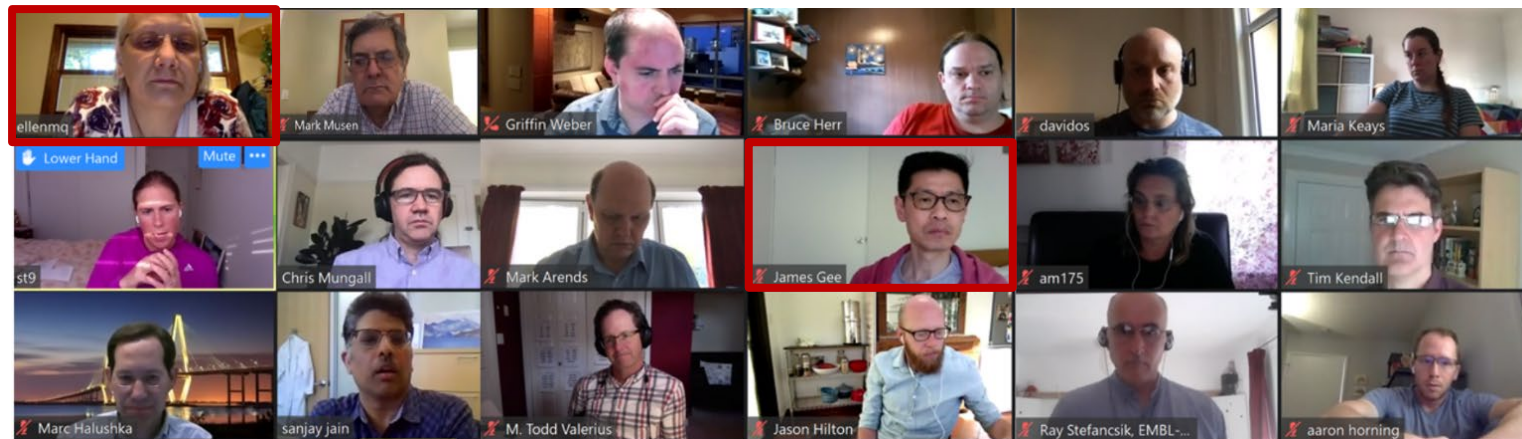
ASCT+B Table Working Group

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 [WG Charter](#).

Upcoming meetings in **2021**: April 7, May 5, 11a-noon ET.

Please [register](#) 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>

Consortium

Allen Brain Atlas

BICCN

CZI

EU H2020

GTEX

GUDMAP

Gut Cell Atlas

HTAN

HuBMAP

KPMP

LungMAP

MRC

RBK

SPARC

TCGA

Wellcome

Size

#Links



Color

NIH

HCA

Organ

Adrenal Gland

Bladder

Bone Marrow & Blood

6 Brain

6 Breast

Cervix

Decidua

Eye

Gonads

Heart

6 Intestine, Large

Intestine, Small

9 Kidney

Liver

10 Lung

Lymph Node

Ovaries

Pancreas

Placenta

Prostate

Skin

Spinal Cord

Spleen

Stomach

Testes

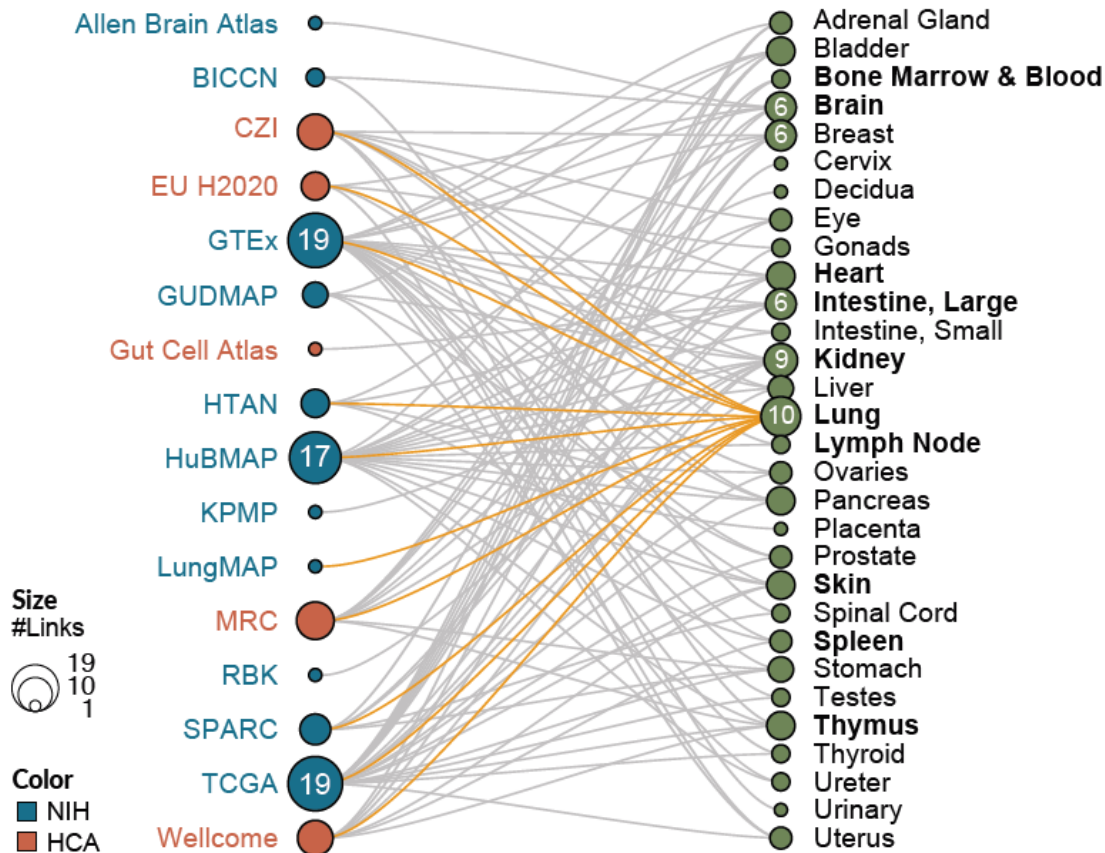
Thymus

Thyroid

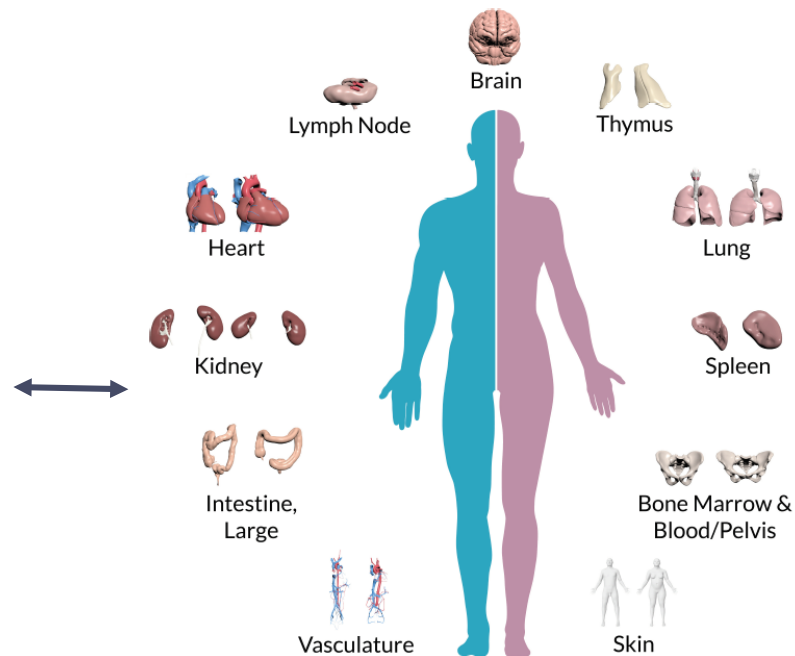
Ureter

Urinary

Uterus



Organ	#AS	#CT	#B Total	#BG	#BP	#AS-AS	#AS-CT	#CT-B
Bone Marrow & Blood/Pelvis	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
Totals:	1,534	622	2,154	1,492	632	3,393	14,987	3,580



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

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



CCF Registration User Interface (RUI)



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., mapping).

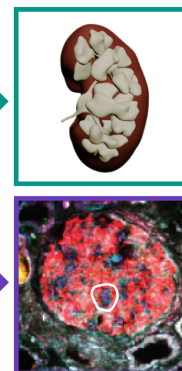
ASCT Table

Structure/Region	Sub structure/Sub region	Cell Type	
Renal Corpuscle	Bowman's Capsule	Parietal epithelial Cell	
	Glomerulus	Podocyte Capillary Endothelial Cell Mesangial Cell	
Proximal Tubule	Loop of Henle, Thin Limb	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, Thick Limb	Descending Thin Limb Cell (general) Ascending Thin Limb Cell (general) Thick Ascending Limb Cell (general)
			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

Ontology

Cell Type
<i>Anatomical Structures Partonomy</i>
kidney
kidney capsule
cortex of kidney
outer cortex of kidney
renal medulla
<i>Cell Types Ontology</i>
connective tissue cell
pericyte cell
mesangial cell
extraglomerular mesangial cell
glomerular mesangial cell

3D Reference Object Library



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

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

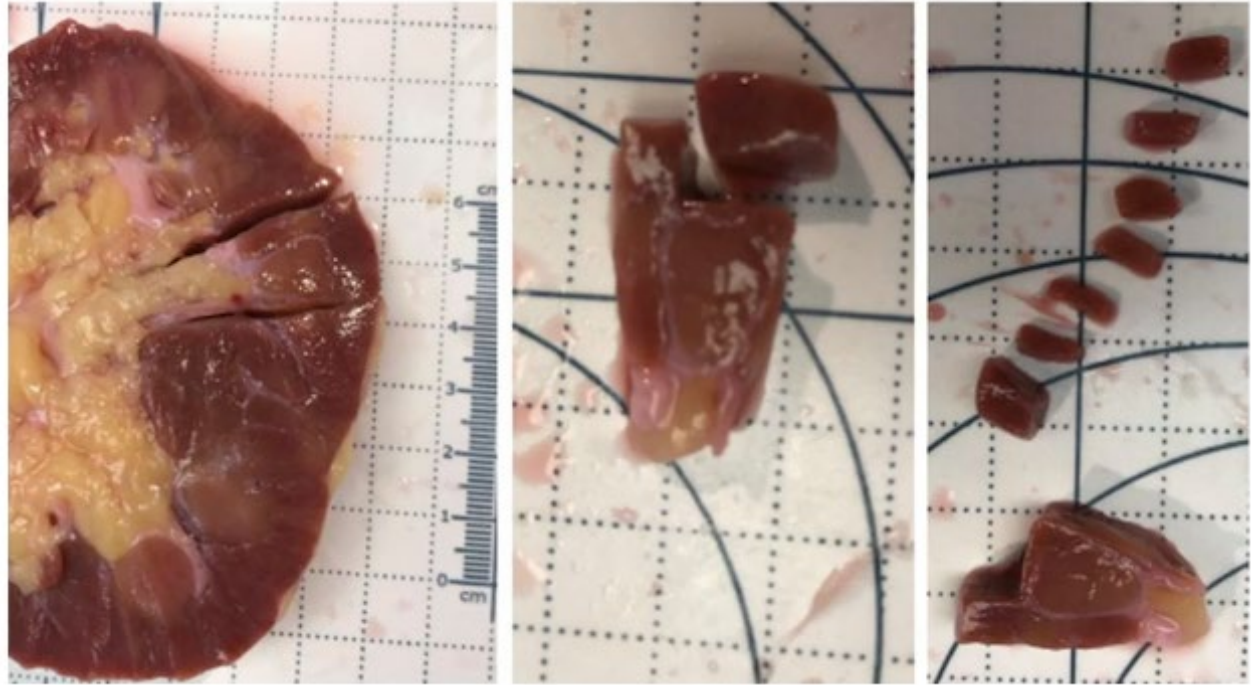
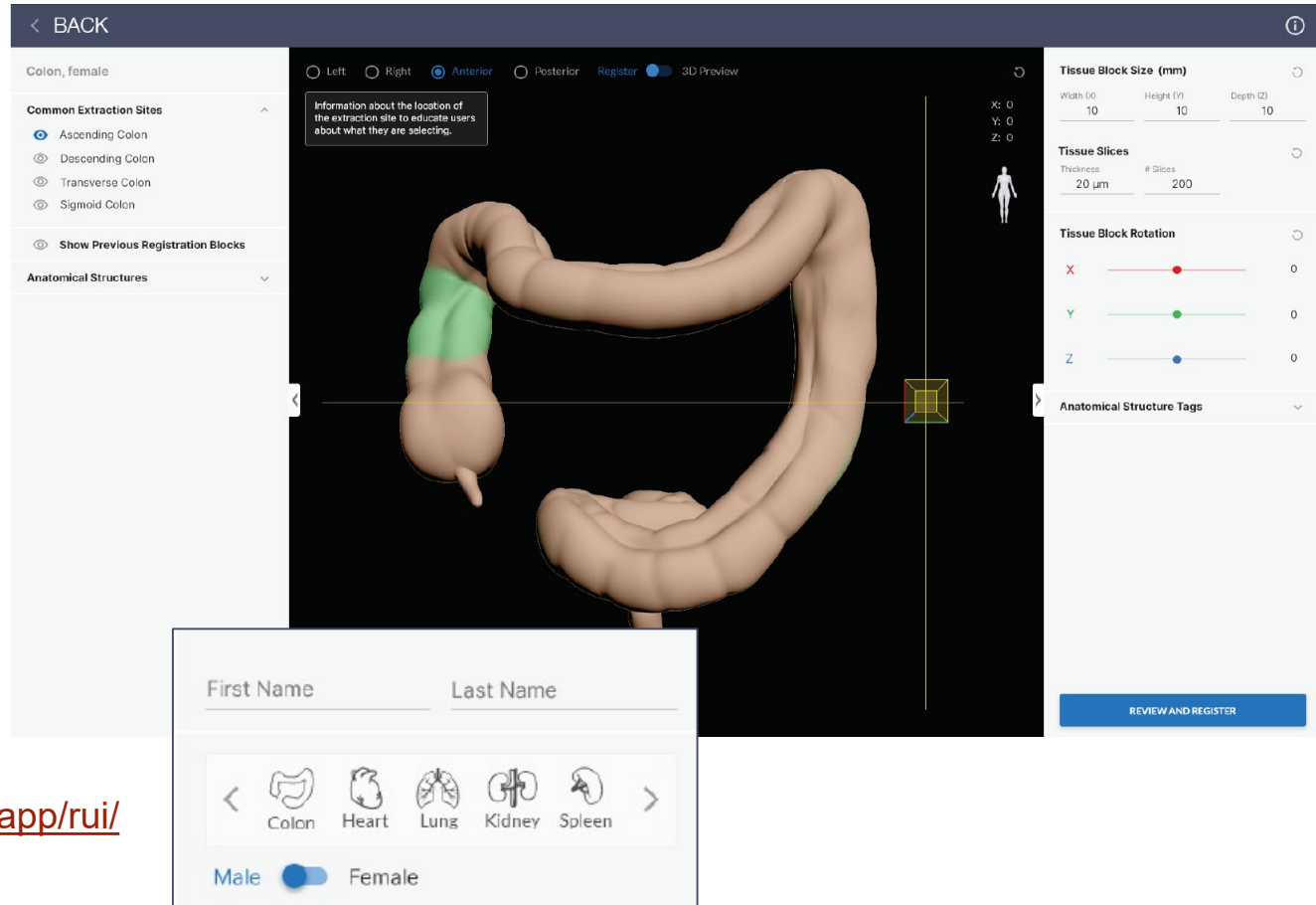


Image provided by Sanjay Jain, TMC-UCSD

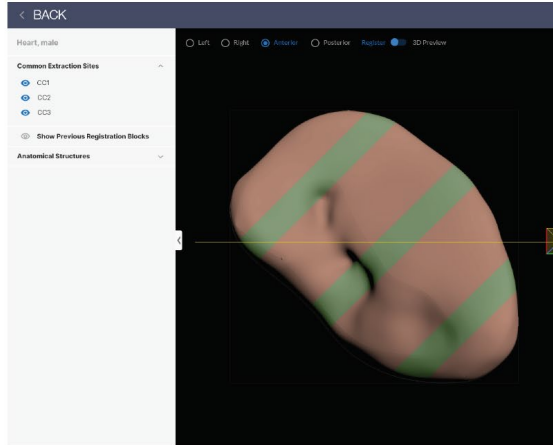
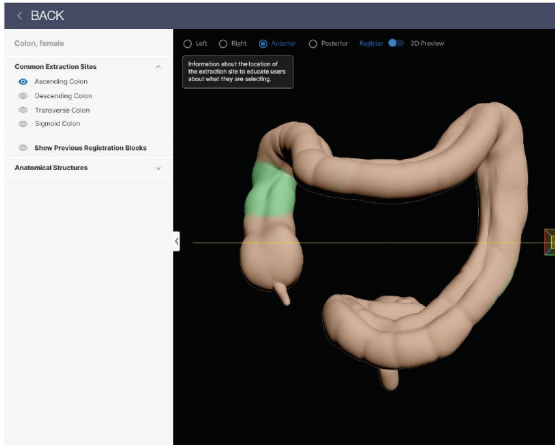
CCF Registration User Interface (RUI) v1.0.0

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/>



Kidney

- Bisection Line

Spleen

- CC1
- CC2
- CC3

Colon

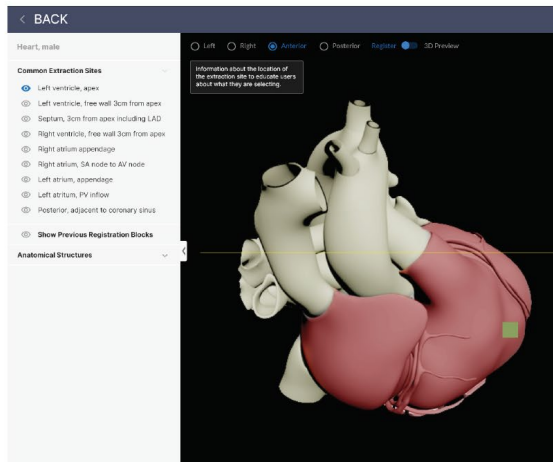
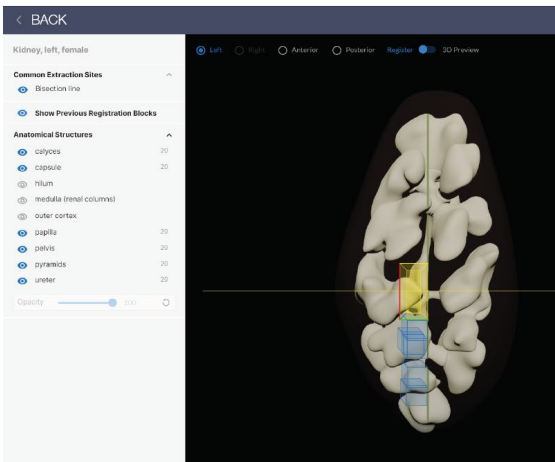
- Ascending Colon
- Descending Colon
- Transverse Colon
- Sigmoid Colon

Heart

- Left atrium, appendage
- Left atrium, PV inflow
- Left ventricle, apex
- Left ventricle, free wall 3cm from apex
- Septum, 3cm from apex including LAD
- Posterior, adjacent to coronary sinus
- Right atrium appendage
- Right atrium, AV (atrioventricular) node
- Right atrium, SA (sinoatrial) node
- Right ventricle, free wall 3cm from apex

Extraction Site Mapping

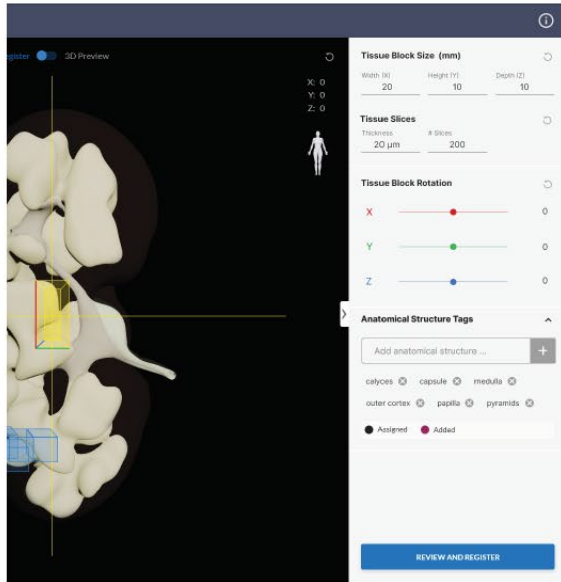
- 7
- 8
- 1
- 2
- 3
- 9
- 5
- 6a
- 6b
- 4



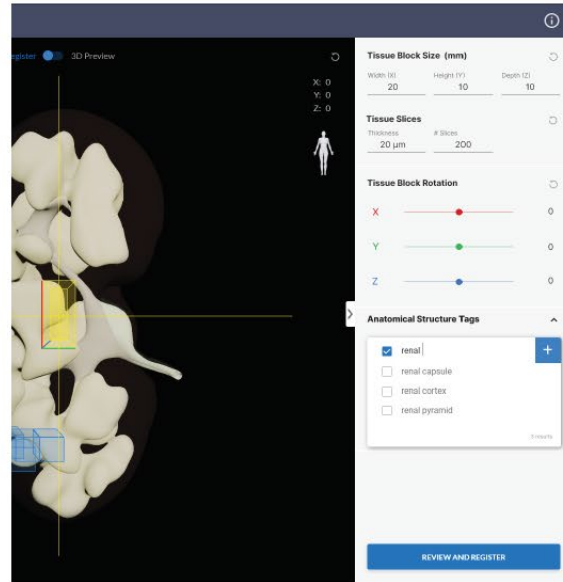
For the first HuBMAP portal release, 48 tissue blocks were registered.

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

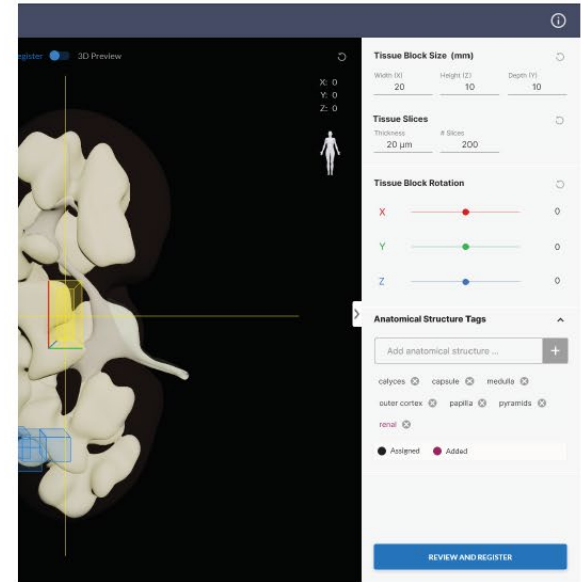
Collision when Tissue Block hits Reference Organ




Tag Search behavior



Custom tag added to list



HuBMAP Upload Portal



BOES@pitt.edu | [Edit Profile](#) [Logout](#)

HuBMAP Display ID Generator

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

Source HuBMAP ID * [Look up](#)

HuBMAP display id: **TEST0005-RK**

type: Organ name:

Organ Type: Kidney (Right)

HuBMAP ID: HBM:264-TTJ-798

Description:

Tissue Sample Type *

Protocol 1

protocols.io DOI *

Protocol document * [Browse](#)

doc, docx and pdf files only

[Add Protocol](#)

Generate IDs for multiple FFPE block samples


Lab IDs and Sample Locations can be assigned on the next screen after generating the HuBMAP IDs

Description

Metadata [+ Add Metadata](#)

Image [+ Add Image](#) Make sure any uploaded images are de-identified

[Generate ID](#) [Cancel](#)



BOES@pitt.edu | [Edit Profile](#) [Logout](#)

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 TEST0005-RK-8

Type: FFPE block

[Assign Lab IDs and Sample Locations](#)

[Return to Search](#)

Assign Lab IDs and Sample Location

	Lab Sample Id	Register Location	SuccessView JSON
TEST0005-RK-6	<input type="text" value="TEST0005-RK-6-A"/>	Register Location	?
TEST0005-RK-7	<input type="text"/>	Register Location	?
TEST0005-RK-8	<input type="text"/>	Register Location	?

[Submit](#)

[close](#)

Implemented by the HIVE IEC

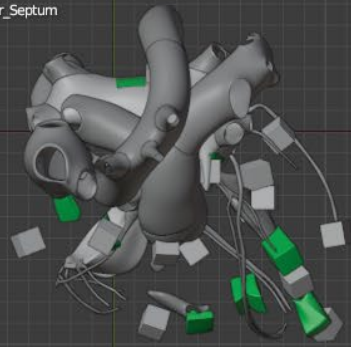
CCF Registration User Interface (RUI)

The screenshot displays the CCF Registration User Interface (RUI) for the HuBMAP project. The interface is divided into several sections:

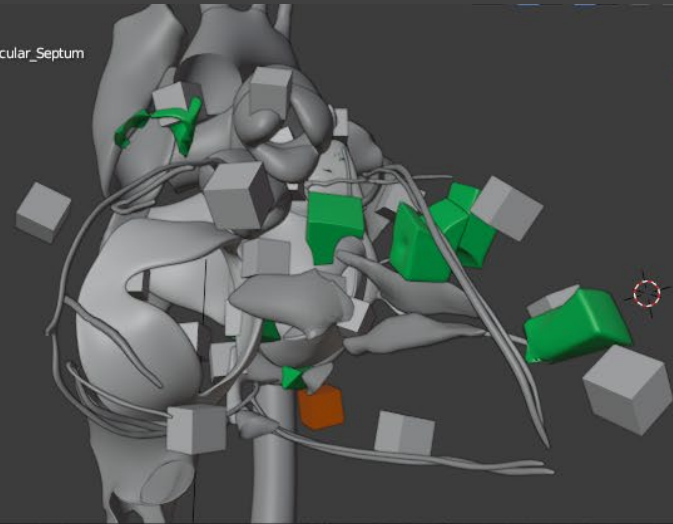
- Header:** "HuBMAP CCF REGISTRATION USER INTERFACE" with a help icon.
- User Information:** Fields for "First Name" (Andreas) and "Last Name" (Bueckle).
- Organ Selection:** Icons for Colon, Heart, Kidney, Spleen, and Stomach. The Kidney is selected.
- Gender and Side:** Radio buttons for "Left", "Right", "Anterior" (selected), and "Posterior". A "Register" toggle is on, and "3D Preview" is also on.
- Anatomical Structures List:**
 - Common Extraction Sites: "Show Previous Registration Blocks"
 - Anatomical Structures:
 - kidney capsule
 - cortex of kidney
 - outer cortex of kidney
 - renal column (highlighted)
 - hilum of kidney
 - renal medulla
 - renal papilla
 - renal pyramid
- 3D View:** A central 3D model of a kidney with a blue rectangular registration block overlaid on it. A mouse cursor is pointing at the block. A small human figure icon is visible on the right side of the view.
- Coordinates:** X: 80, Y: 69, Z: 40.
- Configuration Panels (Right Side):**
 - Tissue Block Size (mm):** Width (X) 8, Height (Y) 6, Depth (Z) 10.
 - Tissue Slices:** Thickness and # Slices fields.
 - Tissue Block Rotation:** Sliders for X, Y, and Z axes, all set to 0.
 - Anatomical Structure Tags:** "Add Anatomical Structures ..." field with a plus icon. Legend: Assigned (black dot), Added (pink dot).
 - REVIEW AND DOWNLOAD** button.

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

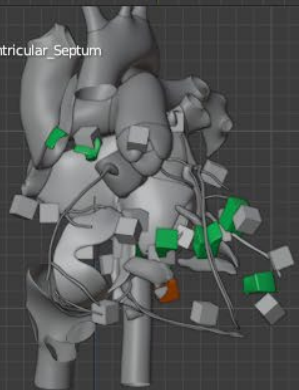
Top Orthographic
(3) HuBMAP | VHM_Interventricular_Septum
Centimeters



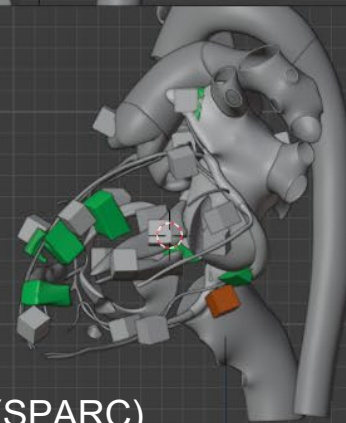
User Perspective
(3) HuBMAP | VHM_Interventricular_Septum



Front Orthographic
(3) HuBMAP | VHM_Interventricular_Septum
Centimeters




Right Orthographic
(3) HuBMAP | VHM_Interventricular_Septum
Centimeters




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

**Public private
partnership panel** with
NIH, Google, Broad, Lilly
and potentially Roche




InnovationDigi 1,393
teams




HuBMAP
Human BioMolecular Atlas Program


Hacking the Kidney Hackathon



 PARTICIPATION OPENS
NOV 5TH, 10:00 AM EST

**TOTAL PRIZE MONEY \$60,000 TO BE AWARDED TO
THE WINNING TEAMS!**

OUR SPONSORS

Google **Deloitte**  **CAS**
A DIVISION OF THE
AMERICAN CHEMICAL SOCIETY

 **Roche**

 **Pistoia Alliance**  **Maven Wave** **DEERFIELD**
Advancing Healthcare®

<https://innovationdigi.com/hubmap-hackathon>



CCF Exploration User Interface (EUI)



CCF Exploration User Interface (EUI)

HuBMAP Sex: Both Age: 1-110 BMI: 13-83 Login

Search ontology terms ...

- body
 - heart
 - lung
 - kidney
 - right kidney
 - left kidney
 - kidney capsule
 - cortex of kidney
 - renal medulla
 - renal column
 - renal pyramid
 - hilum of kidney
 - kidney interstitium
 - kidney calyx
 - renal pelvis
 - ureter
 - renal papilla
 - renal fat pad
 - nephron

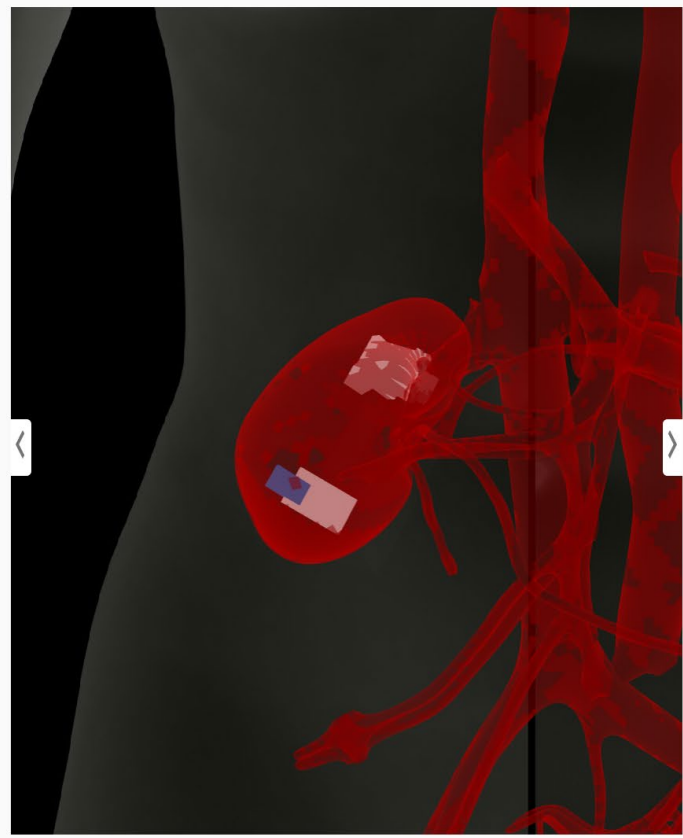
body

- 2 Centers
- 27 Donors
- 41 Samples

	Female, Age 14, BMI 14.7 HBM894.MPVN.828 TMC-Florida First case collected. Incomplete d...	
	Male, Age 18, BMI 27.1 HBM436.GHWX.449 TMC-Florida section is 190um from block surface	
	Male, Age 56, BMI 32.5 HBM696.XTVL.498 TMC-Vanderbilt Age 56, White Male	
	Male, Age 53, BMI 26.5 HBM652.VRLD.292 TMC-Vanderbilt Age 53, Black Male	
	Male, Age 58, BMI 22.0 HBM477.CJKM.888 TMC-Vanderbilt 107-111	
	Male, Age 18, BMI 25.5 HBM473.VKCM.878 TMC-Florida section is 255um from block surface	
	Male, Age 55, BMI 25.4 HBM824.BLXF.883 TMC-Vanderbilt 13-16	



















Search ontology terms ... 

- body
 - heart
 - lung
 - kidney
 - right kidney
 - left kidney
 - kidney capsule
 - cortex of kidney
 - renal medulla
 - renal column
 - renal pyramid
 - hilum of kidney
 - kidney interstitium
 - kidney calyx
 - major calyx
 - minor calyx
 - renal pelvis
 - ureter
 - renal papilla
 - renal fat pad
 - nephron
 - spleen
 - colon



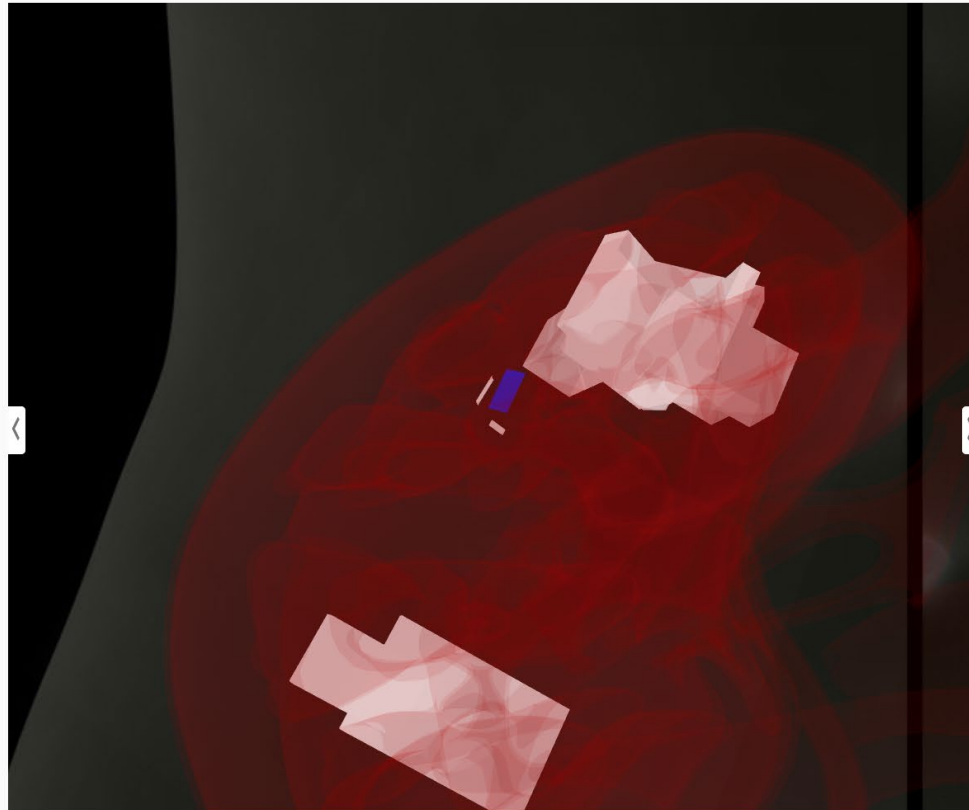
body

- 1 Centers
- 9 Donors
- 40 Samples

	Male, Age 55, BMI 25.4 HBM695 RTLJ.484 TMC-Vanderbilt 13-16	
	Male, Age 21, BMI 21.8 HBM634 MIMGK.572 TMC-Vanderbilt Age 21 , White Male, Trauma Patient	
	Female, Age 44, BMI 28.0 HBM457 NNQN.252 TMC-Vanderbilt Age 44, white female.	
	Female, Age 44, BMI 28.0 HBM465 VKHL.532 TMC-Vanderbilt Age 44, white female.	
	Male, Age 21, BMI 21.8 HBM693 HFFJ.752 TMC-Vanderbilt Age 21 , White Male, Trauma Patient	
	Female, Age 58, BMI 23.0 HBM536 LDTZ.757 TMC-Vanderbilt Age 58, White Female	
	Male, Age 48, BMI 35.3 HBM334 GCCX.874 TMC-Vanderbilt Age 48, White Male	
	Male, Age 31, BMI 32.6 HBM776 PKJF.786 TMC-Vanderbilt Age 21, White Male	
	Female, Age 66, BMI 31.3 HBM284 TRCV.726	












Search ontology terms ... 

- body
 - heart
 - lung
 - kidney
 - right kidney
 - left kidney
 - kidney capsule
 - cortex of kidney
 - outer cortex of kidney
 - renal medulla
 - outer medulla
 - inner medulla
 - renal column
 - renal pyramid
 - hilum of kidney
 - kidney interstitium
 - kidney calyx
 - major calyx
 - minor calyx
 - renal pelvis
 - ureter
 - renal papilla
 - renal fat pad
 - nephron
 - spleen
 - colon
 - small intestine

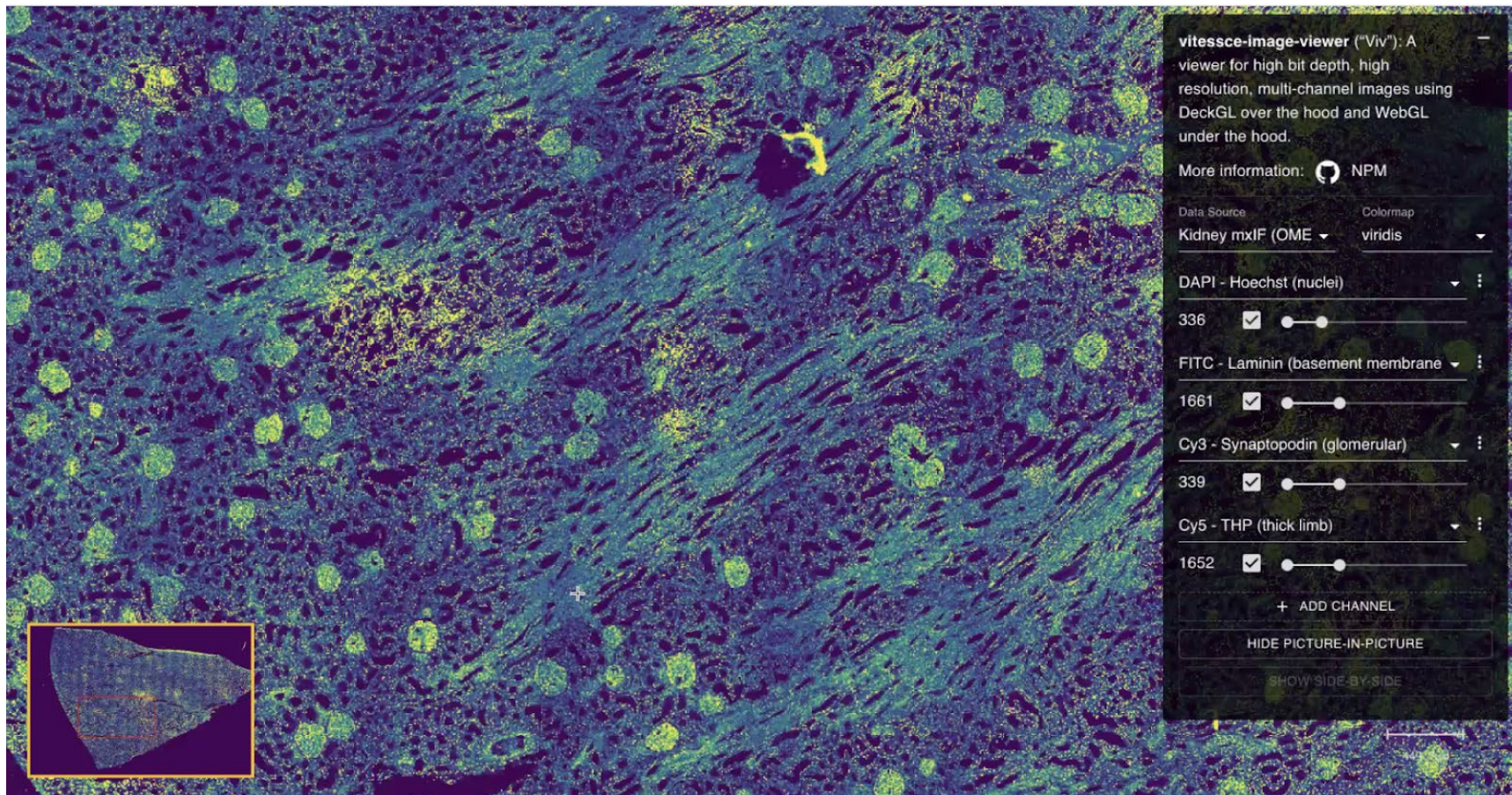


body

2 Centers
9 Donors
14 Samples

- 
CoverNephrectomy
 10.1016/j.jrst.2017.07.006
 KPMP-IJOSU
 Isolated as a part of a kidney st...
- 
Patient B Cortical biopsy
 10.1681/ASN.2016091027
 KPMP-IJOSU
 Biopsy from Nephrology bioban...
- 
Patient A Cortical biopsy
 10.1681/ASN.2016091027
 KPMP-IJOSU
 Biopsy from Nephrology bioban...
- 
Male, Age 55, BMI 25.4
 HBM824.BLXF.883
 TMC-Vanderbilt
 13-16
- 
Female, Age 66, BMI 31.3
 HBM554.ZRCG.496
 TMC-Vanderbilt
 21-24
- 
Female, Age 58, BMI 23.0
 HBM926.VBJV.597
 TMC-Vanderbilt
 Age 58, White Female
- 
Male, Age 62, BMI 34.9
 HBM947.VLDP.894
 TMC-Vanderbilt
 Kidneys 153-156
- 
Female, Age 44, BMI 28.0
 HBM457.NNQN.252
 TMC-Vanderbilt
 Age 44, white female.
- 
Male, Age 21, BMI 21.8
 HBM693.HFJ.752
 TMC-Vanderbilt
 Age 21, White Male, Trauma Pat...
- 
Female, Age 58, BMI 23.0
 HBM536.LDTZ.757
 TMC-Vanderbilt
 Age 58, White Female
- 
Male, Age 48, BMI 35.3

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



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

Human Reference Atlas CCF: Checklist

In support of Common Coordinate Framework (CCF) design (see [CCF Portal](#)):

1. Make sure the Anatomical Structures, Cell Types, and Biomarkers (ASCT+B) that you use/submit are listed in the [ASCT+B tables](#). The tables are authored and reviewed by an international team of anatomists, pathologists, physicians, and other experts, see this [SOP](#).
2. Spatially register all tissue samples using the CCF Registration User Interface (RUI) in the Ingest Portal. End of October 2020, kidney, spleen, heart, colon registration are supported. For other organs, see [SOP](#).
3. After submitting data, review data in the [CCF Exploration User Interface](#) and make sure spatial, semantic, and other metadata are correct.
4. For functional tissue unit (FTU) segmentation, submit a list of FTUs for your organ(s) and make sure FTU names and all relevant cell types (CT) are captured in the ASCT+B table. Use assays/biomarkers (B) that make it possible to identify FTUs—initially manually, later automatically. Submit tissue with 1000 FTUs manually identified FTUs.
5. In support of the [Vasculature-based CCF](#), provide cell segmentation data for blood vessels and different cell types.

For questions, email infoccf@indiana.edu.



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



HuBMAP
HUMAN BIOMOLECULAR ATLAS PROJECT

Visible Human
MOOC

HuBMAP Visible Human MOOC (VHMOOC)

Started Aug 4, 2020

[GO TO CANVAS COURSE](#)

You are enrolled.



INDIANA UNIVERSITY

Course Introduction

This 10h course introduces the HuBMAP project which aims to create an open, global reference atlas of the human body at the cellular level. Among others, the course describes the compilation 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 asynchronously to fit busy schedules. If you have questions or experience issues during registration, please email cnsctr@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
- Ontology, 3D Reference Objects, and User Interfaces
- HuBMAP Portal Design and Usage

Meet the Instructors



Katy Börner, Victor H. Yngve Distinguished Professor of Engineering and Information Science. Founding Director of the Cyberinfrastructure for Network Science Center at Indiana University.



Ellen M. Quardokus, staff in the Chemistry Department and research scientist, Cyberinfrastructure for Network Science Center, SICE with expertise in molecular biology, microscopy, anatomy, and interdisciplinary communication.




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

 Length: 10 hours

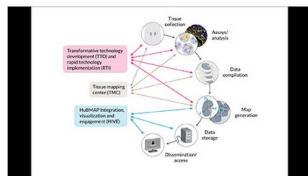
 Department: Cyberinfrastructure Network Science

 Credit: None

 Audience: Biomedical students and professionals interested in single-cell tissue analysis and visualization

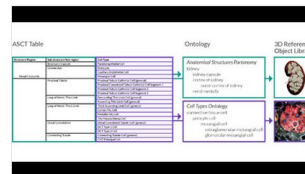
<https://expand.iu.edu/browse/sice/cns/courses/hubmap-visible-human-mooc>

1st HuBMAP Portal Release (Oct. 2020)



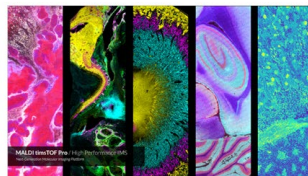
HuBMAP Overview

- Project Goals, Setup, and Ambitions



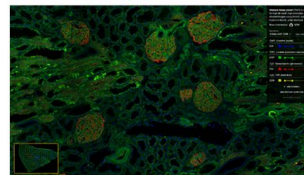
CCF Ontology, 3D Reference Objects, and User Interfaces

- Creating an Atlas of the Human Body



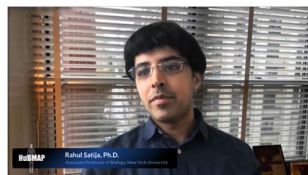
Tissue Data Acquisition and Analysis

- Behind the Scenes at Vanderbilt University



Portal Design and Usage

- Datasets and Software in the 1st HuBMAP Portal Release



Biomolecular Data Harmonization

- An Introduction to Seurat



Open Consent Your Data

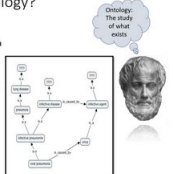
- In Support of Research

2nd HuBMAP Portal Release (Dec. 2020)

What is an Ontology?

A data structure that specifies, for a given application area,

- Entities
- Properties of entities
- Relationships among entities



Ontologies 101

- A gentle introduction on how to use ontologies to organize the world.



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

- What are ASCT+B tables and how they are used.

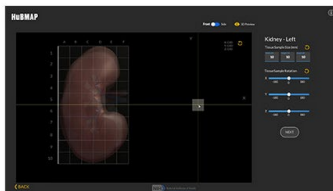
Forthcoming

- CODEX Data and Cell Segmentation by Gary Nolan
- Portal Design and Usage (Summer 2021 Update)

Learning Module Example:

CCF Ontology, 3D Reference Objects, and User Interfaces—Creating an Atlas of the Human Body

Videos



Registration User Interface (RUI)

- [RUI Application](#) ↗
- [RUI Intro Video](#) ↗



Exploration User Interface (EUI)

- [EUI Application](#) ↗
- [EUI Intro Video](#) ↗



NLM 3D

- [Interview with Kristen Browne](#) ↗

Explore 3D Reference Organs

Started: Aug 30, 2020 at 11:30pm

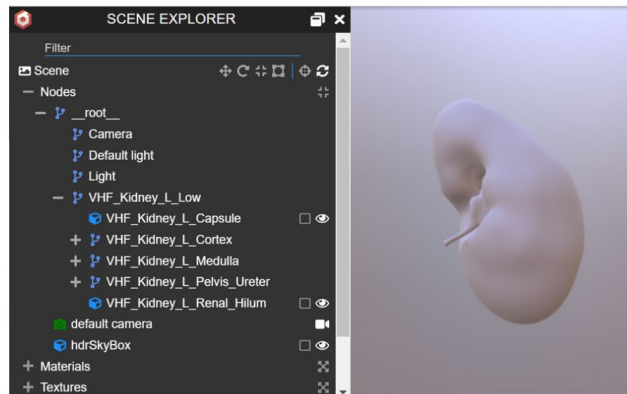
Quiz Instructions

Two 3D reference organs (kidney and spleen) have been made freely available as part of the 1st HuBMAP Portal Release.

The 3D reference objects files are provided in the GLB format, a binary form of the nested Graphics Library Transmission Format (<https://www.khronos.org/gltf/>). These files can be viewed and explored using free web browser, **Babylon.js** (<https://sandbox.babylonjs.com>). If you are a programmer, note that these files can also be accessed programmatically via API-neutral runtime asset delivery of 3D scenes and models using the JSON standard.

To explore these 3D models in a web browser:

1. First, visit the Hubmap Github project source objects (https://github.com/hubmapconsortium/hubmap-ontology/tree/master/source_objects), and download the GLB file for left female kidney (VHF_Kidney_L_Low.glb, 96KB).
2. Next, visit the **Babylon.js** website and view the 3D kidney by dragging and dropping the GLB file into the browser.
3. In the Scene Explorer on left, click on + symbol to expand Nodes, root, VHF_Kidney_L_Low and other subtrees. Click on eye symbol to turn different parts of the 3D kidney model on/off. Click on square to turn on/off the bounding box (i.e., smallest 3D volume in which all object points lie) for each anatomical structure. To see inner structures, turn outer structures off.



While you explore the kidney, make sure to record the number of renal pyramids for the left female kidney, and report back your finding in the self-check quiz below.

Register Tissue Block via RUI

Due No due date

Points 5

Questions 1

Time Limit None

Instructions

The Registration User Interface (RUI) Prototype is a tool developed for HubMAP that supports the registration of three-dimensional (3D) tissue blocks within 3D reference organs. Surgeons and others involved in the tissue procurement process can use the interface to size a virtual tissue block in three dimensions and then to position and rotate the 3D tissue block within a 3D reference organ so its placement mirrors the real-world tissue block extraction site.

The prototype RUI is freely available to use at:

<https://hubmapconsortium.github.io/ccf-3d-registration> [↗]

Registration data can be saved in JSON format to support spatial search and browsing of tissue data in the Exploration User Interface (EUI).

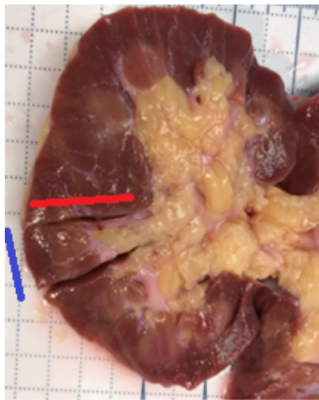


Figure 1. Example kidney tissue block

Please register the exemplary kidney tissue block, shown above, using the RUI using these steps (also shown in our tutorial):

Manually Annotate Human Tissue

-/5 Points

Calculated by:
Most Recent

Unlimited Attempts

Available



Details

Machine learning algorithms can be used to identify and count the number of functional tissue units (FTUs) present in a tissue section. For the kidney, we are interested in identifying and counting the number of glomeruli. Glomeruli have a ball-shaped structure and are composed of capillary blood vessels that filter waste products out of blood to form urine, see Fig. 1.

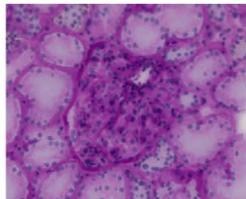
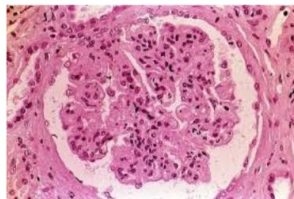


Figure 1. Example of a renal glomeruli

Machine learning algorithms benefit from training data, i.e., human annotations of tissue data that correctly identify glomeruli. For this assignment, please complete the following steps to annotate a kidney tissue sample to help generate machine learning training data and to measure and reduce variability in human annotation data.

1. Install **QuPath** (<https://qupath.github.io/>)
 - If your installed version is lower than 0.2, please update the QuPath to the latest version by visiting the website or by selecting "**Help - Check for updates (web)**" in the tool menu.
2. To open larger images, update the setting for larger memory in QuPath from
 - Navigate to help and select "Show setup options"

Help

Show setup options

- Change the maximum memory from the required **16GB** to our recommendation of **32GB**.

Memory



NEW Modules Released for XMas 2020

All Sections

Dear all, We are proud to release 2 new modules for XMas 2020: Ontologies 101 A gentle introduction on ho...

Posted on:

Dec 18, 2020 at 9:17am



ASCT+B and RUI Onboarding Videos

All Sections

Hello everyone! As you may know, we have had a big amount of new teams joining HuBMAP recently, so we ...

Posted on:

Nov 19, 2020 at 1:28pm



Azimuth: New App for Reference-Based Single-Cell Analysis Released

All Sections

The Satija Lab, the developers of Seurat (an R toolkit for single cell genomics), has released an exciting new w...

Posted on:

Nov 19, 2020 at 11:31am



HuBMAP "Hacking the Kidney" Kaggle Competition is now live!

All Sections

Dear VHMOOC students, The Kaggle Competition titled HuBMAP: Hacking the Human Kidney is now live! V...

Posted on:

Nov 19, 2020 at 10:47am



Welcome to the course!

All Sections

Dear Students, Welcome to the HuBMAP Visible Human MOOC, or VHMOOC! The course opened Tuesday, ...

Posted on:

Sep 1, 2020 at 9am



HuBMAP Visible Human MOOC (VHMOOC)

Started Aug 4, 2020

[GO TO CANVAS COURSE](#)

You are enrolled.



INDIANA UNIVERSITY

Course Introduction

This 10h course introduces the HuBMAP project which aims to create an open, global reference atlas of the human body at the cellular level. Among others, the course describes the compilation 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 asynchronously to fit busy schedules. If you have questions or experience issues during registration, please email cnsctr@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
- Ontology, 3D Reference Objects, and User Interfaces
- HuBMAP Portal Design and Usage

Meet the Instructors



Katy Börner, Victor H. Yngve Distinguished Professor of Engineering and Information Science, Founding Director of the [CyberInfrastructure for Network Science Center](#) at Indiana University.



Ellen M. Quardokus, staff in the Chemistry Department and research scientist, CyberInfrastructure for Network Science Center, SICE with expertise in molecular biology, microscopy, anatomy, and interdisciplinary communication.



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

Length: 10 hours

Department: CyberInfrastructure Network Science

Credit: None

Audience: Biomedical students and professionals interested in single-cell tissue analysis and visualization

<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.



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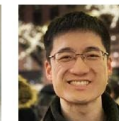
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Q&A

