HuBMAP CCF User Interfaces

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HuBMAP CCF WS

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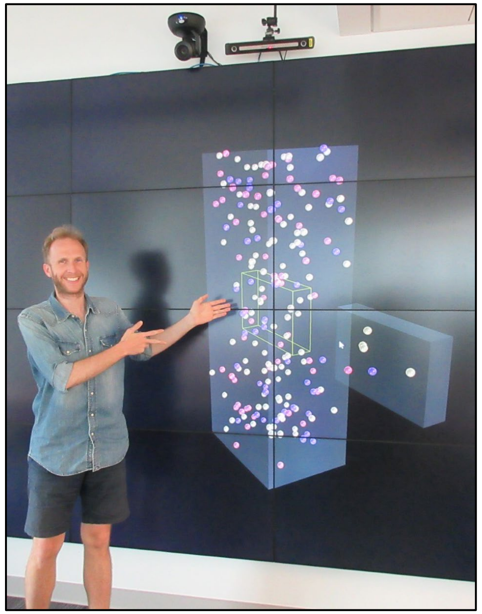
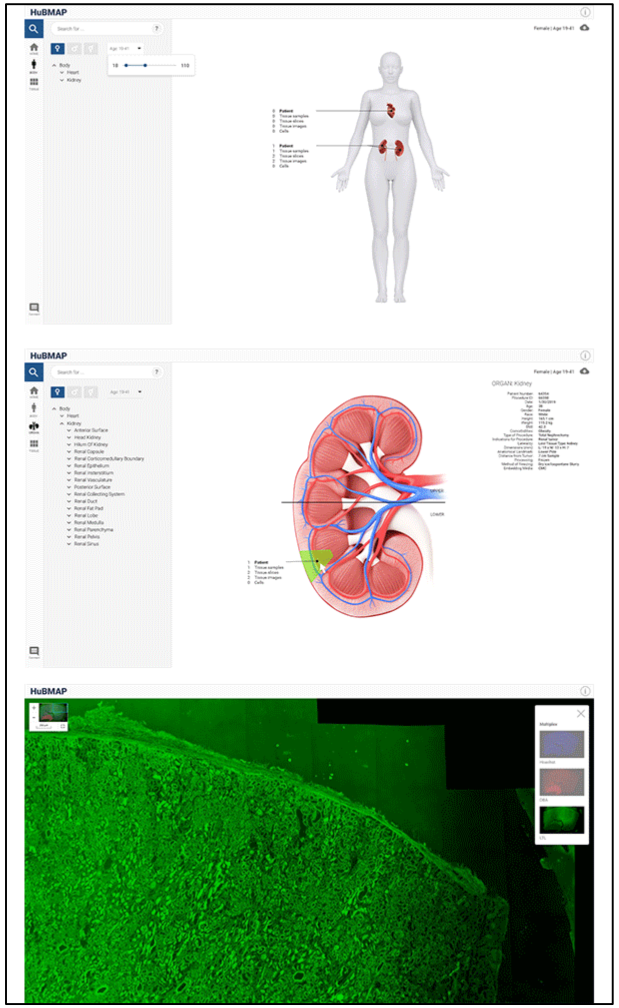
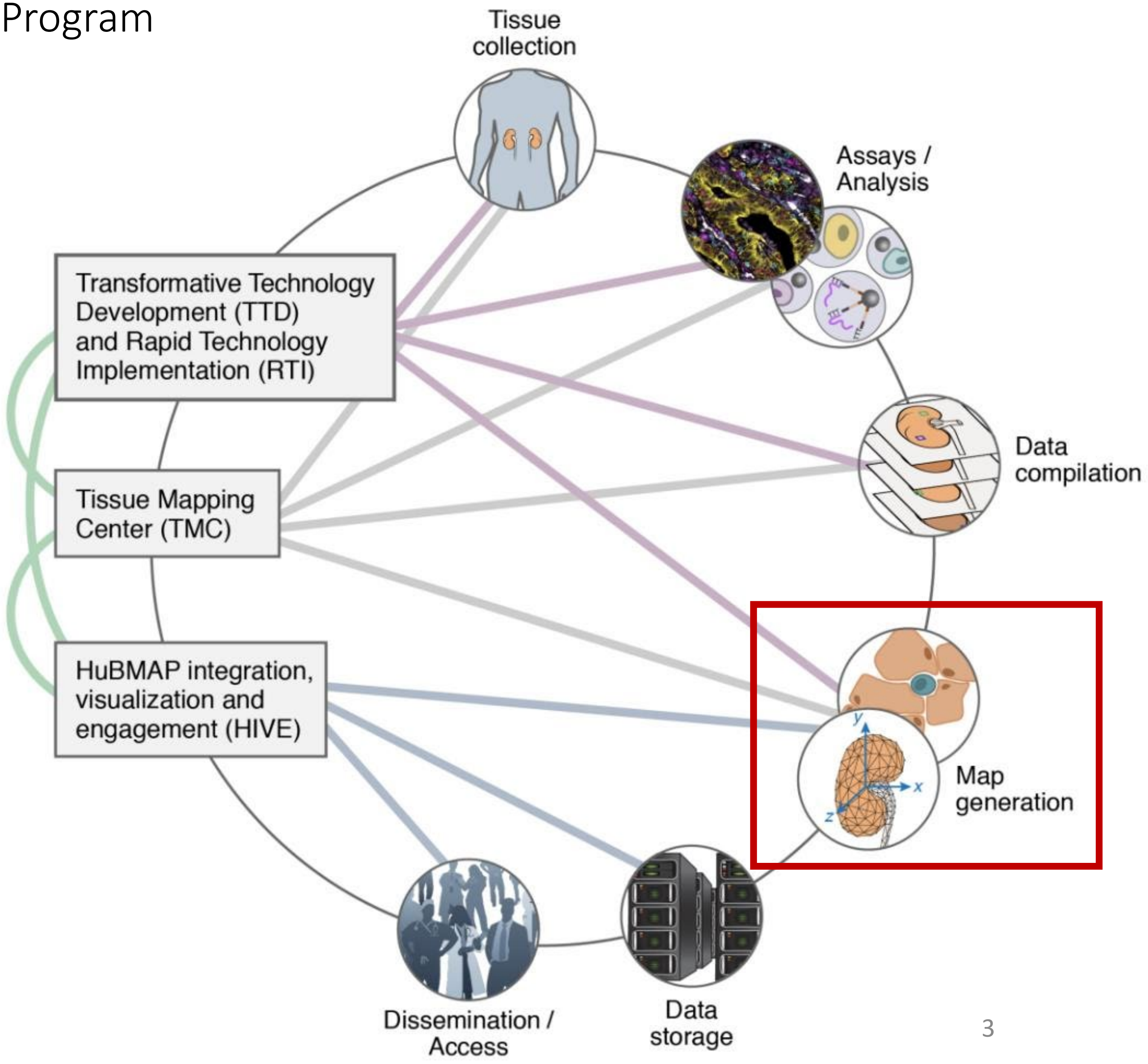
June 27, 2019





HuBMAP CCF Data & User Interfaces

Mapping the Human Body at Cellular Resolution—
The NIH Common Fund Human BioMolecular Atlas Program
Snyder et al. https://arxiv.org/abs/1903.07231



Mapping the Human Body at Cellular Resolution—
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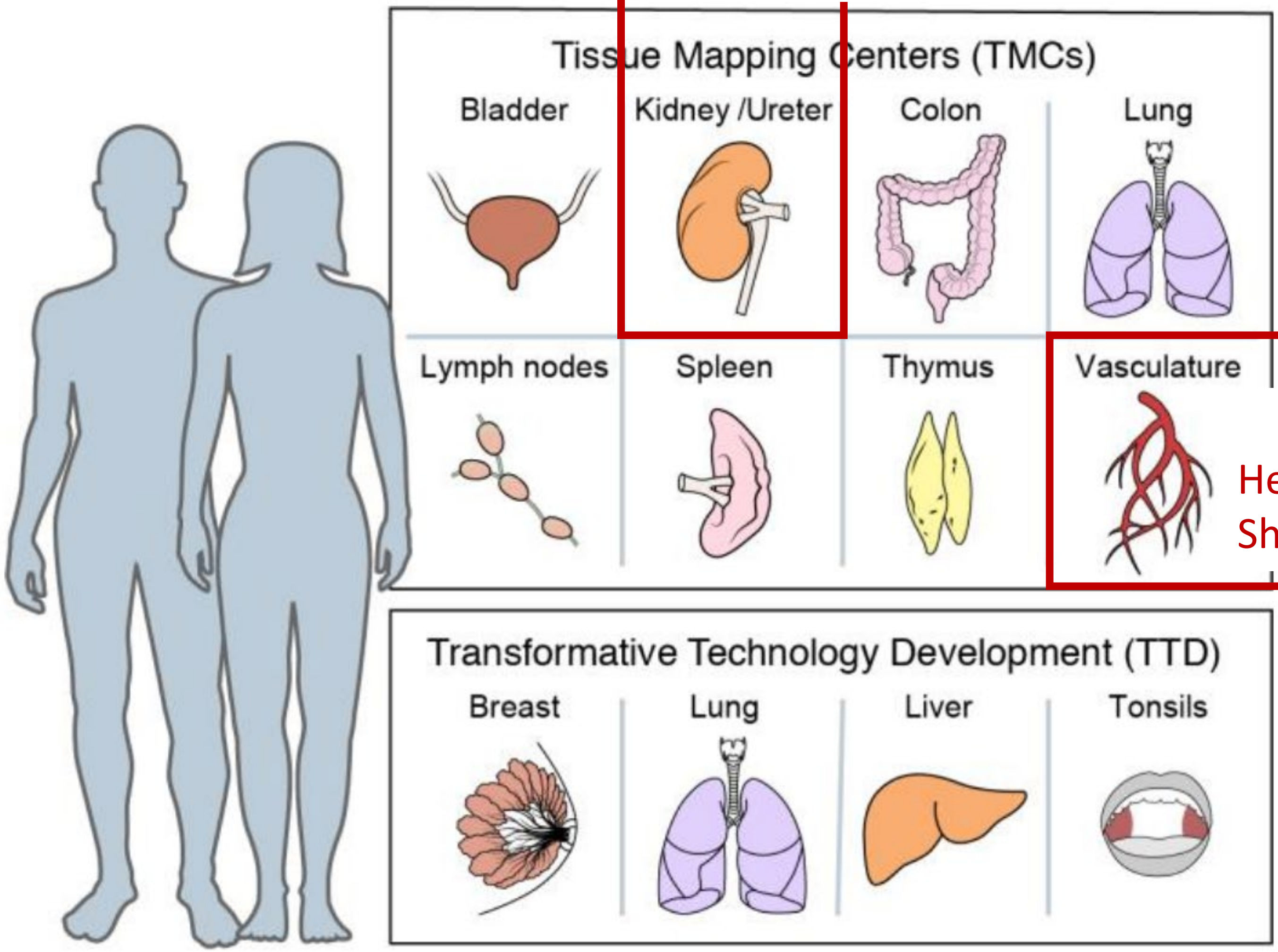
Kidney: Jeff Spraggins, TMC-VU; Sanjay Jain, TMC-UCSD



Heart:
Shin Lin, UW, TMC-CalTech

Mapping the Human Body at Cellular Resolution—
The NIH Common Fund Human BioMolecular Atlas Program
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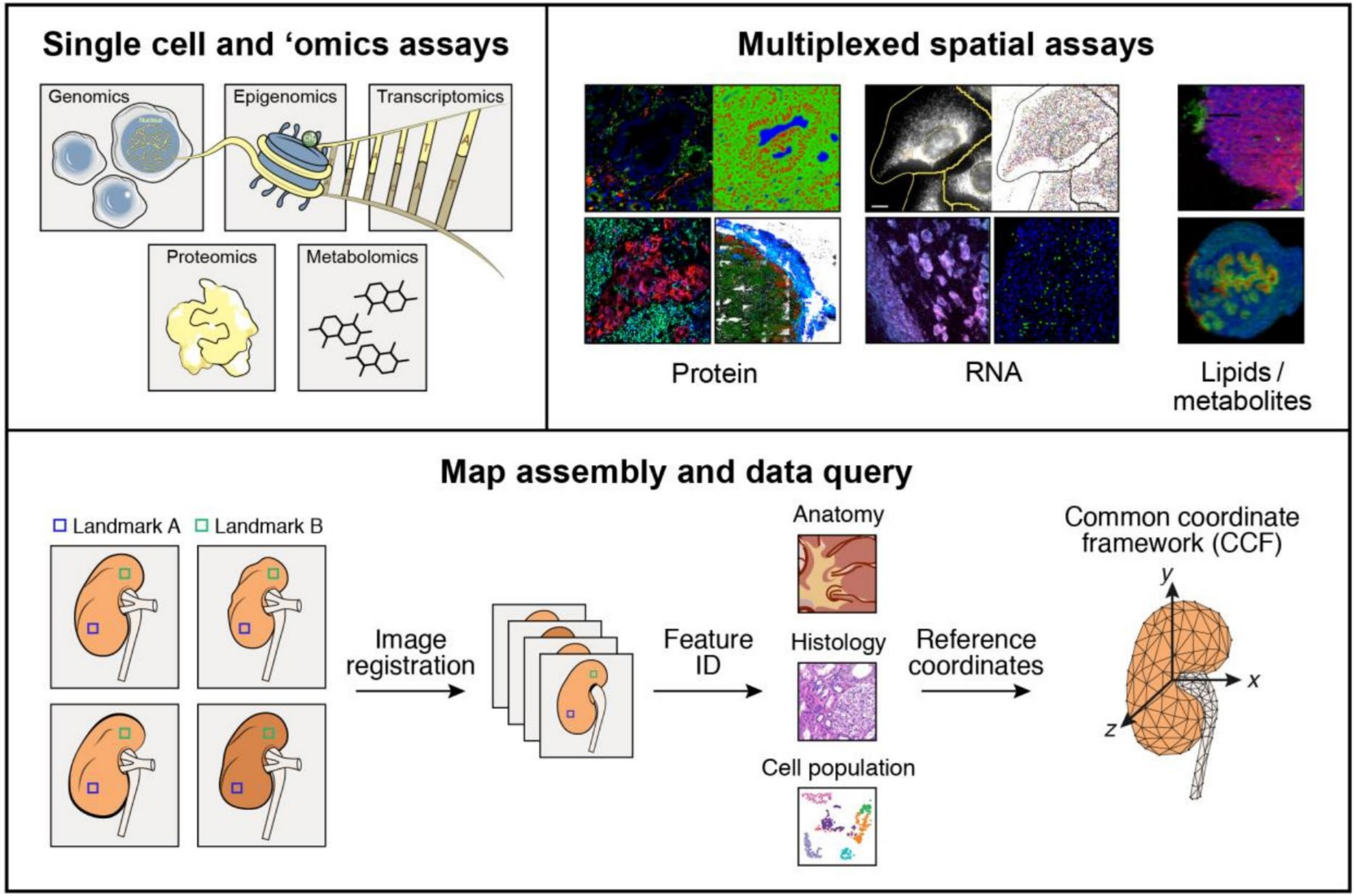
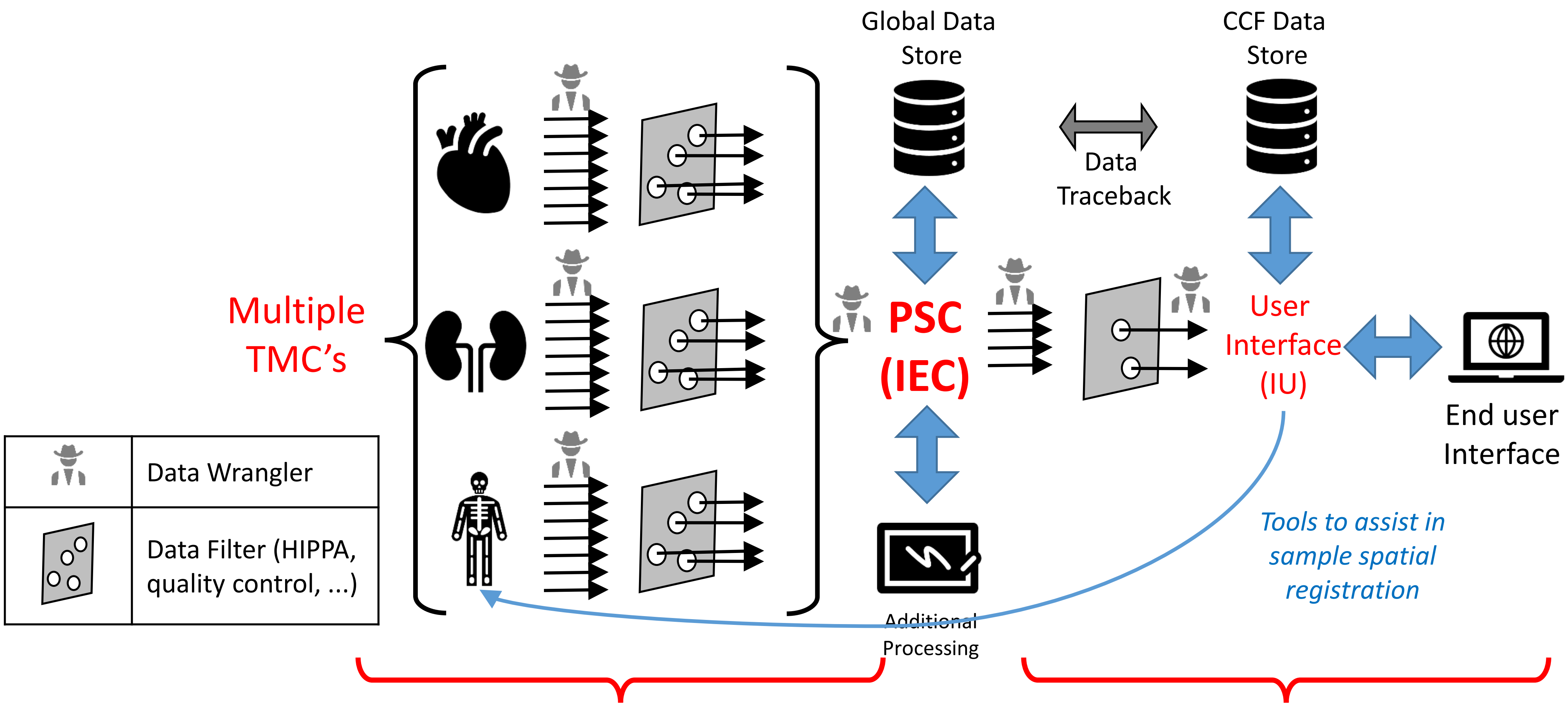


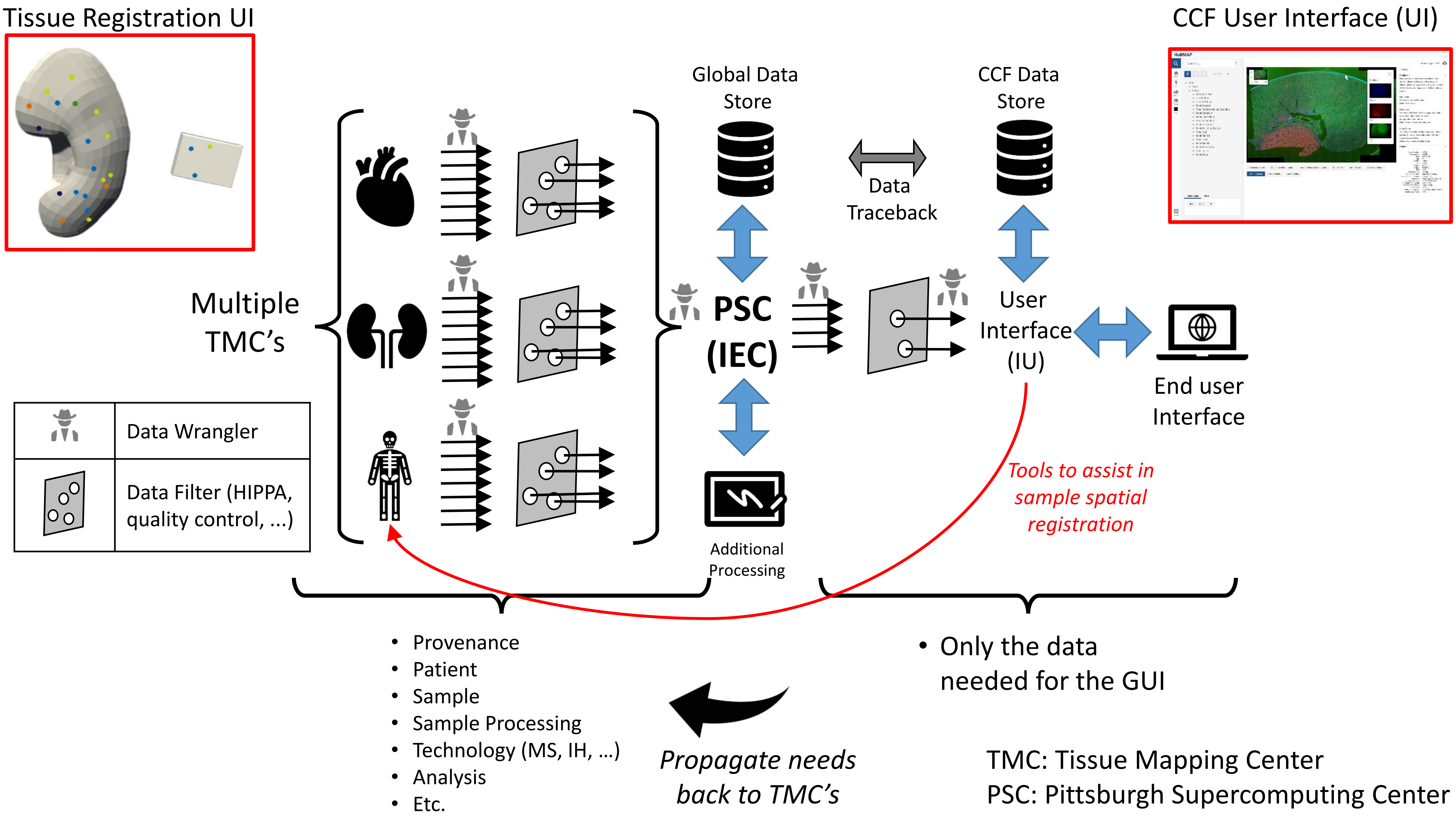


- Provenance
- Patient
- Sample
- Sample Processing
- Technology (MS, IH, ...)
- Analysis
- Etc.

Propagate needs back to TMC's

- Only the data needed for the GUI

TMC: Tissue Mapping Center
PSC: Pittsburgh Supercomputing Center

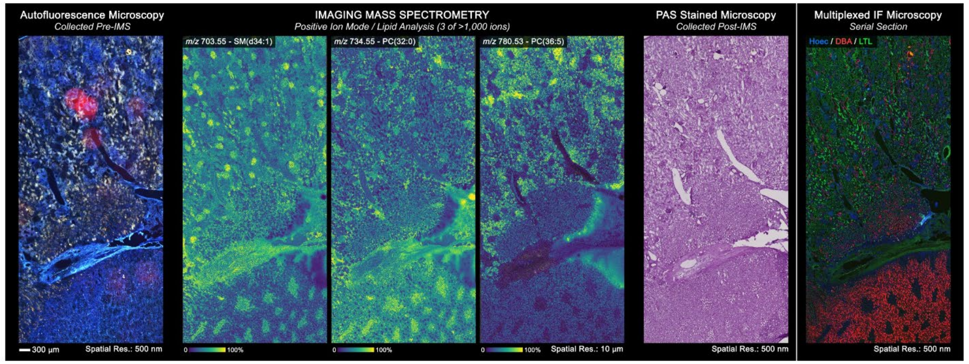


Tissue Registration UI
CCF User Interface (UI)
Global Data Store
CCF Data Store
Data Traceback
Multiple TMC's
PSC (IEC)
User Interface (IU)
End user Interface
Additional Processing
Data Wrangler
Data Filter (HIPPA, quality control, ...)
Tools to assist in sample spatial registration
Provenance
Patient
Sample
Sample Processing
Technology (MS, IH, ...)
Analysis
Etc.
Only the data needed for the GUI
Propagate needs back to TMC's
TMC: Tissue Mapping Center
PSC: Pittsburgh Supercomputing Center

Data. Is very heterogeneous. Must provide guidance.

Kidney: Jeff Spraggins et al., VU

See data on Globus, BIOMIC_patient-64354



Clinical and Spatial Metadata (21 rows)

Cell Types, on right

Cell type	Subset A	Subset B	Subset C
Tubular Epithelium	Proximal tubular cells	S1	
		S2	
		S3	
	Loop on Henle	Thin descending limg	
		Thin ascending limb	
		Thick limb	medullary
			cortical
		Macula Densa	
	Distal convoluted tubule		
	Connecting segment		
	Collecting duct	Principal cells	
		Intercalated cells	Type A
			Type B
Glomerulus	Epithelium	Visceral	
		Parietal	
	Mesangial cells		
Vasculature	Endothelium	Glomerular	
		Peritubular	
		Lymphatic	
	Pericytes		
	Juxta Glomerular Cells		
Interstitium	Fibroblasts	Myofibroblasts	
		EPO producing cells	
		Medullary fibroblasts	
	Mononuclear cells	Resident macrophages	
		Dendritic cells	
	Lymphocytes	T cells	
		B cells	
		NK cells	

Cell States (9 rows)

Cell states	Subset A
Proliferating cells	S-phase
	G2/M
Cell cyle arrest	G0
	G1/S
	G2/M

Heart: Shin Lin, UW

Year 1: Tissue data for 1-2cm cubed volumes from 9 sites for 1 heart from 1 individual.

Data Dictionary (115 rows)

Field # Sort	Field Label Sort	Field Name Sort	Field Units	Field Data	Lookup Tal	Low Value	High Value	Valid value	IsNullable	Parent Fiel	Parent Fiel	Can Child b	ReadOnly Sort
9	Donor //ABO:	abo		char(3)	lkup_abo				TRUE				FALSE
10	Donor //Date of birth:	dob		datetime					TRUE				FALSE
11	Donor //Gender:	gender		char(1)	lkup_gender			M,F	TRUE				FALSE
12	Details //Age:	age_in_months		smallint		0	1188		TRUE			FALSE	FALSE
13	Details //Age Unit:	age_unit		char(1)	lkup_age_unit			M,Y	TRUE	age_in_months			TRUE
14	Details //Height:	hgt_cm	cm	decimal(5, 2)		1	241.3		TRUE				FALSE
15	Donor hgt_ft //	hgt_ft	ft	int		0	7		TRUE				TRUE
16	Donor hgt_in //	hgt_in	in	int		0	11		TRUE				TRUE
17	Details //Weight:	wgt_kg	kg	decimal(7, 4)		0.454	294.835		TRUE				FALSE
18	Donor wgt_lb //	wgt_lb	lbs	decimal(3, 0)		2	650		TRUE				TRUE
19	Donor //Ethnicity/race:	race		bigint	lkup_race_subcat_multi				FALSE				FALSE
30	Details //History of diabe	hist_diabetes		smallint	lkup_histdiab_dur				TRUE				FALSE
31	Donor //History of cance	hist_cancer		smallint	lkup_histcancer_site				TRUE			FALSE	FALSE
32	Donor History of cancer ,	cancer_oth_ostxt		varchar(50)		1	50		TRUE	hist_cancer	999		FALSE
33	Details //History of hyper	hypertension		smallint	lkup_histhype_dur				TRUE			FALSE	FALSE

Cell Types (14)

endothelial cells	
	arterial
	capillary
	venous
	lymphatic
cardiomyocytes	
	atrial
	ventricular
	nodal
fibroblasts	
	fibroblasts
	myofibroblasts
immune cells	
	macrophages

Data: Clinical

Kidney: Jeff Spraggins et al., VU

Clinical and Spatial Metadata (21 rows)

Sample Number:	20
Patient Number:	64354
Procedure ID:	66598
Date:	1/30/2019
Age:	38
Gender:	Female
Race:	White
Height:	165.1 cm
Weight:	115.2 kg
BMI:	42.3
Comorbidities:	Obesity
Type of Procedure:	Total Nephrectomy
Indications for Procedure:	Renal tumor
Laterality:	Left
Tissue Type:	kidney
Dimensions (mm):	L: 19 x W: 13 x H: 7
Anatomical Landmark:	Lower Pole
Distance from Tumor:	7 cm
Sample Processing:	Frozen
Method of Freezing:	Dry Ice/Isopentane Slurry
Embedding Media:	CMC

Heart: Shin Lin, UW

Data Dictionary (115 rows)

Field # Sort	Field Label Sort	Field Name Sort	Field Units	Field Data	Lookup Tal	Low Value	High Value	Valid value
9	Donor //ABO:	abo		char(3)	lkup_abo			
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33	Details //History of hyper	hypertension		smallint	lkup_histhype_dur			

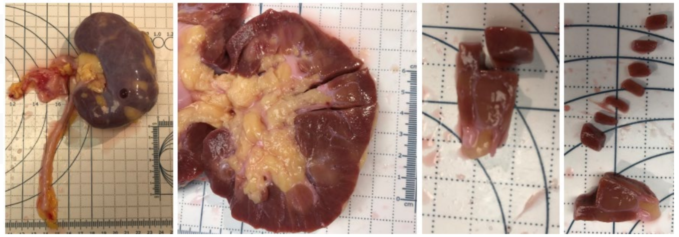
Data: 3D Tissue

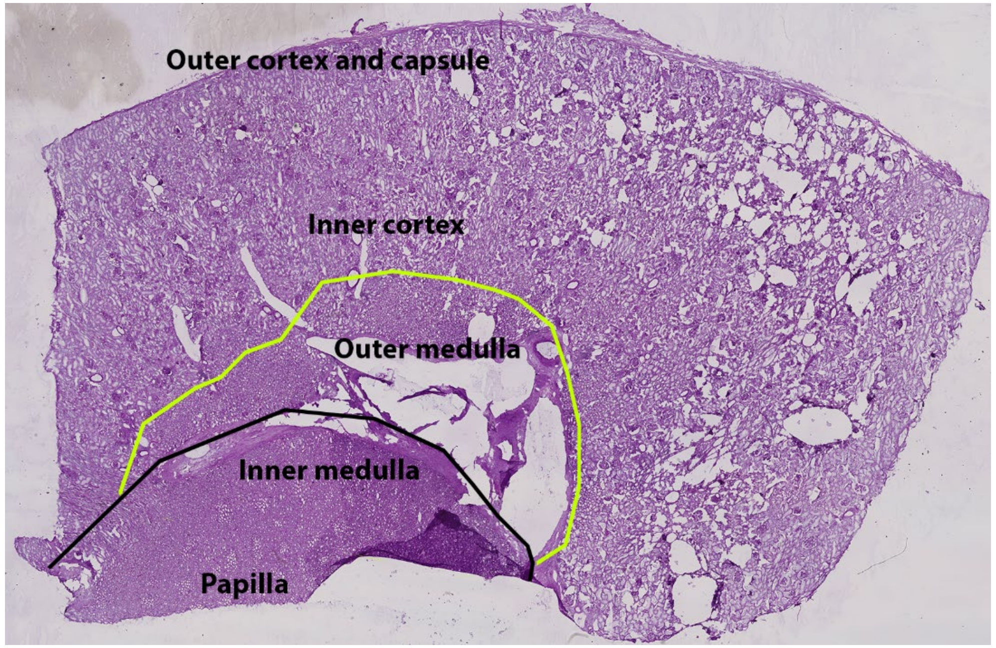
Kidney: Jeff Spraggins et al., VU

See data on Globus, BIOMIC_patient-64354

- BIOMIC_patient-64354_clinical_and_spatial_metadata.xlsx
- BIOMIC_patient-64354_data_guide.pptx
- BIOMIC_patient-64354_overview.png
- BIOMIC_patient-64354_Sample-20-Histology.tif
- neg_ion_mode_section
- pos_ion_mode_section

BUKMAP, Zhang Group

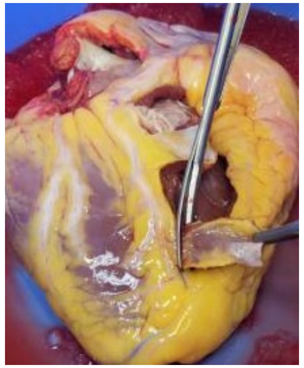




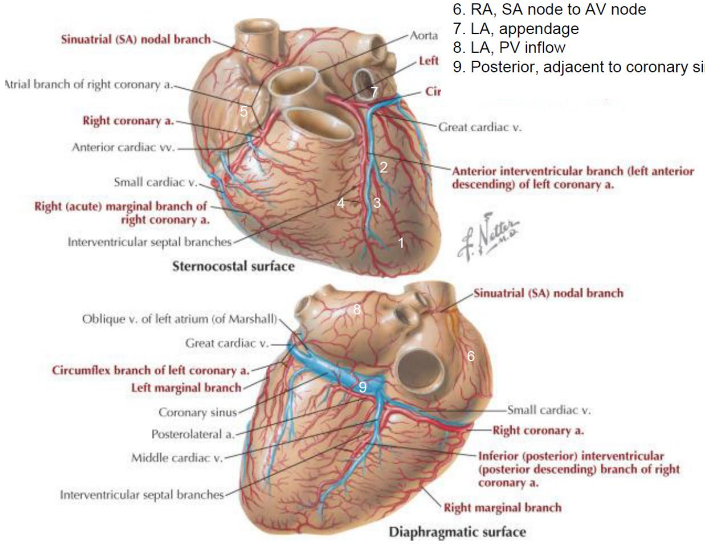
Heart: Shin Lin, UW

Year 1: Tissue data for 1-2cm cubed volumes from 9 sites for 1 heart from 1 individual.

Terminology; Coordinates and photos to spatialize



Sites	Distinctive features
1. LV, apex	
2. LV, free wall 3 cm from apex	
3. septum, 3cm from apex including LAD	major arterial vessel, Purkinje fiber CM
4. RV, free wall 3 cm from apex	
5. RA appendage	
6. RA, SA node to AV node	pacemaker CM
7. LA, appendage	
8. LA, PV inflow	
9. Posterior, adjacent to coronary sinus	major venous vessel



Data: TMCs x Organs x Data Types x Technologies

BUKMAP, Zhang Group

Organs (10)	Data Types (13)	Technologies (~25)
1. Bladder	1. Imaging - Proteins	CODEX;DART-FISHrp;IF;IHC;LRET-IF;MALDI Imaging MS;PER-DEI
2. Blood Vessel (Heart)	2. Imaging - RNA	DART-FISH;LRET-ISH;MERFISH;PER-DEI;seqFISH;smFISH
3. Breast	3. Imaging - DNA	PER-DEI
4. Colon	4. Imaging - Other	Lipid and Metabolite MALDI Imaging MS
5. Kidney	5. scRNAseq	snDropseq;scRNAseq
6. Liver	6. scDNAseq	scATACseq;scTHSseq;SNAREseq
7. Lung	7. scProteomics	IMC
8. Spleen	8. bulk-Proteomics	LC-MS/MS
9. Thymus	9. bulk-RNA	?
10. Tonsil	10. bulk-DNA	?
	11. Metabolomics	LC-MS/MS;nano-POTS
No Bone Marrow	12. Lipids	LC-MS/MS;nano-DESI
and Pancreas.	13. Other	Autofluorescence;PAS stained microscopy

CCF Data Wiki

Minimum Information Standard

hubmapconsortium / ccf-data-wiki Private

Unwatch 3 Star 0 Fork 0

Code Issues 0 Pull requests 0 Wiki Insights

Home

Edit New Page

Bruce Herr II edited this page 2 days ago · 5 revisions

Welcome to the CCF Data Wiki!

Organ	CalTech	UCSD	Stanford	Vanderbilt	Florida
Heart	✓				
Kidney		✓		✓	
Bowel			✓		
Thymus					✓
Spleen					✓
Lymph Nodes					✓
Lung		✓			
Bladder		×			
Colon			×		

Legend:

- ✓ - Organ proposed and survey submitted
- × - Organ was proposed, but no survey has been submitted

Pages 12

Links

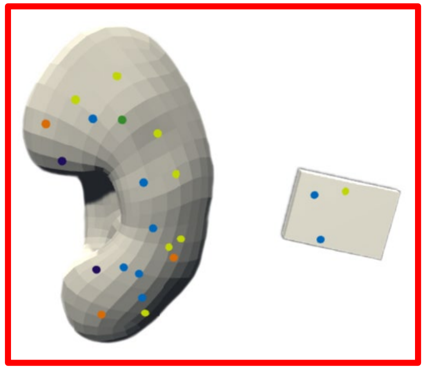
- Home

Templates

- TMC-Organ-Template

Clone this wiki locally

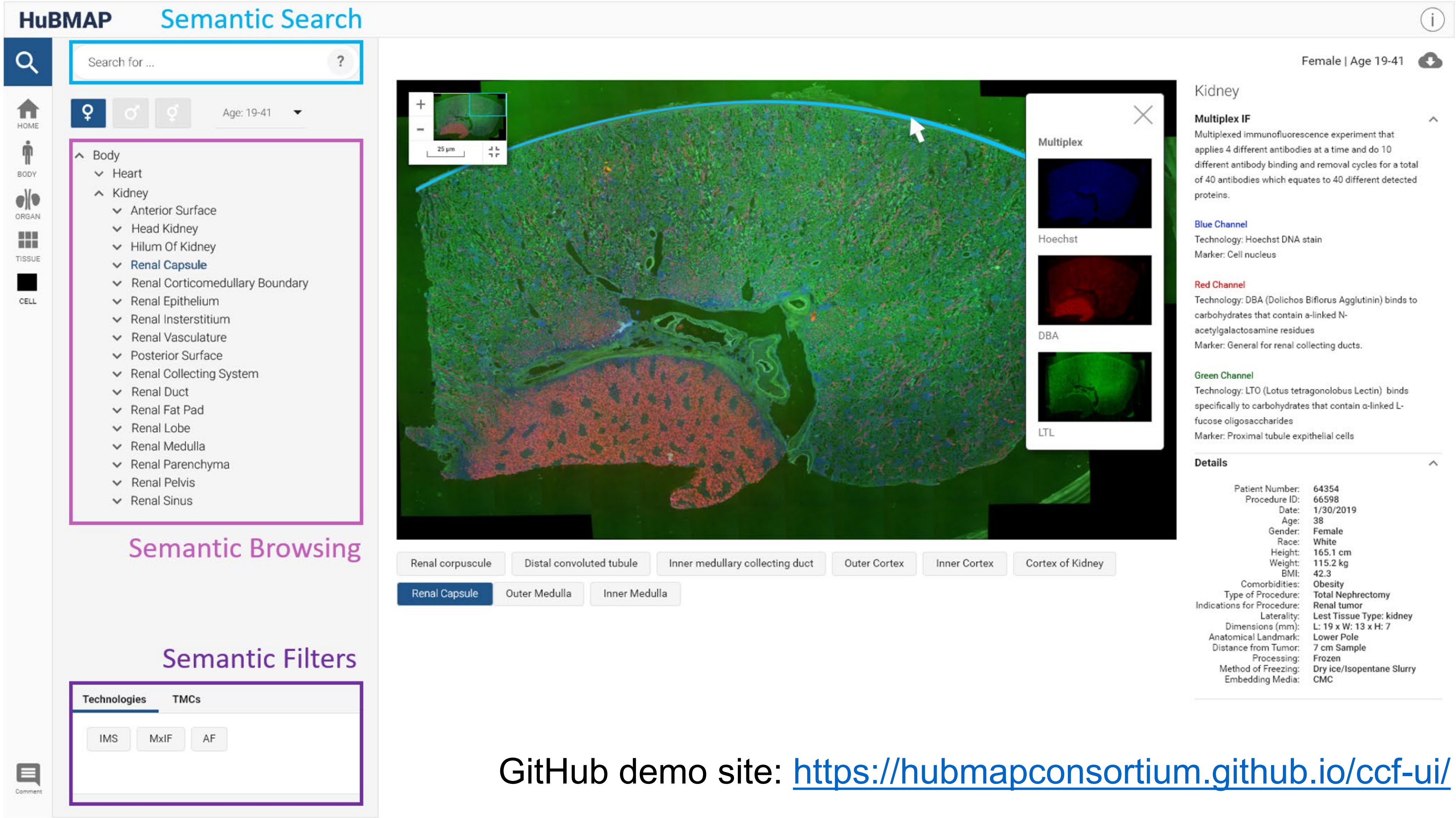
https://github.com/hubmapcc



https://github.com/hubmapconsortium/ccf-data-wiki/wiki

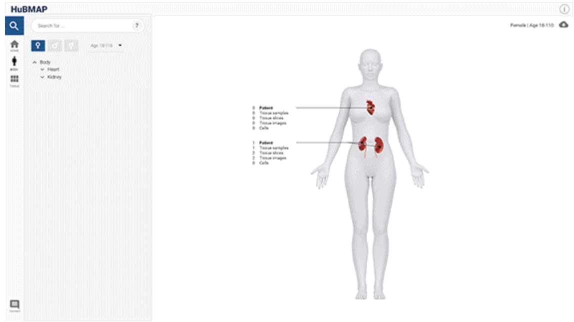
CCF User Interfaces (UI)

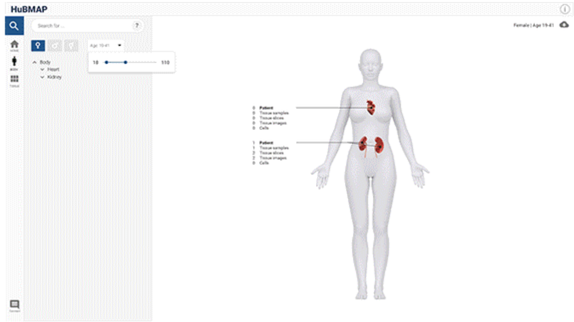
CCF User Interface (UI)

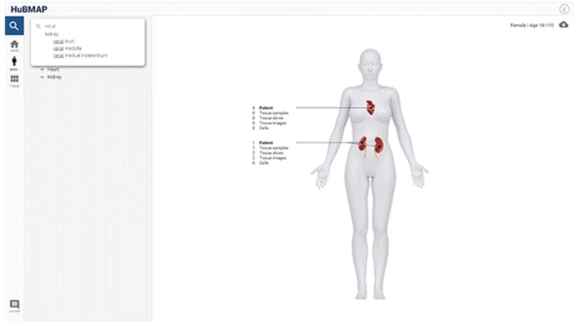


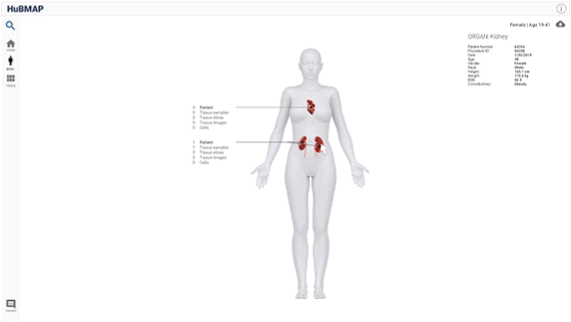
GitHub demo site: https://hubmapconsortium.github.io/ccf-ui/

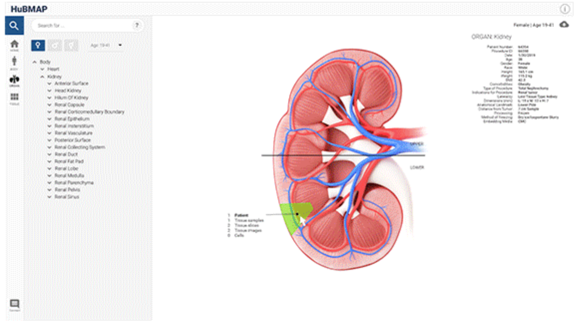
CCF User Interface (UI)

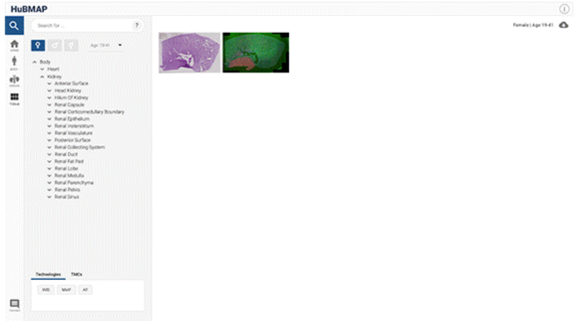


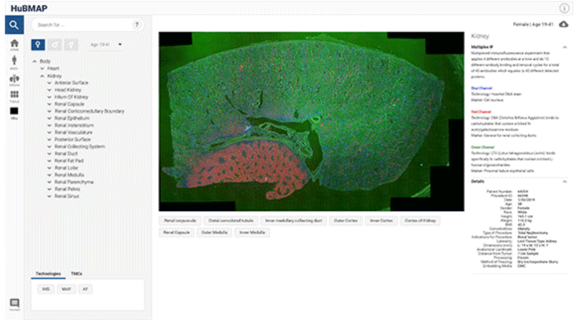


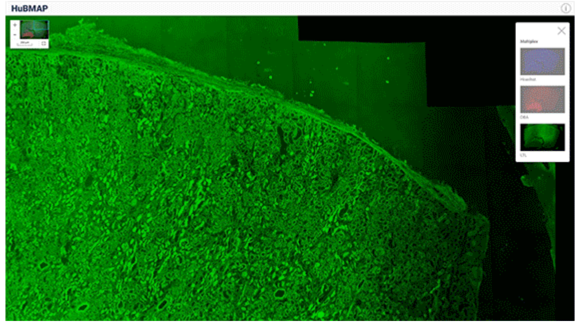


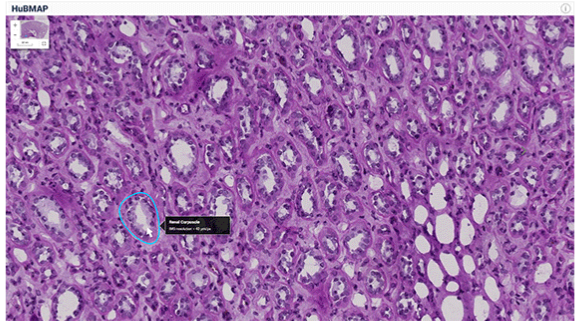












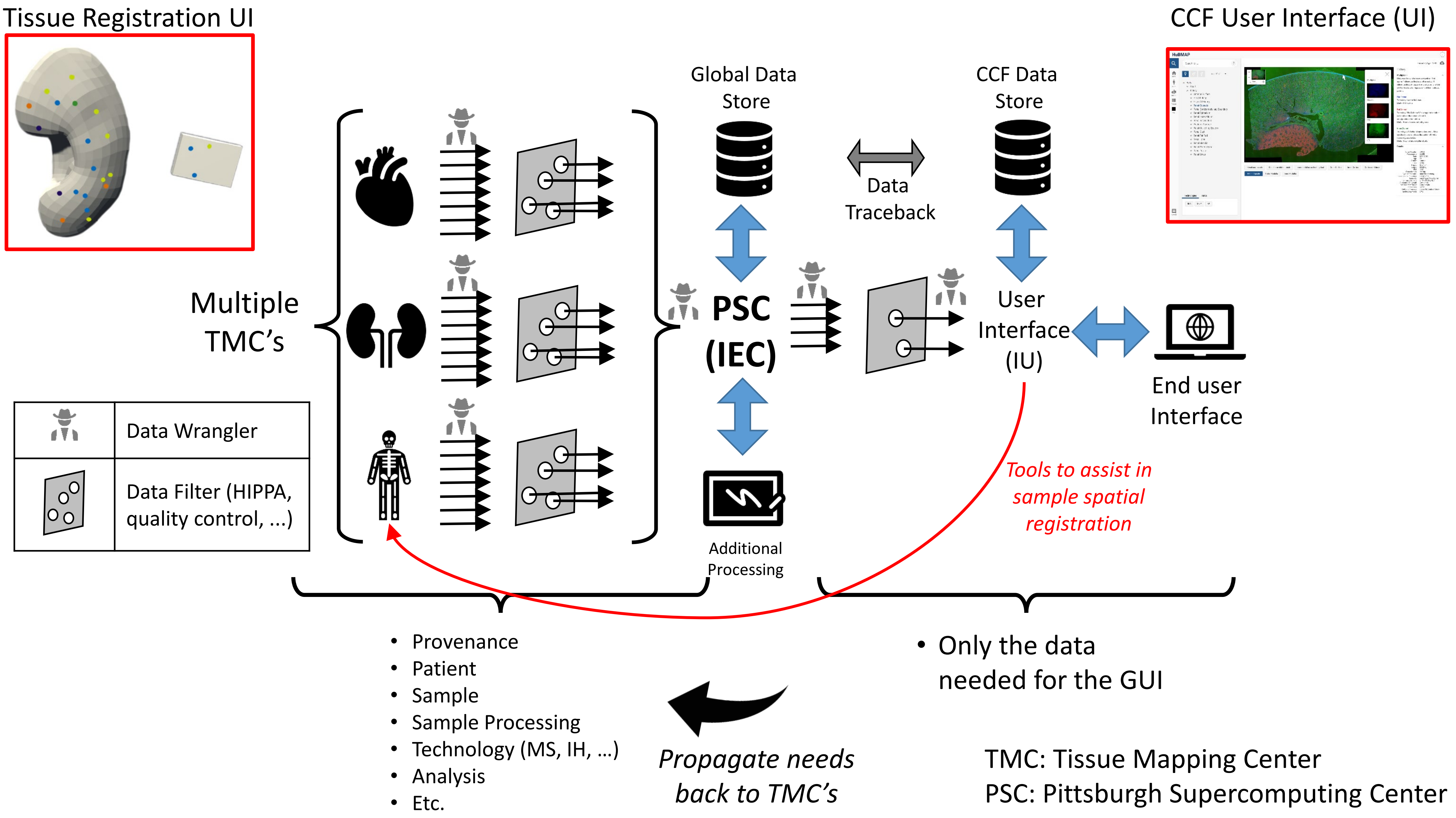
CCF User Interface (UI)

MC-IU has released CCF user interface v0.5.0, a proof-of-concept version of the CCF UI.
The user interface supports:

- Visual browsing of tissue samples and metadata at the whole body, organ, tissue, and cell level.
- Filtering by metadata (age, gender, TMC, and technology), results are presented at all views.
- Submission of questions and comments on the CCF UI.
- Semantic search by ontology, results are presented at all levels.
- Data download at the whole body, organ, tissue, and cell level, i.e., link to https://sampledata.hubmapconsortium.org.

See also:
Recorded demo: https://www.youtube.com/watch?v=rWMqKQc_00w&feature=youtu.be
GitHub link to code: https://github.com/hubmapconsortium/ccf-ui
GitHub demo site: https://hubmapconsortium.github.io/ccf-ui/
Original specs: https://drive.google.com/open?id=1tqUzmVLxwqcGprtRIevfY86YvHHPEsDR

Live Demo!



Tissue Registration UI
CCF User Interface (UI)
Global Data Store
CCF Data Store
Data Traceback
Multiple TMC's
PSC (IEC)
User Interface (IU)
End user Interface
Data Wrangler
Data Filter (HIPPA, quality control, ...)
Additional Processing
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Provenance
Patient
Sample
Sample Processing
Technology (MS, IH, ...)
Analysis
Etc.
Only the data needed for the GUI
Propagate needs back to TMC's
TMC: Tissue Mapping Center
PSC: Pittsburgh Supercomputing Center

Tissue Registration UI: Heart (depending data availability)

Align 9 tissue samples in 3D heart using a combi of

- Rough placement using human expertise/3D pattern matching and
- Fine adjustments using machine learning

Virtual tissue samples will be sized 1-2cm cubed, numbered (1 … 9), and oriented (left-right, top and bottom tissue slice of z-stack).

Measure error from

- precision of tissue sample procurement and
- placement in the 3D browser

We hypothesize that placement accuracy will improve when additional information (e.g., landmarks, major scaffolds, MR/CT scan of heart after 9 samples were extracted) is being visible in virtual organ.

Sites	Distinctive features
1. LV, apex	
2. LV, free wall 3 cm from apex	
3. septum, 3cm from apex including LAD	major arterial vessel, Purkinje fiber CM
4. RV, free wall 3 cm from apex	
5. RA appendage	
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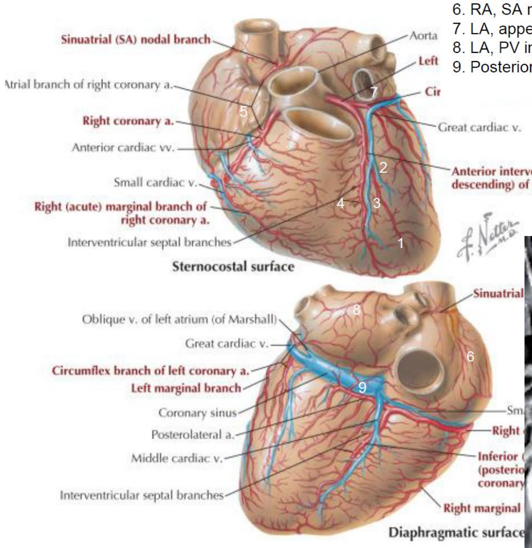
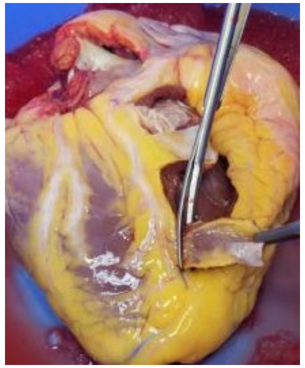
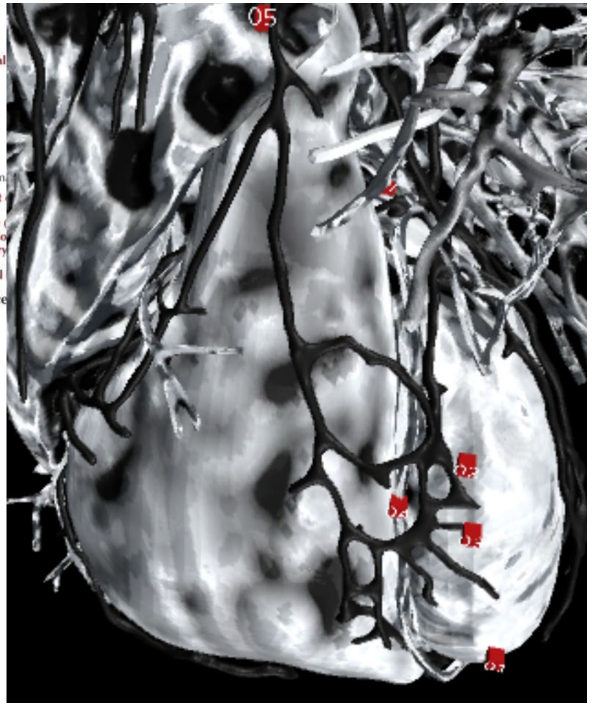




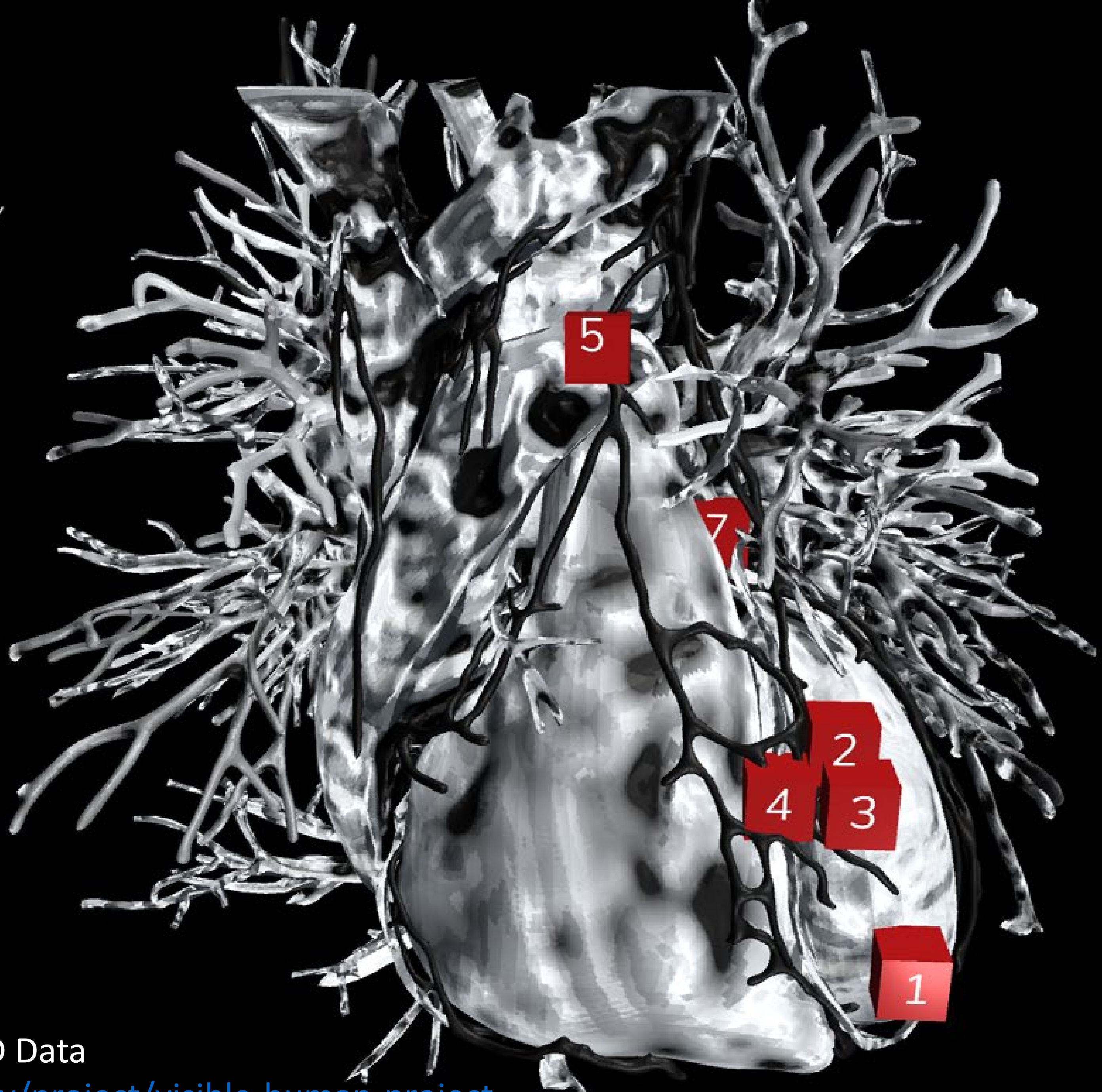


Human heart with data overlay
Developer: Andreas Bueckle

Show/hide

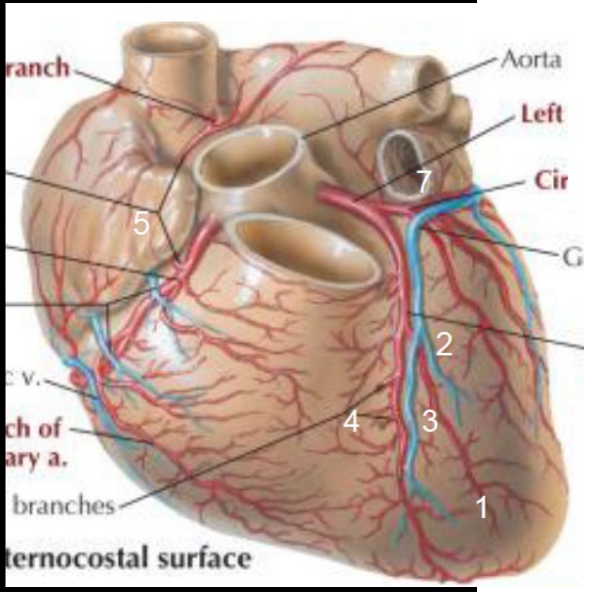
- ☑ Coronary arteries
- ☑ Coronary veins
- ☑ Left atrium
- ☑ Left ventricle
- ☑ Right atrium
- ☑ Right ventricle
- ☑ Markers

Adjust camera speed



Currently Selected

Please click any of the red markers!



Heart model from NLM3D Data
https://lhncbc.nlm.nih.gov/project/visible-human-project

Tissue Registration UI: Kidney

(depending data availability)

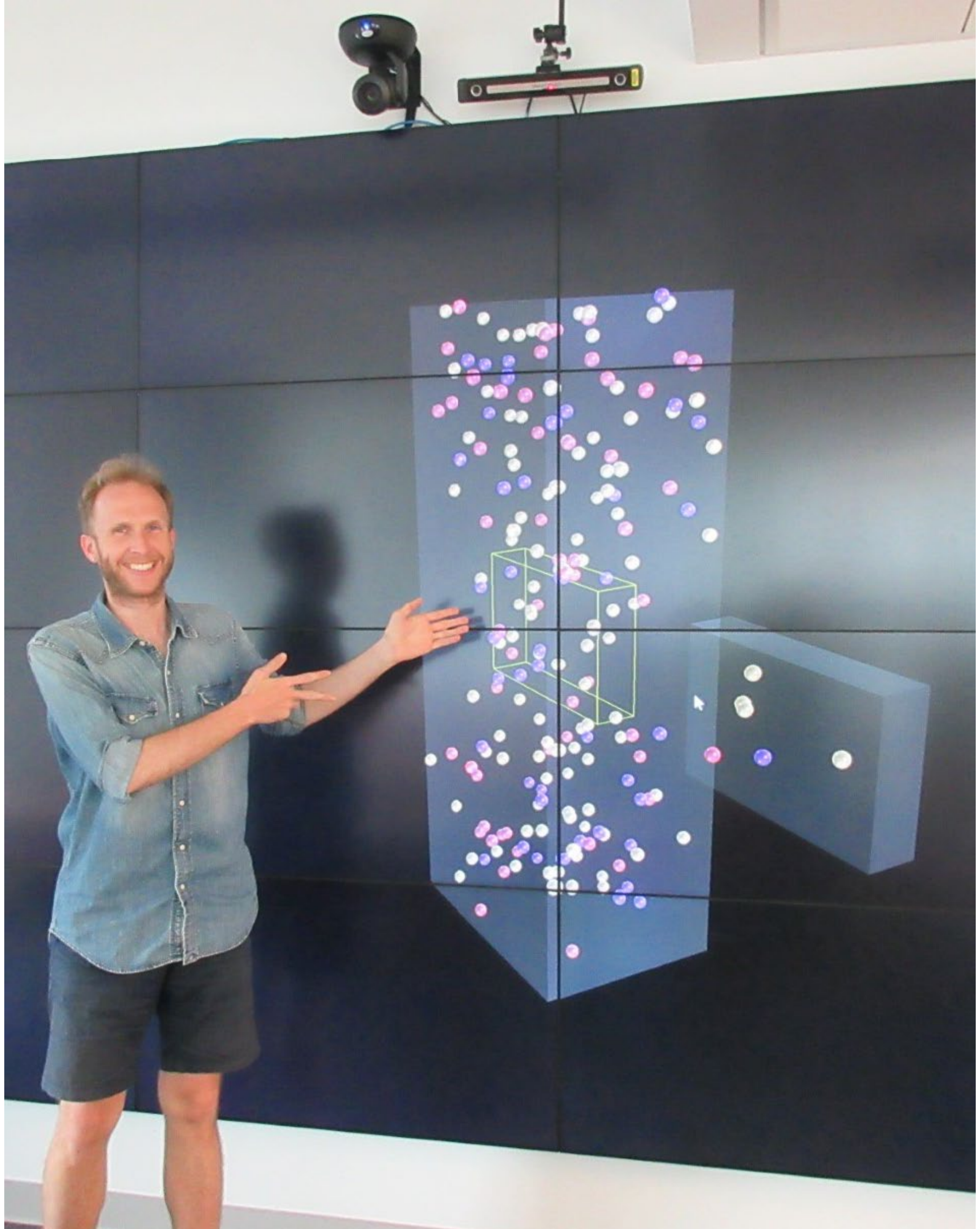
- Exploit human pattern recognition and fine motor skills (by surgeons) to register tissue in organs.
- Add info on anatomical landmarks (fiducial marks), cell types, molecular data to support alignment.
- LATER: Use human alignment data as training data for machine learning algorithms, to better support manual alignment OR to possibly fully automatize alignment.

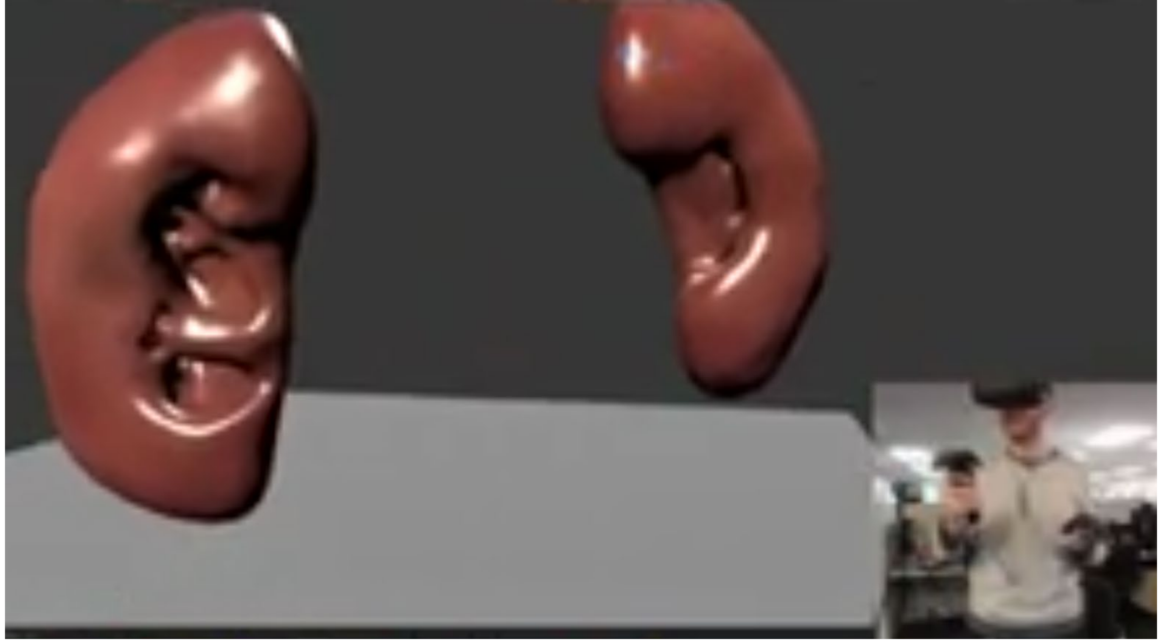
VIVE™ | VIVE Virtual Reality System

vive.com

How many of you have used a VIVE or space mouse?

Kidney model from NLM3D Data
https://lhncbc.nlm.nih.gov/project/visible-human-project

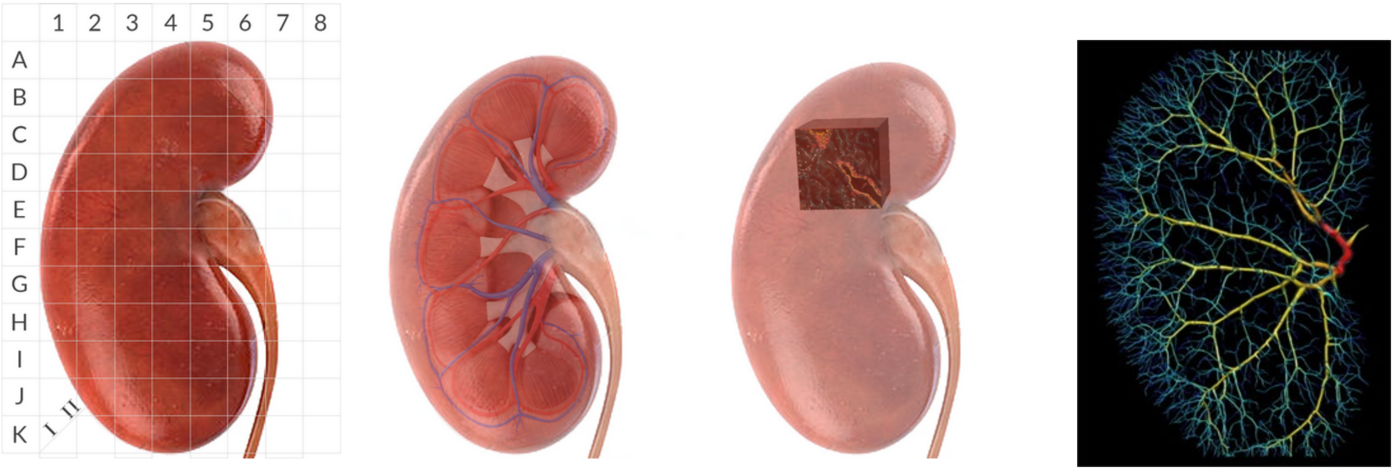




Kidney model from NLM3D Data
https://lhncbc.nlm.nih.gov/project/visible-human-project

KPMP GLUE grant proposal in progress.

For the kidney, there exist no predefined tissue extraction sites. The current kidney Registration UI uses a grid system and a picture of a kidney slice to guide placement, see **Fig. 3 left and middle**. Funding of this GLUE grant will make it possible to use 3D image volumes collected from intact kidney tissue within KPMP that feature anatomically meaningful structures of different cell types, see **Fig. 3 right**.



Structural morphology of renal vasculature. Nordsletten et al. 2006. https://doi.org/10.1152/ajpheart.00814.2005

Figure 3: 3D grid system (left), 2D image (middle), 3D tissue reconstructions from KPMP (right)

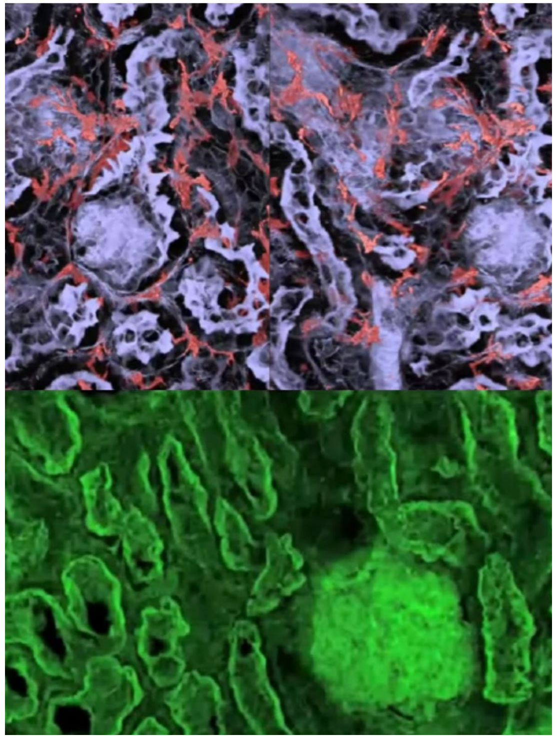
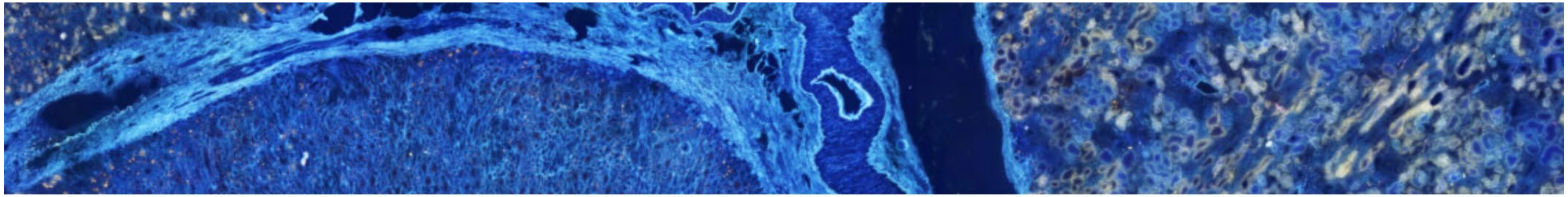


Fig. 4. KPMP volumetric data.

See presentation by Seth Winfree for details *https://ccfws.cns.iu.edu*

Using the 3D grid system, a user can use 3D coordinates to refer to a particular area in the kidney, e.g., A-4-II would correspond to the lower-middle part of the kidney, on the inside (occluded in this view). Using the 2D image, sample placement within a semi-transparent reference kidney object is guided by anatomical structures. Using KPMP data, it will be possible to show complex volumetric structures inside the 3D reference kidney to allow for more granular alignment at the molecular level.

CCF Workshop (MC-IU, Jeff Spraggins, TMC-Vanderbilt, Sanjay Jain, TMC-UCSD)



HuBMAP Human BioMolecular Atlas Program | COMMON COORDINATE FRAMEWORK WORKSHOP CCFWS-01

Time & Date

9:00am–5:00pm EDT on May 9, 2019

All slides, video recordings are at https://ccfws.cns.iu.edu

Goals

HuBMAP will develop a common reference map or coordinate system called the Common Coordinate Framework (CCF). As stated in the Common Coordinate Framework Meeting (CCFM) document, a CCF makes it possible to uniquely and effectively define and name any location in the human body. A set of robust origin points (serving as landmarks) make it possible to reference organs, tissues, cells over different anatomical scales, tolerate human variability and function across lifespan and disease, and help integrate heterogeneous data layers and a wide range of reference maps such as whole body spatial maps, genetic variant maps, and coordinate systems that align with vascular pathways.

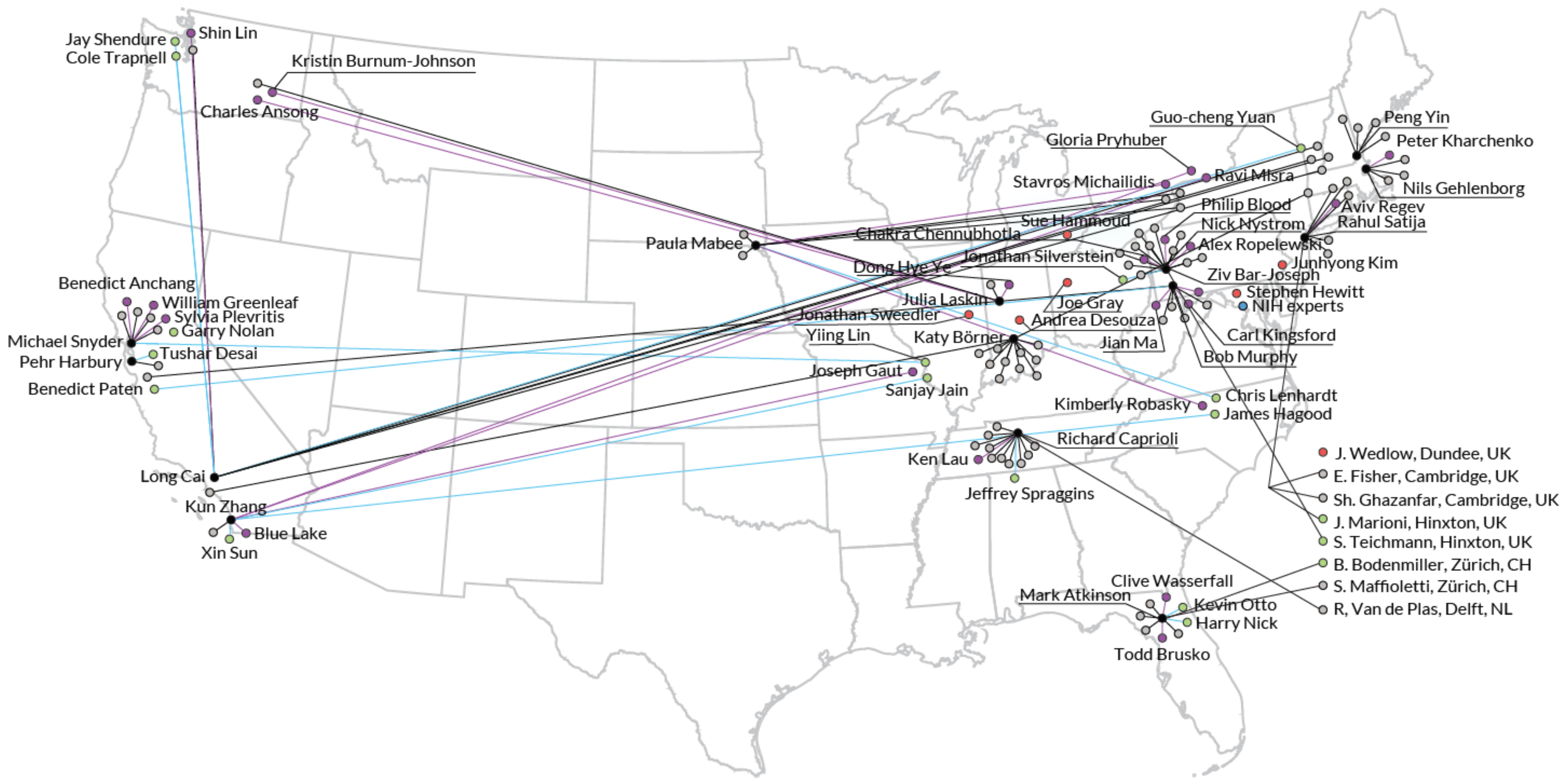
This CCF workshop will focus on a kidney-specific CCF and atlas but also discuss other relevant CCF/atlas efforts. It will feature presentations and discussions on:

- CCF metadata—what data are currently captured, how can they be unified across tissue mapping centers (TMCs), what additional data are needed to meet stakeholder (research) needs.
- CCF ontologies—what ontologies exist and are used in what part of the data pipeline; what 'desirable properties' and 'success criteria' exist?
- CCF mapping and numerical construction—including dealing with human variation and using CCF user interfaces as a means to properly register data and review data completeness.
- General principles and processes that can inform CCF design for other organs and continuous adaptation of CCF to emerging technologies and ever changing user requirements.

The ultimate goal is a set of draft guidelines for TMCs detailing what data to provide in which formats to maximize CCF mapping accuracy and data utility.

Geospatial Layout of HuBMAP Teams

MC-IU within HuBMAP (http://hubmapconsortium.org)
04/16/2019



Legend

Label: Experts
Color: Role

Nodes and Edges

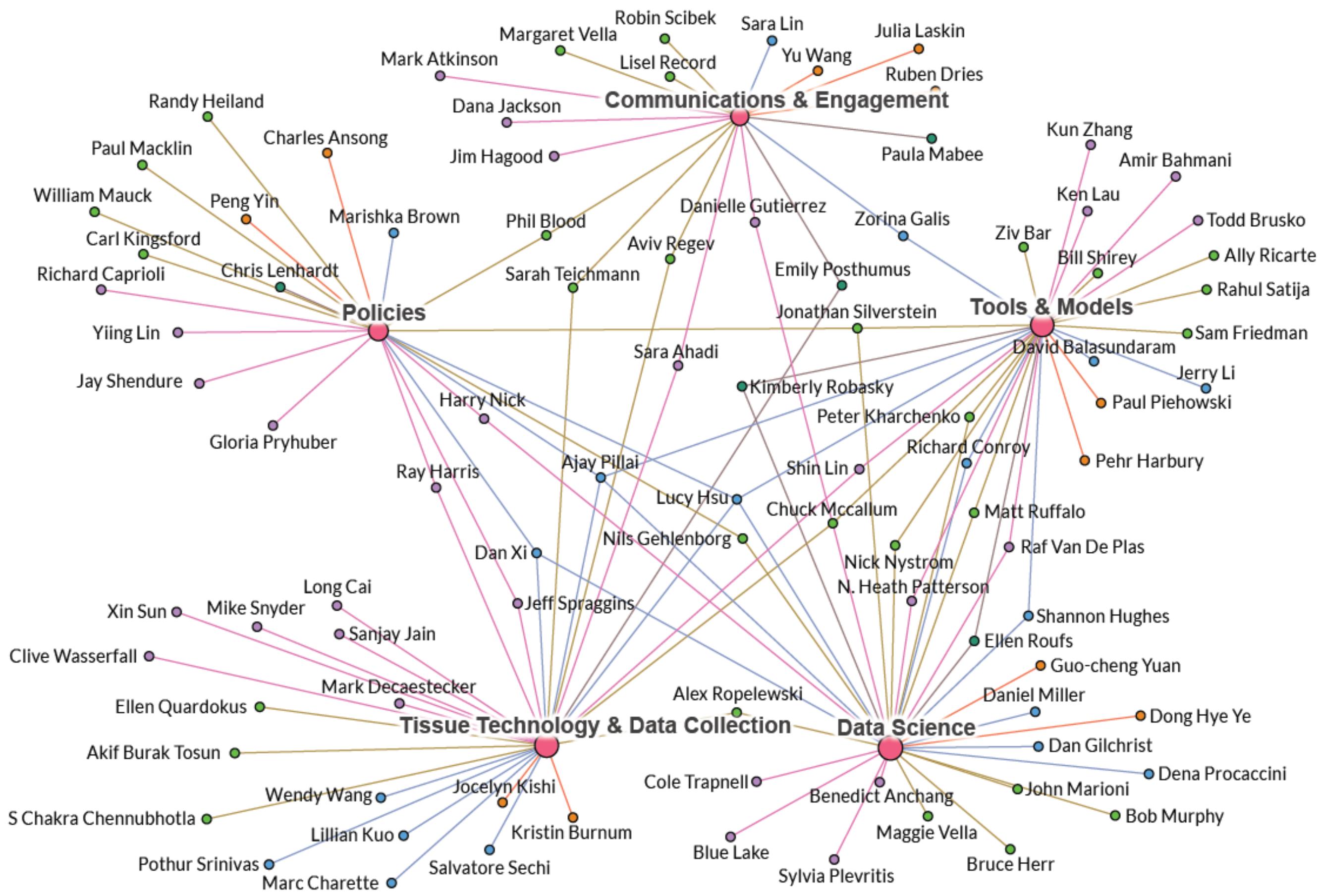
- PI (Contact)
- PI
- Co-Investigator
- NIH
- EPC

How To Read This Visualization

This geospatial map shows the collaboration network of 134 experts. Principal investigators (PIs) are placed at their exact geolocation. Team members are placed nearby and are linked to PIs. Nodes and edges are colored according to their roles.

Bimodal Network of Experts and Working Groups

MC-IU within HuBMAP (https://hubmapconsortium.org)
04/09/2019



Legend

Label: Experts
Working Groups
Color: Team Type

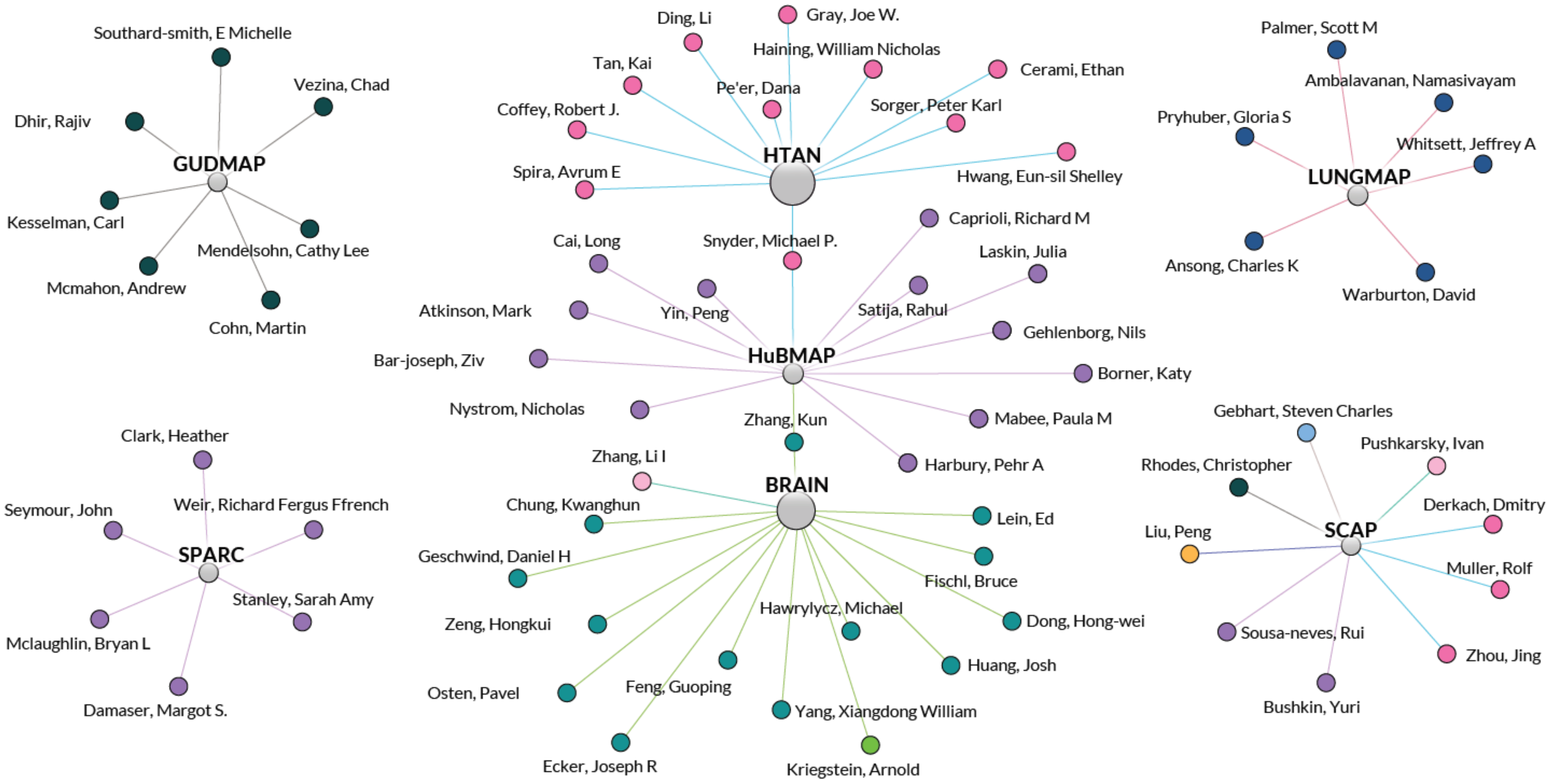
Nodes and Edges
- WGs
- HIVE
- TTD
- TMC
- NIH
- CC

How To Read This Visualization

This bimodal network represents a network between five working groups and 126 experts of those groups. Nodes and edges are colored according to the team type that expert belongs to. Working group nodes are sized by the total number of experts in the group.

Bimodal Network of PI (Contacts) and NIH Projects

MC-IU within HuBMAP (https://hubmapconsortium.org)
04/22/2019



Legend

Label: PI (Contacts)
NIH Projects
Maximum = 71,882,084
Minimum = 3,065,740

- OD
- NIMH
- NCI
- NIDDK
- NHLBI
- NCCIH
- NHGRI
- NIGMS

How To Read This Visualization

This bimodal network represents a network between six NIH projects and 73 PI (Contacts). Nodes and edges are colored according to the Funding Institute & Center that project of Pi (Contact) is financed from. NIH project's node sizes based on award amount.