

# **Multi-Level, Multi-Modal CCF UI for Data Providers and Users** within the **Human BioMolecular Atlas Program (HuBMAP)**

MC-IU Team:

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HuBMAP HIVE Q3 Demo Day

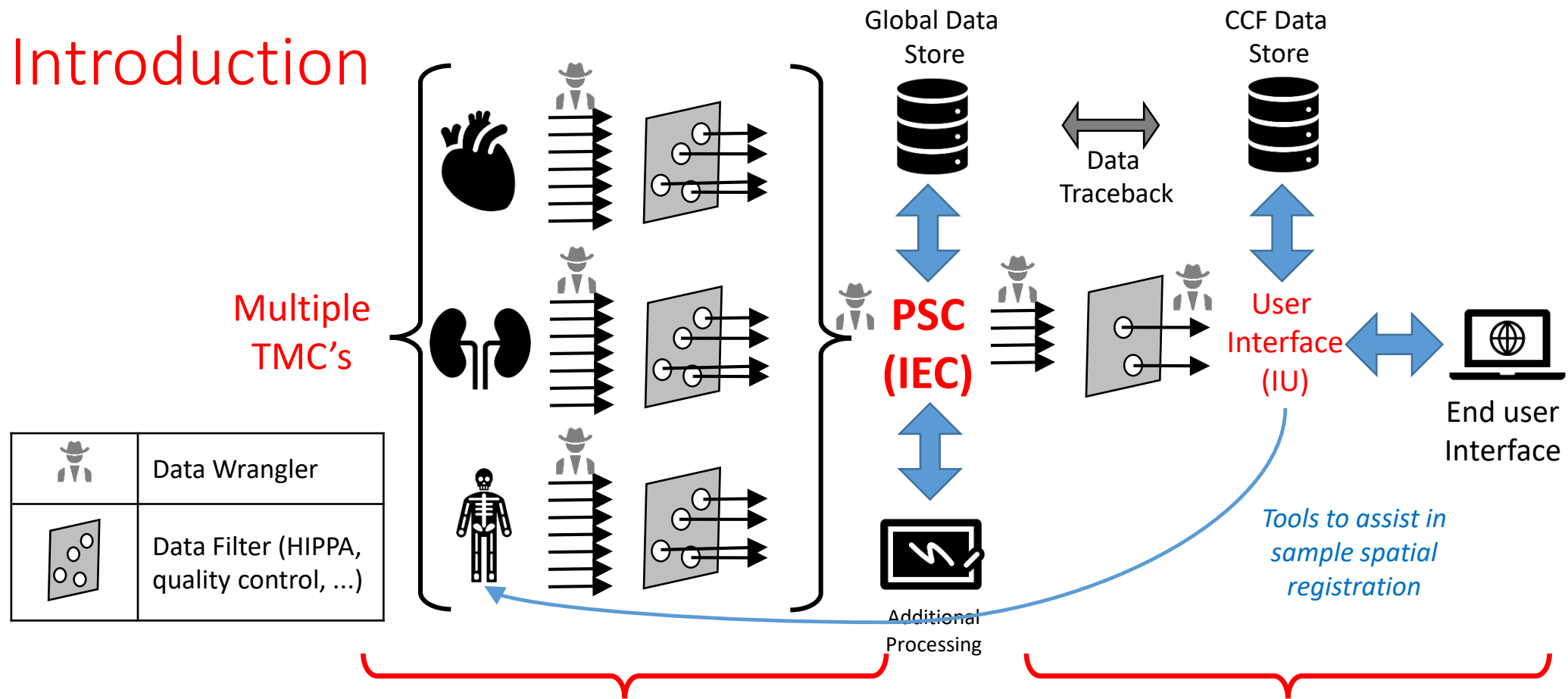
Harvard Medical School, Boston, MA

*June 27, 2019*

# Overview

- Introduction
- Y1 Q3 Progress Report
  - CCF Ontology
  - CCF Meta-Data Review
  - CCF Data Wiki
  - CCF User Interface (UI)
- Y2 Plans (June 21, 2019 - June 20, 2020)
  - CCF Mapping and Ontologies
  - CCF UI and Tissue Registration UI
  - Visual Human Massive Open Online Course (VHMOOC)
  - User Studies

# Introduction



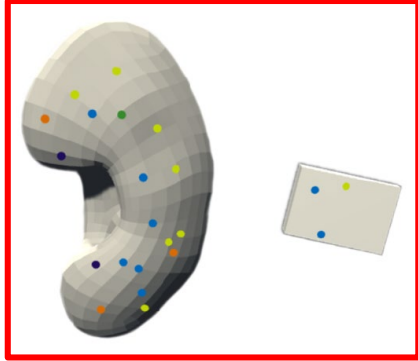
- Provenance
- Patient
- Sample
- Sample Processing
- Technology (MS, IH, ...)
- Analysis
- Etc.

*Propagate needs back to TMC's*

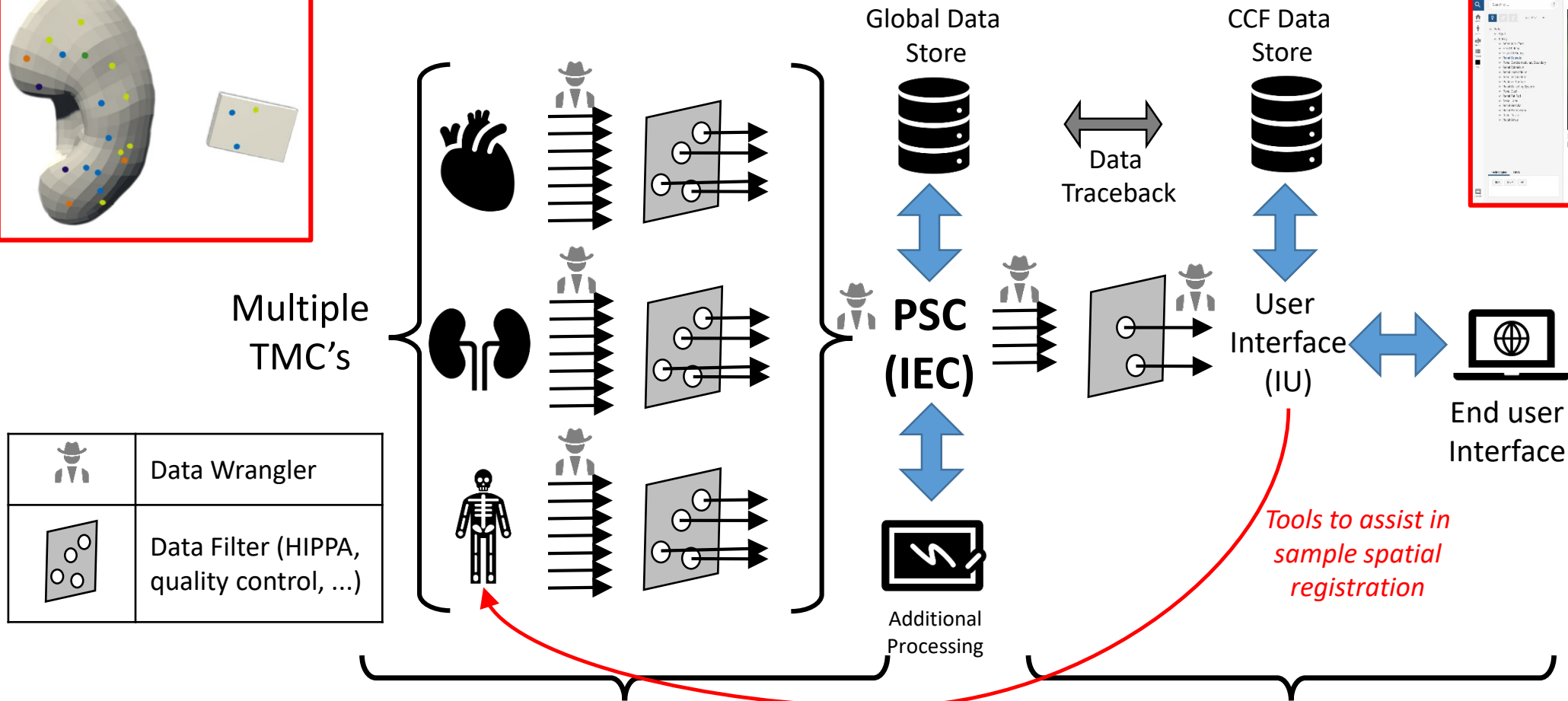
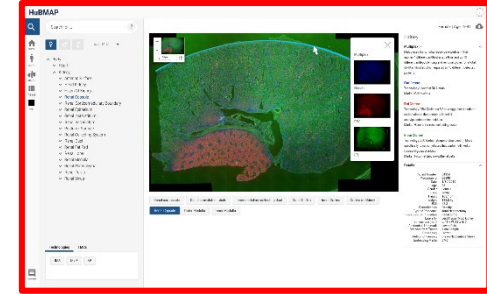
- Only the data needed for the GUI

TMC: Tissue Mapping Center  
PSC: Pittsburgh Supercomputing Center

## Tissue Registration UI



## CCF User Interface (UI)



	Data Wrangler
	Data Filter (HIPPA, quality control, ...)

- 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

# Y1 Q3 Progress - Ontology for Kidney

# CCF Ontology: some guiding principles

- Reuse existing ontologies and data formats developed for projects similar to HuBMAP to the greatest extent possible
  - GUDMAP / RBK
  - Human Cell Atlas
  - ...
- Reuse domain-specific ontologies and data formats
  - OME-Tiff (Open Microscopy Community advanced image format)
  - MIAME (Minimum Information About a Microarray Experiment)
  - ...
- Leverage HuBMAP domain expertise!
  - Each TMC is an expert in its organ. Capture this in the organ-specific ontologies.
- Use a standard Ontology format and development tools
  - We will use OWL
  - Include test cases in the ontology itself (e.g. both A-box and T-box) for testing, validation and demonstration purposes.
- Cross-link with existing ontologies as much as possible
- Need partOf trees for simplified navigation in GUI.

# CCF: Source Ontologies

## Anatomic/Phenotypic

- Uberon
- Foundational Model of Anatomy (FMA)  
(has anatomical terms NOT in Uberon)
- Human Phenotype Ontology (HPO)
- Phenotype and Trait Ontology (PATO)
- Organ specific: Kidney Tissue Atlas Ontology (KTAO) and LungMAP

## Tissue/Data Collection

- Biological Spatial Ontology (BSPO)
- Ontology of Biomedical Investigations (OBI)
- EDAM (Bioinformatics concepts)

## Open Biological and Biomedical Ontology (OBO)

**Foundry** is a collective of ontology developers that are committed to collaboration and adherence to shared principles.

**BioPortal** is a collection of ontologies for biomedical research.

## (Sub-)Cellular

- Cell Ontology (CL)
- Gene Ontology (GO)
- Chemical Entities of Biological Interest (ChEBI)
- RNA Ontology (RNAO)
- Protein Ontology (PR)
- Cell Behavior Ontology (CBO)

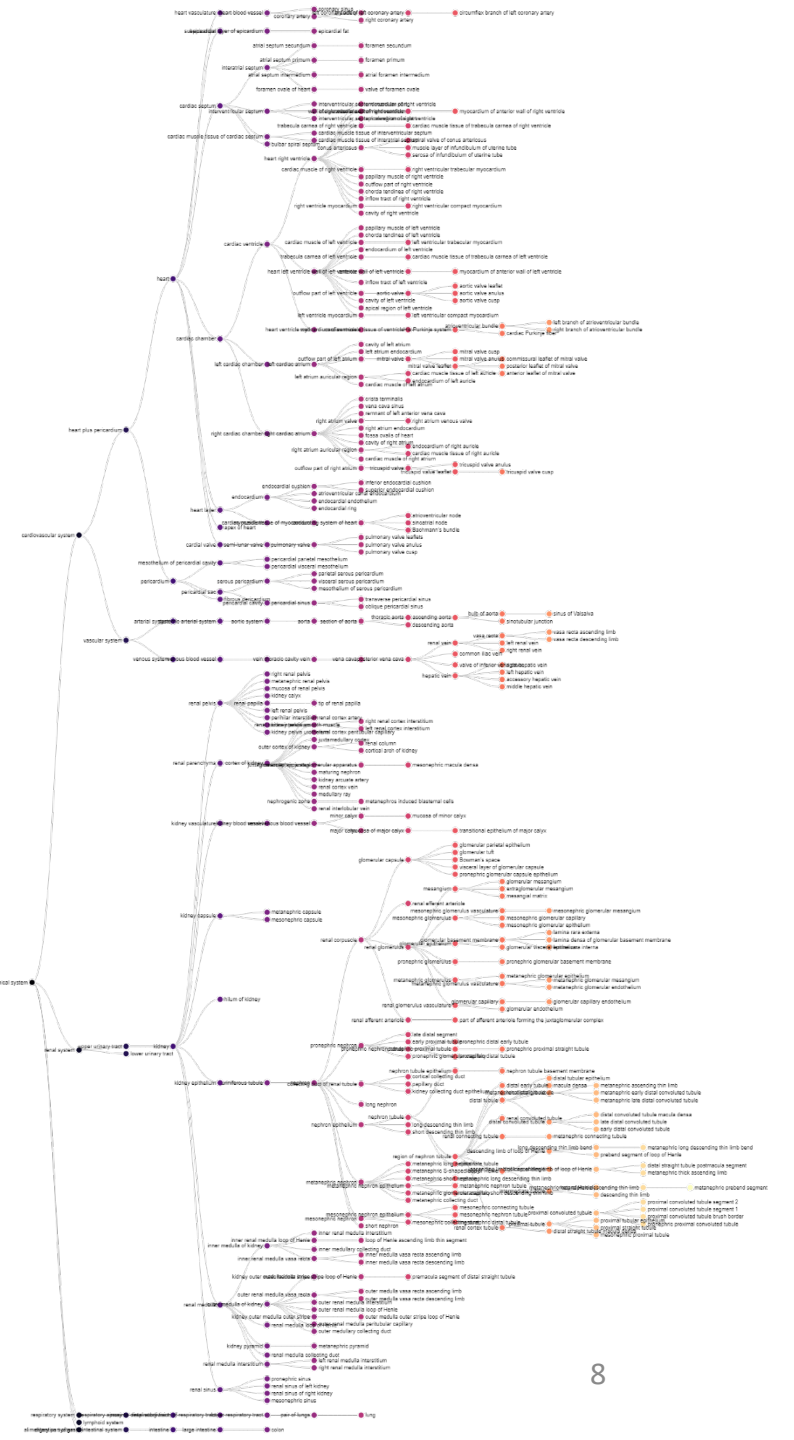
## Metadata

- Basic Formal Ontology (BFO)
- Information Artifact Ontology (IAO)
- Ontology of units of Measure (OM)
- Provenance, Authoring and Versioning ontology (PAV)
- VIVO (Identifying researchers)

## MeSH and NCI Thesaurus

# Current CCF Ontology

- Uses Uberon and user-supplied tables of terms to create a SLIM ontology
- Users (initially TMCs) can request missing terms as needed
- "partOf" and other paratomy terms used to help relate concepts
  - Requires domain expertise!
  - Individual TMCs will need to pitch in for their specific organs to refine
- [Click here to visualize the current CCF ontology](#)









# Y1 Q3 Progress – CCF Meta-Data Review

# IU CCF Initial (v0.5.0) Image Formats

**Basic image**: OME-Tiff as the base “image” format based on:

- 2D to 4D data (includes movies)
- more than three “color channels”
- More flexible “color” data format (int, float, etc.)

**Regions of images**: SVG with annotations  
(aligned with a particular OME-Tiff)

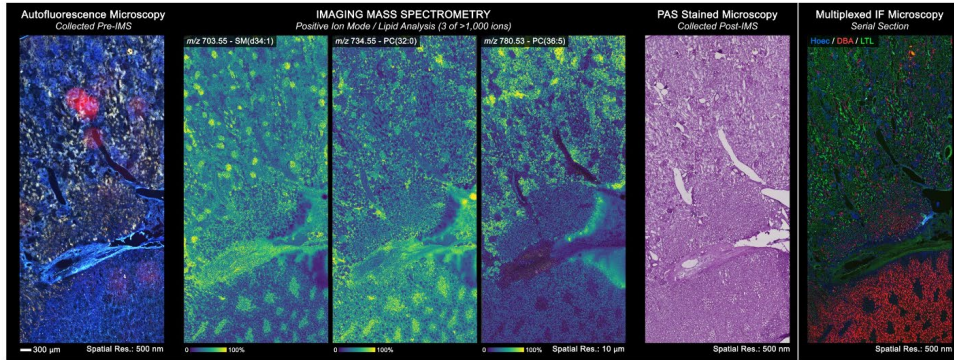
**Volumetric** (e.g., computed tomography, MR, ultrasound, ...)

- Data normally represented as volumes or surfaces

# 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 type	Subset A	Subset B	Subset C
Tubular Epithelium	Proximal tubular cells	S1	
		S2	
		S3	
Loop on Henle		Thin descending limb	
		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	
Vasculature	Mesangial cells		
	Endothelium	Glomerular	
		Peritubular Lymphatic	
Pericytes	Juxta Glomerular Cells		
Interstitial	Fibroblasts	Myofibroblasts	
		EPO producing cells	
		Medullary fibroblasts	
	Mononuclear cells	Resident macrophages	
		Dendritic cells	
Lymphocytes		T cells	
		B cells	
		NK cells	

Cell Types, on right

Cell States (9 rows)

Cell states	Subset A
Proliferating cells	S-phase G2/M
Cell cycle 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	IsNull	Parent Field	Parent Field	Can Child	Read Only	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 diabetes:	diabetes				smallint	lkup_histdiab_dur					TRUE					FALSE	
31	Donor	//History of cancer:	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	FALSE
33	Details	//History of hypertension:	hypertension				smallint	lkup_histtype_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 Table	Low Value	High Value	Valid value
9	Donor	//ABO:		abo			char(3)	lkup_abo			
10	Donor	//Date of birth:		dob			datetime				
11	Donor	//Gender:		gender			char(1)	lkup_gender			M,F
12	Details	//Age:		age_in_months			smallint		0	1188	
13	Details	//Age Unit:		age_unit			char(1)	lkup_age_unit			M,Y
14	Details	//Height:		hgt_cm		cm	decimal(5, 2)		1	241.3	
15	Donor	hgt_ft //		hgt_ft		ft	int		0	7	
16	Donor	hgt_in //		hgt_in		in	int		0	11	
17	Details	//Weight:		wgt_kg		kg	decimal(7, 4)		0.454	294.835	
18	Donor	wgt_lb //		wgt_lb		lbs	decimal(3, 0)		2	650	
19	Donor	//Ethnicity/race:		race			bigint	lkup_race_subcat_multi			
30	Details	//History of diabe	hist_diabetes				smallint	lkup_histdiab_dur			
31	Donor	//History of cance	hist_cancer				smallint	lkup_histcancer_site			
32	Donor	History of cancer	, cancer_oth_ostxt				varchar(50)		1	50	
33	Details	//History of hyper	hypertension				smallint	lkup_histhype_dur			

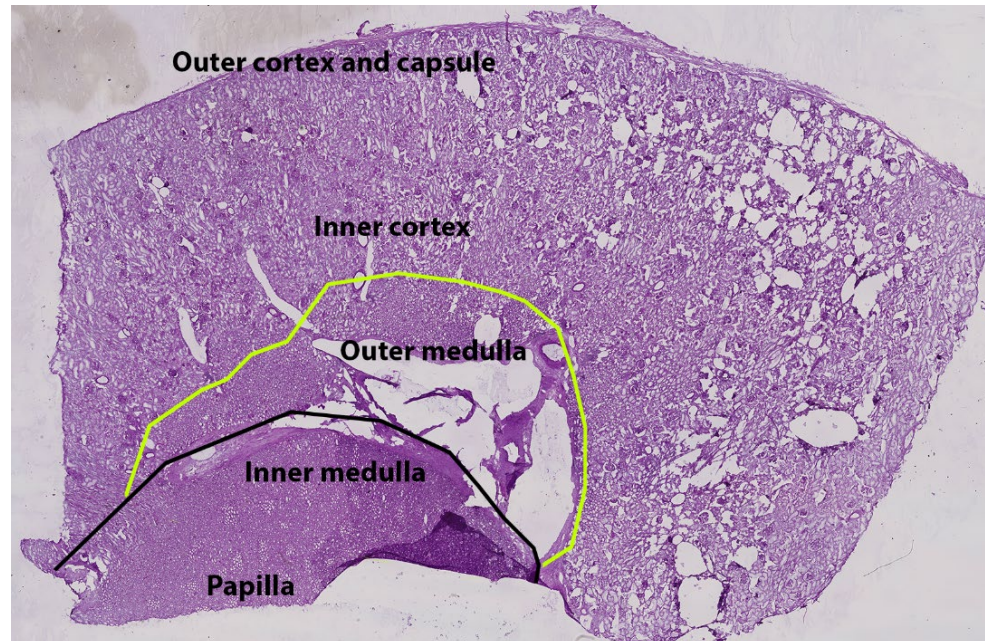
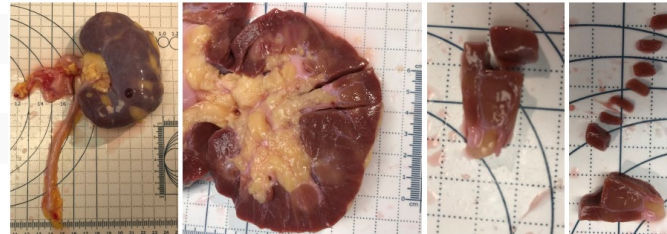
# Data: 3D Tissue

**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

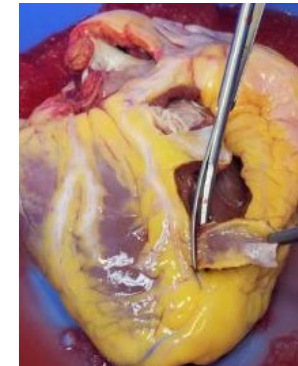
BUKMAP, Zhang Group



**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



<u>Sites</u>	<u>Distinctive features</u>
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

**Sternocostal surface labels:** Sinuatrial (SA) nodal branch, Atrial branch of right coronary a., Right coronary a., Anterior cardiac vv., Small cardiac v., Right (acute) marginal branch of right coronary a., Interventricular septal branches, Aorta, Left, Cir, Great cardiac v., Anterior interventricular branch (left anterior descending) of left coronary a.

**Diaphragmatic surface labels:** Oblique v. of left atrium (of Marshall), Great cardiac v., Circumflex branch of left coronary a., Left marginal branch, Coronary sinus, Posterolateral a., Middle cardiac v., Interventricular septal branches, Sinuatrial (SA) nodal branch, Small cardiac v., Right coronary a., Inferior (posterior) interventricular (posterior descending) branch of right coronary a., Right marginal branch.

# Data: TMCs x Organs x Data Types x Technologies

BUKMAP, Zhang Group

## Organs (10)

1. Bladder
2. Blood Vessel (Heart)
3. Breast
4. Colon
5. **Kidney**
6. Liver
7. Lung
8. Spleen
9. Thymus
10. Tonsil

No Bone Marrow  
and Pancreas.

## Data Types (13)

1. Imaging - Proteins
2. Imaging - RNA
3. Imaging - DNA
4. Imaging - Other
5. scRNAseq
6. scDNAseq
7. scProteomics
8. bulk-Proteomics
9. bulk-RNA
10. bulk-DNA
11. Metabolomics
12. Lipids
13. Other

## Technologies (~25)

- CODEX;DART-FISHrp;IF;IHC;LRET-IF;MALDI Imaging MS;PER-DEI  
**DART-FISH**;LRET-ISH;MERFISH;PER-DEI;seqFISH;smFISH  
PER-DEI  
Lipid and Metabolite MALDI Imaging MS  
snDropseq;**scRNAseq**  
scATACseq;scTHSseq;SNAREseq  
IMC  
LC-MS/MS  
?  
?  
LC-MS/MS;nano-POTS  
LC-MS/MS;nano-DESI  
Autofluorescence;PAS stained microscopy



# Review of Meta-data formats of similar projects

## Other NIH Centers

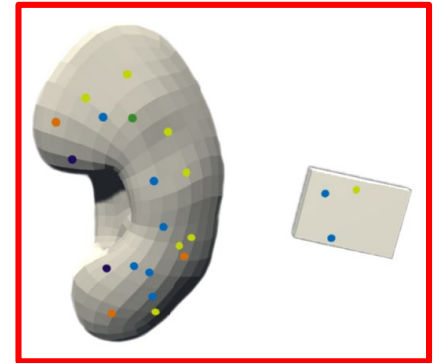
- GenitoUrinary Development Molecular Anatomy Project (GUDMAP)
- (Re)Building a Kidney (RBK)
- Kidney Precision Medicine Project (KPMP)

## Other Efforts

- Human Cell Atlas (HCA)
- ApiNATOMY

# 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

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

Edit New Page

## Welcome to the CCF Data Wiki!

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

Pages 12

Links

- Home

Templates

- TMC-Organ-Template

Clone this wiki locally

<https://github.com/hubmapcc>

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

### Legend:

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

# Y1 Q3 Progress - CCF User Interface (UI)

# Y1 Q3 Progress - CCF User Interface (UI)

The screenshot displays the HuBMAP Semantic Search interface. At the top, the search bar is empty, and the user profile is identified as 'Female | Age 19-41'. The left sidebar contains navigation icons for Home, Body, Organ, Tissue, and Cell. A 'Semantic Browsing' section lists various anatomical regions, with 'Kidney' expanded to show sub-regions like 'Renal Capsule' and 'Renal Cortex'. Below this, 'Semantic Filters' allow selection of technologies (IMS, MxIF, AF). The main area features a large kidney tissue image with a 25 µm scale bar and a 'Multiplex' panel showing three channels: Hoechst (blue), DBA (red), and LTL (green). A 'Details' panel on the right provides patient and procedure information, including Patient Number 64354, Procedure ID 66598, and Date 1/30/2019. The patient is a 38-year-old female, white, with a height of 165.1 cm and weight of 115.2 kg. The procedure was a Total Nephrectomy for a Renal tumor, with dimensions of 19 x 13 x 7 mm. The tumor was located at the lower pole, 7 cm from the sample, and was frozen in dry ice/isopentane slurry.

**HuBMAP Semantic Search**

Search for ... ?

Female | Age 19-41

**Body**

- Heart
- Kidney**
  - Anterior Surface
  - Head Kidney
  - Hilum Of Kidney
  - Renal Capsule
  - Renal Corticomedullary Boundary
  - Renal Epithelium
  - Renal Interstitium
  - Renal Vasculature
  - Posterior Surface
  - Renal Collecting System
  - Renal Duct
  - Renal Fat Pad
  - Renal Lobe
  - Renal Medulla
  - Renal Parenchyma
  - Renal Pelvis
  - Renal Sinus

**Semantic Browsing**

Renal corpuscle | Distal convoluted tubule | Inner medullary collecting duct | Outer Cortex | Inner Cortex | Cortex of Kidney

Renal Capsule | Outer Medulla | Inner Medulla

**Semantic Filters**

Technologies | TMCs

IMS | MxIF | AF

**Kidney**

**Multiplex IF**

Multiplexed immunofluorescence experiment that applies 4 different antibodies at a time and do 10 different antibody binding and removal cycles for a total of 40 antibodies which equates to 40 different detected proteins.

**Blue Channel**

Technology: Hoechst DNA stain  
Marker: Cell nucleus

**Red Channel**

Technology: DBA (Dolichos Biflorus Agglutinin) binds to carbohydrates that contain a-linked N-acetylgalactosamine residues  
Marker: General for renal collecting ducts.

**Green Channel**

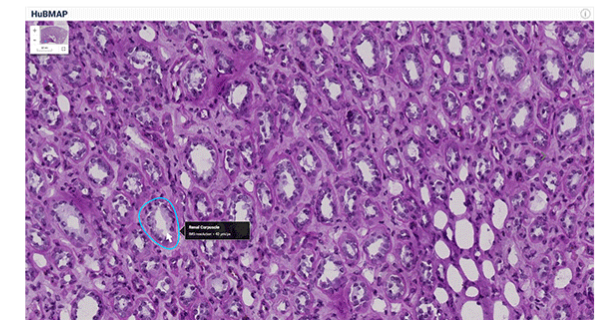
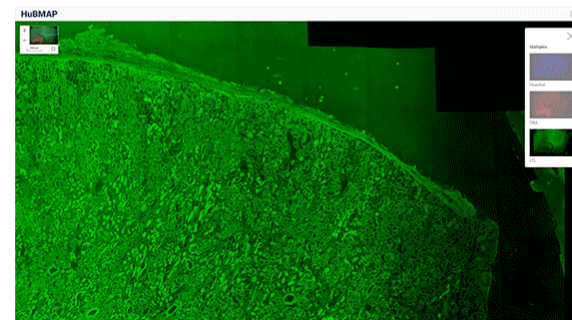
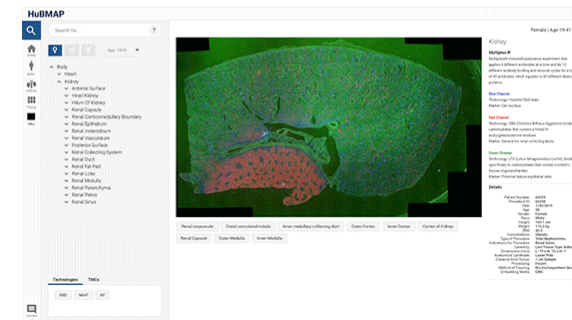
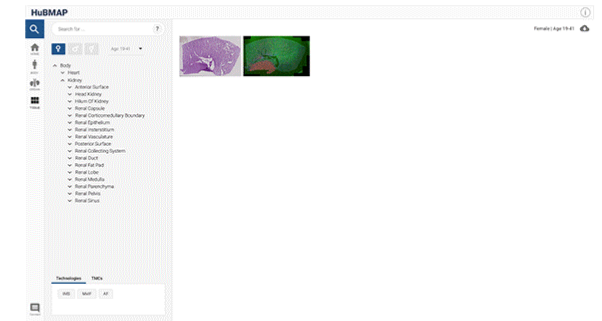
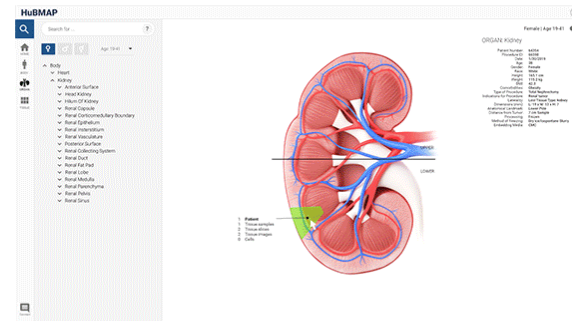
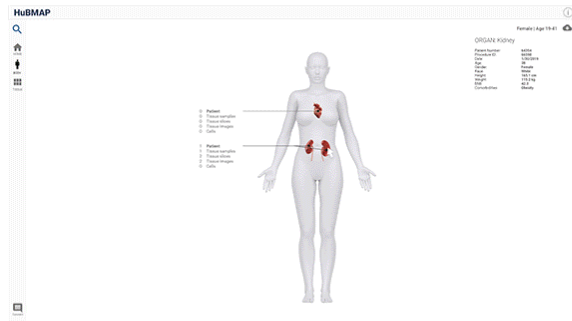
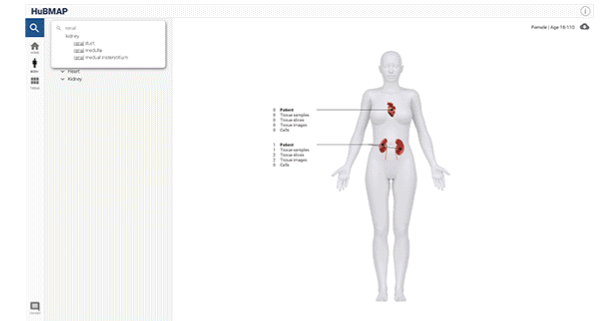
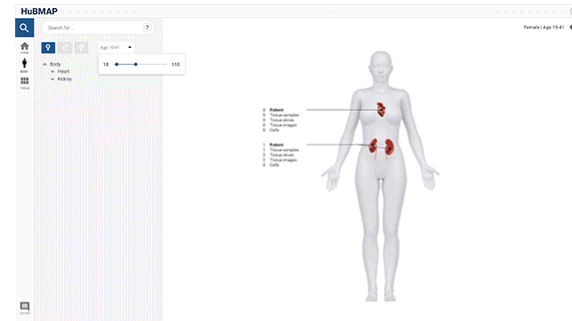
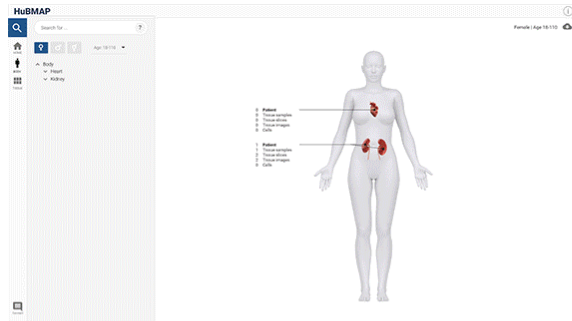
Technology: LTO (Lotus tetragonolobus Lectin) binds specifically to carbohydrates that contain a-linked L-fucose oligosaccharides  
Marker: Proximal tubule epithelial cells

**Details**

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  
Lateralality: 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

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

# Y1 Q3 Progress - CCF User Interface (UI)



# Y1 Q3 Progress - 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](https://www.youtube.com/watch?v=rWMqKQc_00w&feature=youtu.be)

GitHub link to code: <https://github.com/hubmapconsortium/ccf-ui>

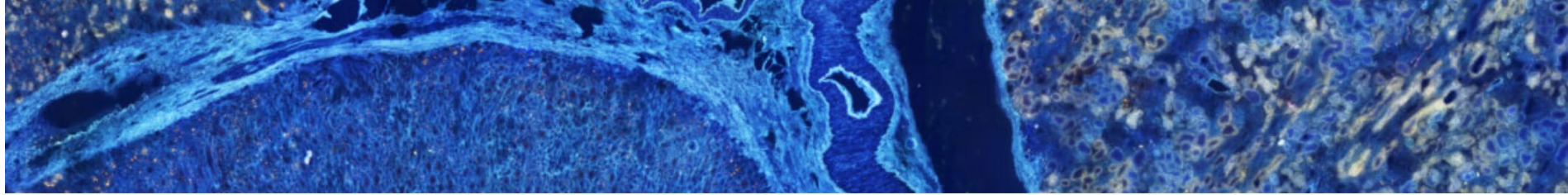
GitHub demo site: <https://hubmapconsortium.github.io/ccf-ui/>

Original specs: <https://drive.google.com/open?id=1tqUzmVLxwqcGprtRlevfY86YvHHPEsDR>

**Live Demo!**



# CCF Workshop



**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.

# Y2 Plans

- CCF Mapping and Ontologies
- CCF UI and Tissue Registration UI
- Visual Human Massive Open Online Course (VHMOOC)
- User Studies

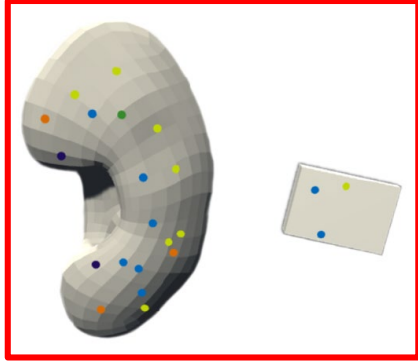


# Y2 Plans: CCF Mapping and Ontologies

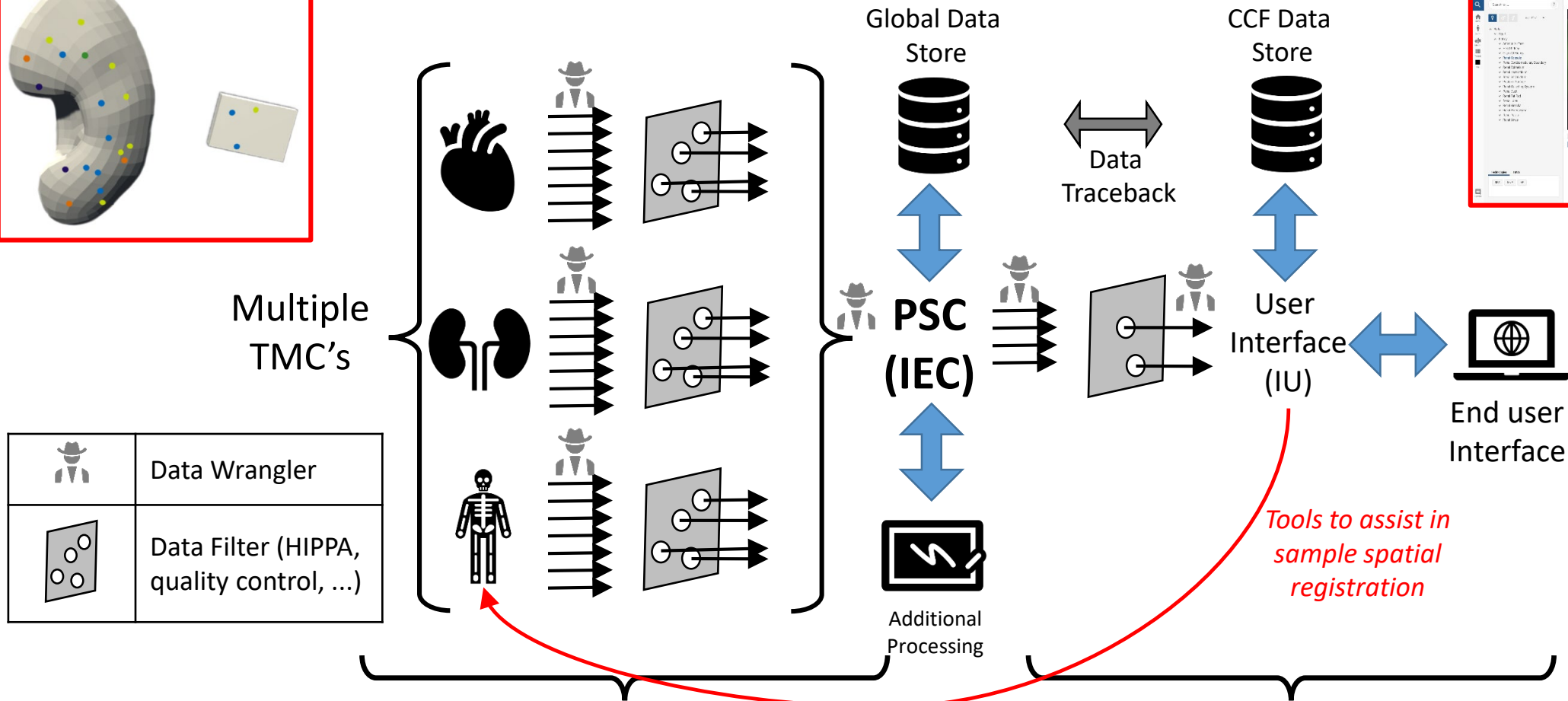
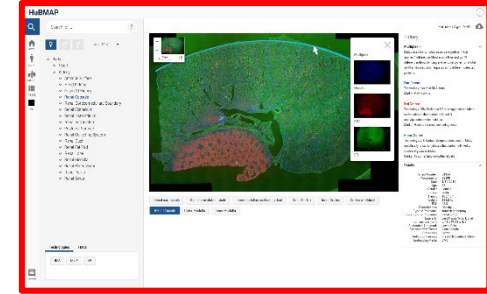
- Complete kidney ontology and switch to “part of” hierarchy
- V1.0.0 Data format specifications for image data including specification of identified regions
- Patient, sample and technology metadata ontologies in collaboration with the tissue centers
- Lung ontology

# Y2 Plans: CCF UI and Tissue Registration UI

## Tissue Registration UI



## CCF User Interface (UI)



- 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: Heart (depending data availability)

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

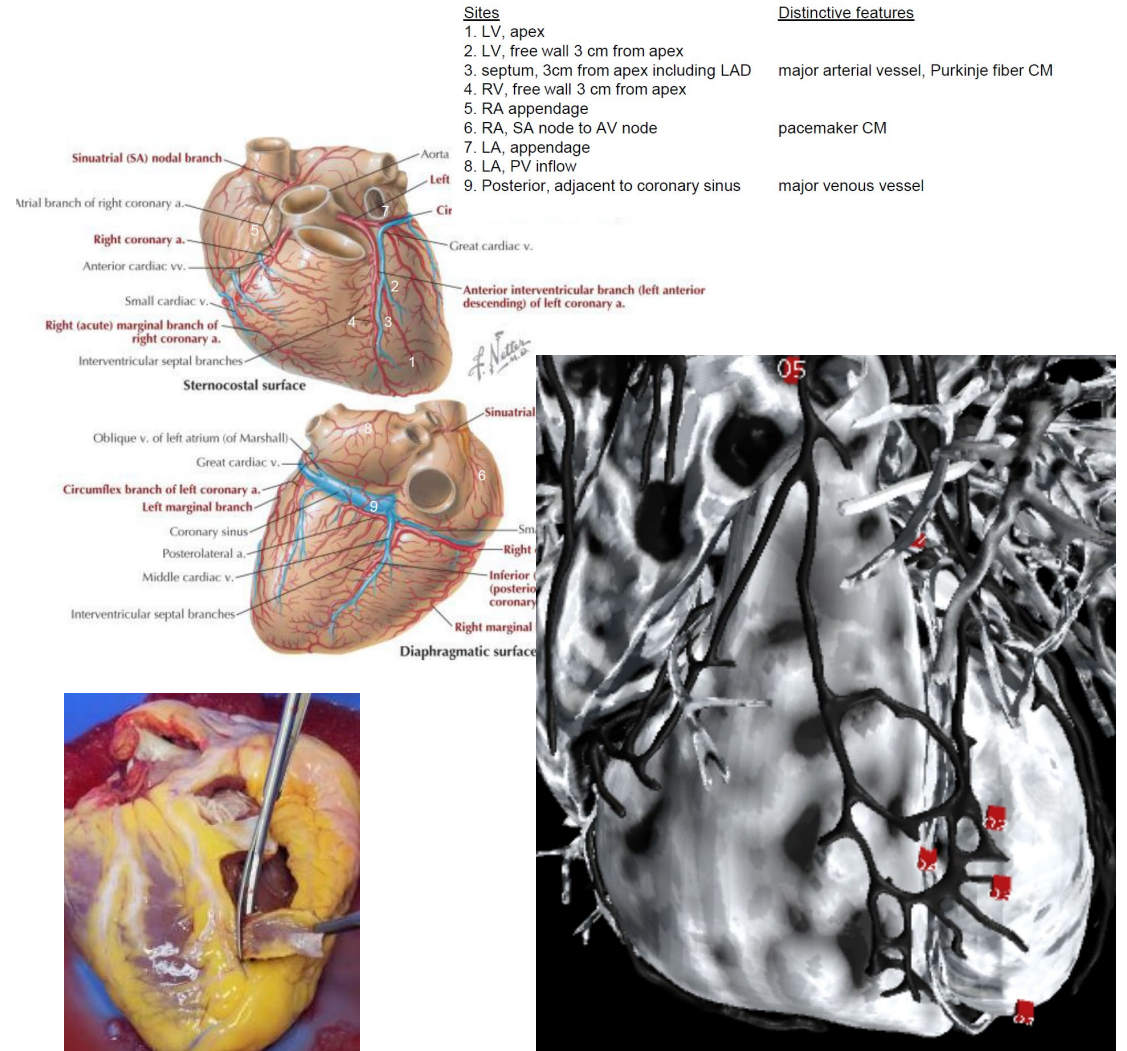
- Rough placement using human expertise/3D pattern matching and
- Fine adjustments using machine learning

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.

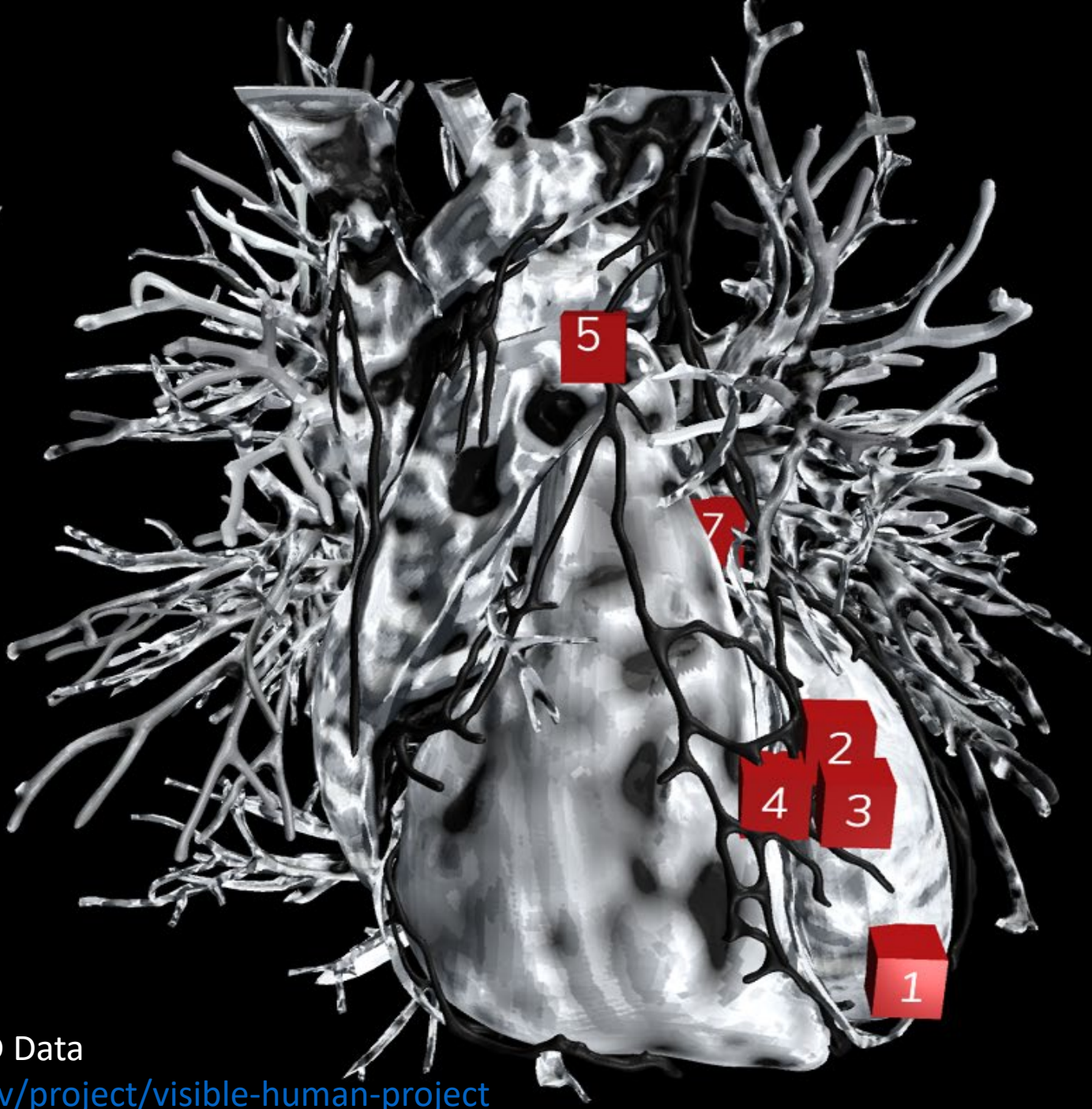




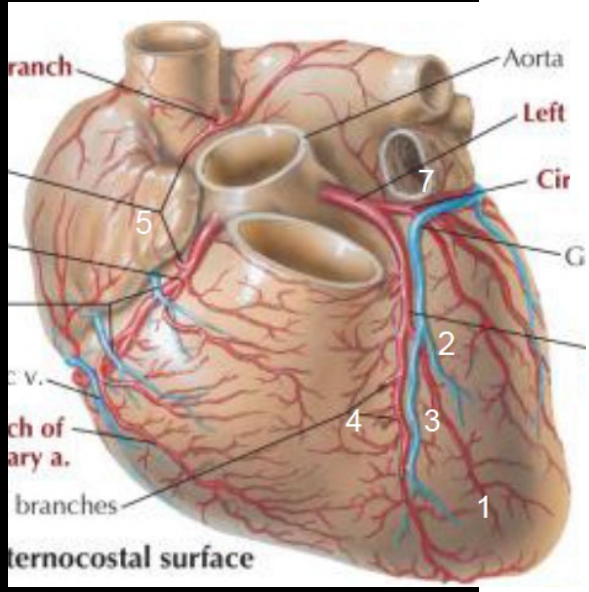
Human heart with data overlay  
Developer: Andreas Bueckle

- 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!



# Tissue Registration UI: Kidney

(depending data availability)

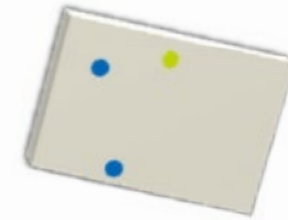
- Exploit human pattern recognition and fine motor skills (by surgeons) to register tissue in organs.
- Add info on anatomical landmarks, cell types, molecular data to support alignment.
- LATER: Use human alignment data as training data for machine learning algorithms, to better support manual alignment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



VIVE™ | VIVE Virtual Reality System  
vive.com



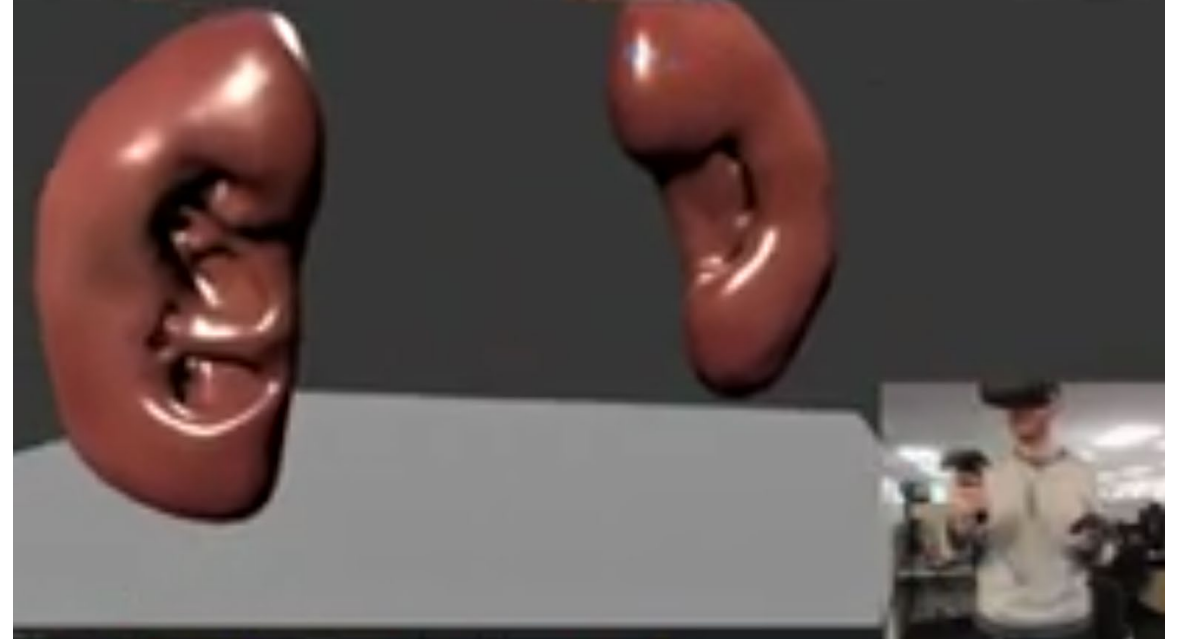
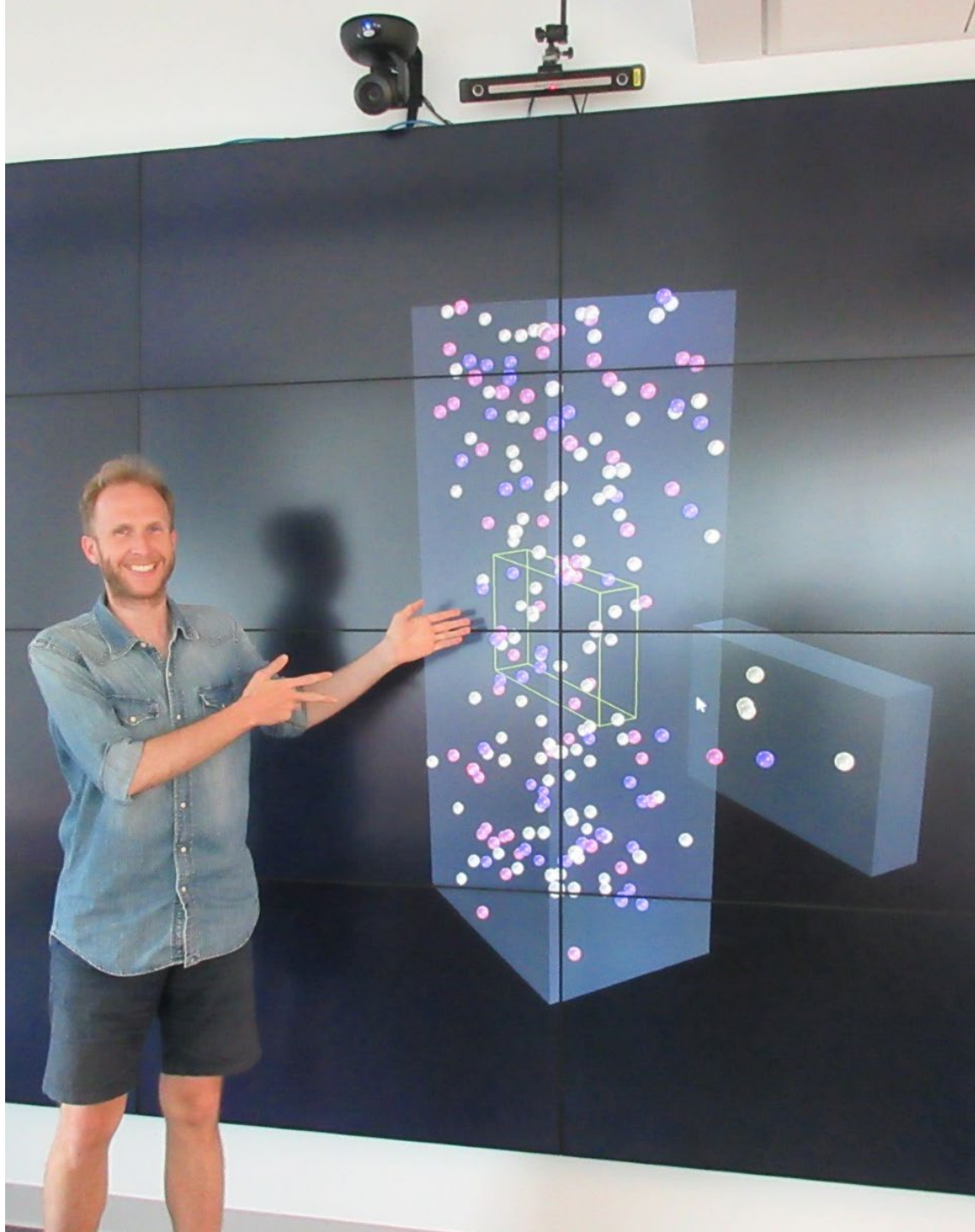
**How many of you have used  
a VIVE or space mouse?**



Kidney model from NLM3D Data

<https://lhncbc.nlm.nih.gov/project/visible-human-project>



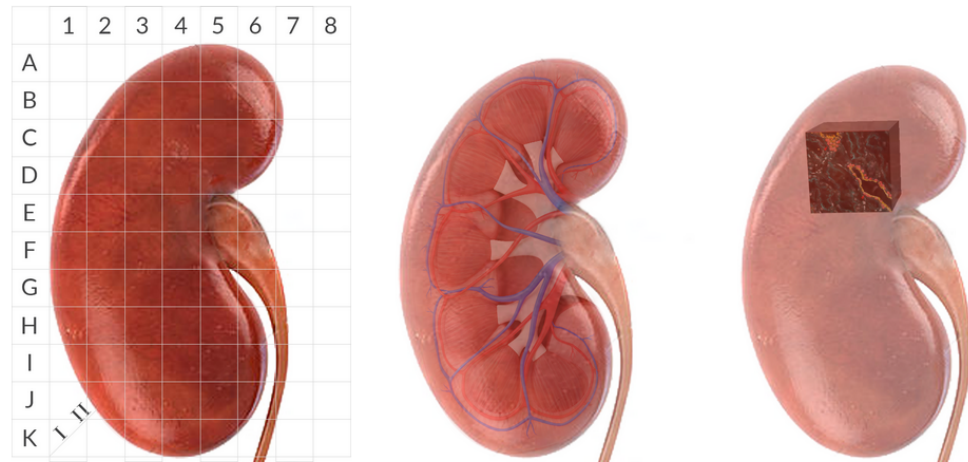


Kidney model from NLM3D Data

<https://lhncbc.nlm.nih.gov/project/visible-human-project>



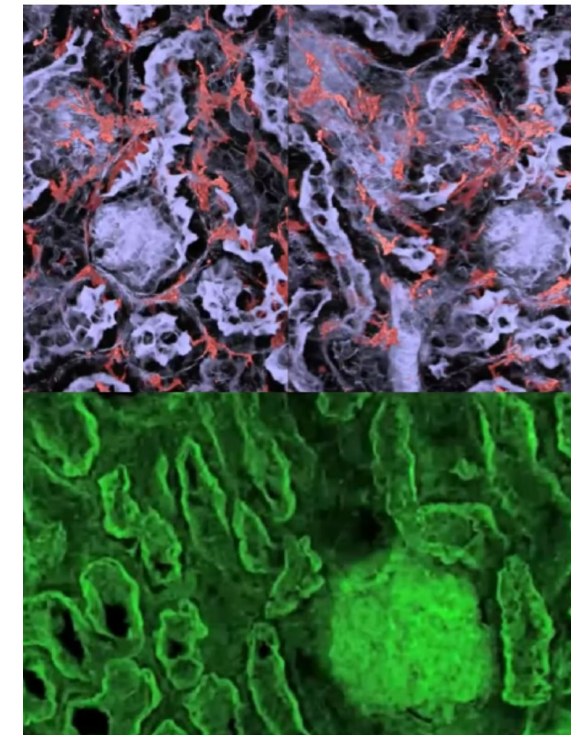
For the kidney, there exist no predefined tissue extraction sites. The current kidney Registration UI uses a grid system and a picture of a kidney slice to guide placement, see **Fig. 3 left and middle**. Funding of this GLUE grant will make it possible to use 3D image volumes collected from intact kidney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



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

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.

KPMP GLUE grant  
proposal in progress.



**Fig. 4.** KPMP volumetric data.

See presentation by Seth Winfree for details

<https://ccfws.cns.iu.edu>



# Y2 Plans: CCF UI

- Use the CCF UI to serve a **Kidney Micro Atlas**.
- Go from Proof of Concept to fully-realized application
  - Fully integrate heart and kidney data
  - Integrate Tissue Registration UI data
  - Integrate expanded CCF Ontology
  - Connect to data/queries via IEC APIs and infrastructure
- Collaborate on a common Tissue Viewer

## Y2 Plans:

# Visual Human Massive Open Online Course (VHMOOC)

Research and develop a Visual Human Massive Open Online Course (VHMOOC) that helps communicate the

- quality and coverage of HuBMAP data,
- utility and proper usage of CCF Tissue Registration, CCF UI, and HuBMAP tools, and
- demonstrate new single-cell analysis and CCF mapping techniques.

First interviews with experts will be run at the HuBMAP meeting at Stanford U.

**Please let MC-IU know if you are interested/available to showcase your work.**

# Y2 Plans: User Studies

Conducting in-depth interviews with experts to understand user needs (Y1Q3, will continue in Y2Q1)

Information gathered will inform both the Tissue Registration UI and the Common Coordinate Framework UI.

Identified 6 draft personas (Y1Q3, will refine in Y2)

Generator, Analyst, Technologist, Computationalist, Data Provider, Educator/StudentBased on interviews, user stories, surveys, and comparisons with similar projects (HCA, KPMP)

We welcome your feedback on their applicability across the project. Review and provide feedback at <https://bit.ly/2ZFHWYW>.

Developed methodology and obtained IRB approval for user studies to be conducted in Y2 (Y1Q3)

Task-oriented user testing to improve the CCF user interface. Administered online, with HuBMAP members and other biological researchers who are representative of users based on their research interests.

## Educator/Learner

Focus: Learning  
Data Use: Data consumption  
Role: Uses data across many roles with the goal of learning

## Data Provider

Focus: Data sharing  
Data Use: Distribute data  
Role: Ensures data meets standards for sharing with others

## Computationalist

Focus: Modeling/Simulations  
Data Use: Consumes and generates new data  
Role: Designing algorithms and models for simulations

## Technologist

Focus: Technology/Process advancement  
Data Use: Consumes and generates data  
Role: Works with a variety of software/hardware to test hypotheses around improving software/hardware/process.

- Need to have access to all types of animal samples for download to use in processes, such as to use methods used in technological processes.
- Need access to sample metadata to determine what processes were used to generate the samples in efforts to improve local processes, compare results, or develop a better method.
- Need metadata and samples to learn about trends in the field.
- Need to know what protocols others are using in order to make improvements.
- Need 3D models/2D images to understand technologies used to excise cell-level interactions.
- Need to be able to enable/disable technologies used on samples to

## Outcome

Uses data to create/improve processes or technologies to support the Computationalist.

## Analyst

Focus: Data consumption  
Data Use: Consumes data  
Role: Compares digitized samples at a computer or similar device.

## Generator

Focus: Data creation  
Data Use: Generates tissue data  
Role: Uses technologies to produce data from physical samples

- Need to have access to data in order to test/validate processes/methods used in the lab.
- Need to have access to standards/protocols in order to produce data that Data Providers can then submit to HuBMAP in a usable format that follows stringent scientific process.
- Need to download data in a usable format in order to use with local data for the purpose of securing grants or publication.

## Outcome

The primary goal is to use various technologies to generate data from tissue samples to be used by others for purposes such as diagnosis, building models, etc.