

Kidney Metadata and Ontology Design (HuBMAP)

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underlined: most directly involved in ontology development

Intelligent Systems Engineering
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May 9, 2019

Motivation

Mapping Components (MC): Spatial maps of biomolecular data

Given anatomical and molecular data, develop and validate:

1) Terminologies/Ontologies (Semantics)

- Reference concepts, e.g., organs, organ parts, cell types, cell states
- Fiduciary concepts: Well-defined landmarks that can be provided by TMCs and used by MC to spatially orient data with respect to 3D structures

2) 3D Spatial Models interlinked with terminology/ontology

- Across levels (gross anatomy/organ, tissue, cell level) using hierarchical containment to localize the sample within the body
- Make landmarks visible in 3D models

3) Interface for semantic and spatial search, filter, review, download of data.

- Use ontology for query expansion (elastic search), semantic browsing, and as controlled vocabulary (e.g., turning on/off male/female or different cell states).
- Use 3D models for spatial browsing, confirmation of proper tissue registration, exploring cell context, etc.

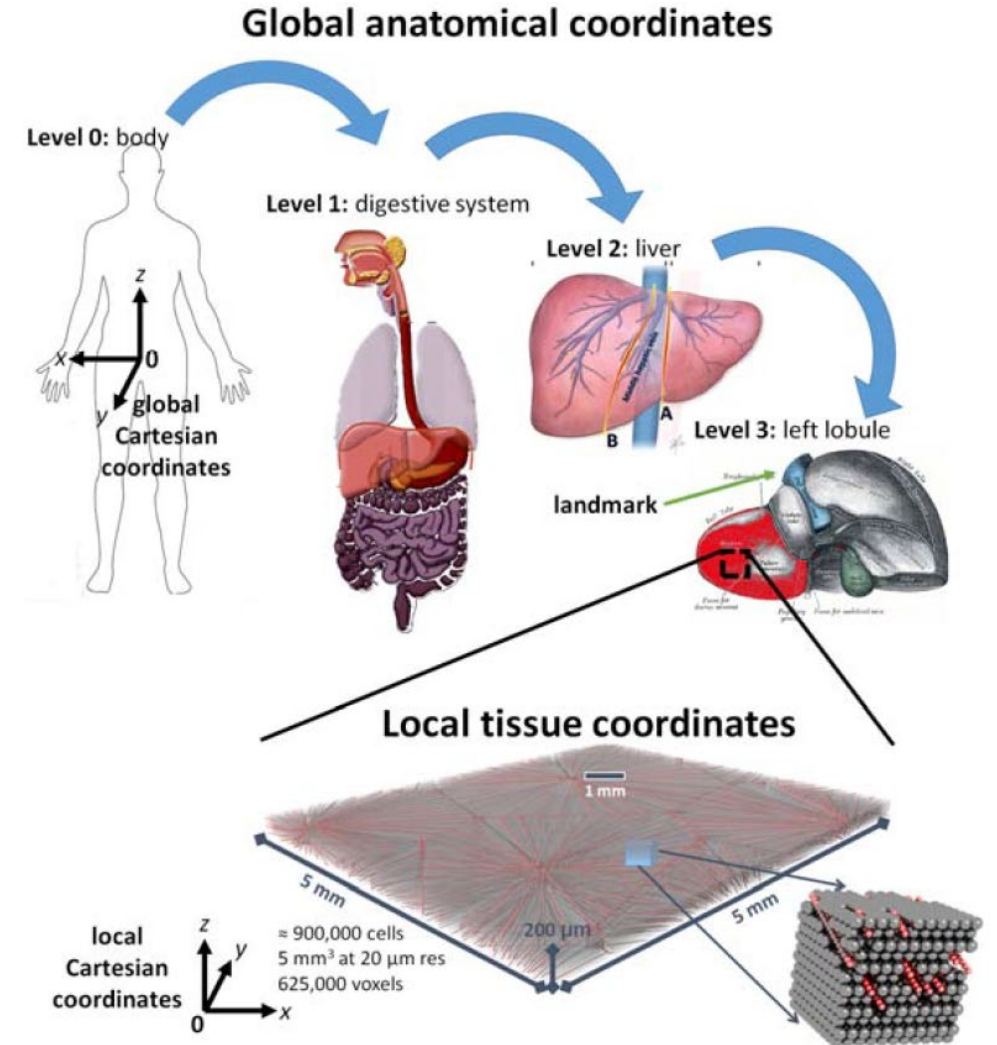
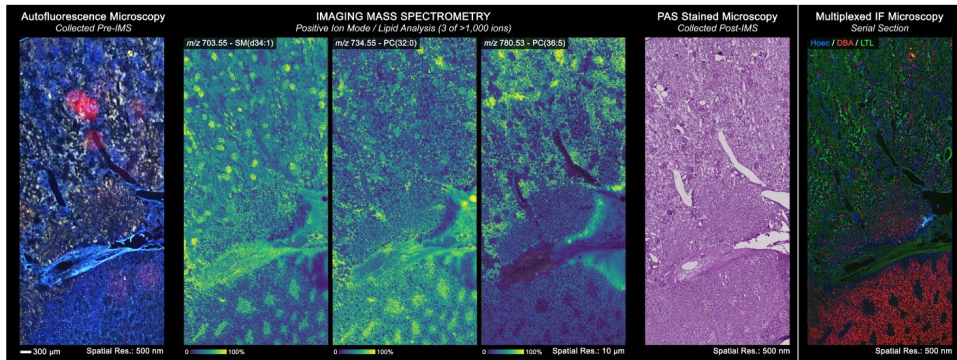


Fig. 5. CCF concept, navigating through the global anatomical coordinate system to insert a synthetic tissue sample (from PhysiCell⁴) into the left liver lobe with a local coordinate system.

We must plan for heterogeneous data

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	Principal cells	Type A
		Intercalated cells	Type B
Glomerulus	Epithelium	Visceral	
		Parietal	
Vasculature	Endothelium	Mesangial cells	
		Glomerular	
		Peritubular	
	Pericytes	Lymphatic	
		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:	hist_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:	hist_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

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

Jeff invited feedback on current fields and format.

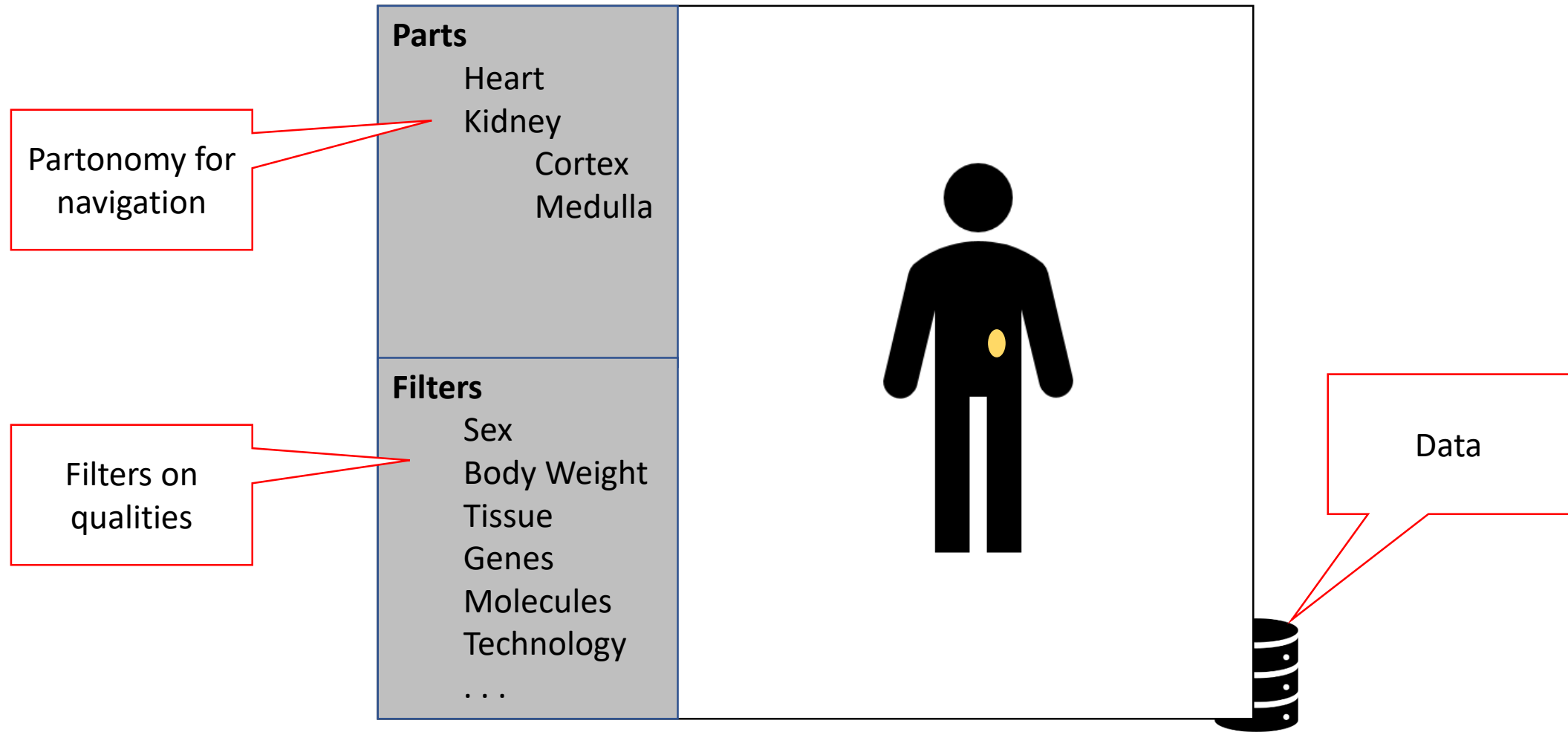
Heart: Shin Lin, UW

Data Dictionary (115 rows)

Field #	Sort	Field Label	Sort	Field Name	Sort	Field Units	Field Data	Lookup Tal	Low Value	High Value	Valid value
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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			

Please complete **TMC Landmarks Survey** at <https://goo.gl/forms/x9F8cP1GlzprDxbI2> (complete one survey per organ)

Goal: Facilitate navigation of multiscale data



Overall CCF Approach

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 Microcopy 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
- May need separate partOf (or class/subclass) 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)

(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

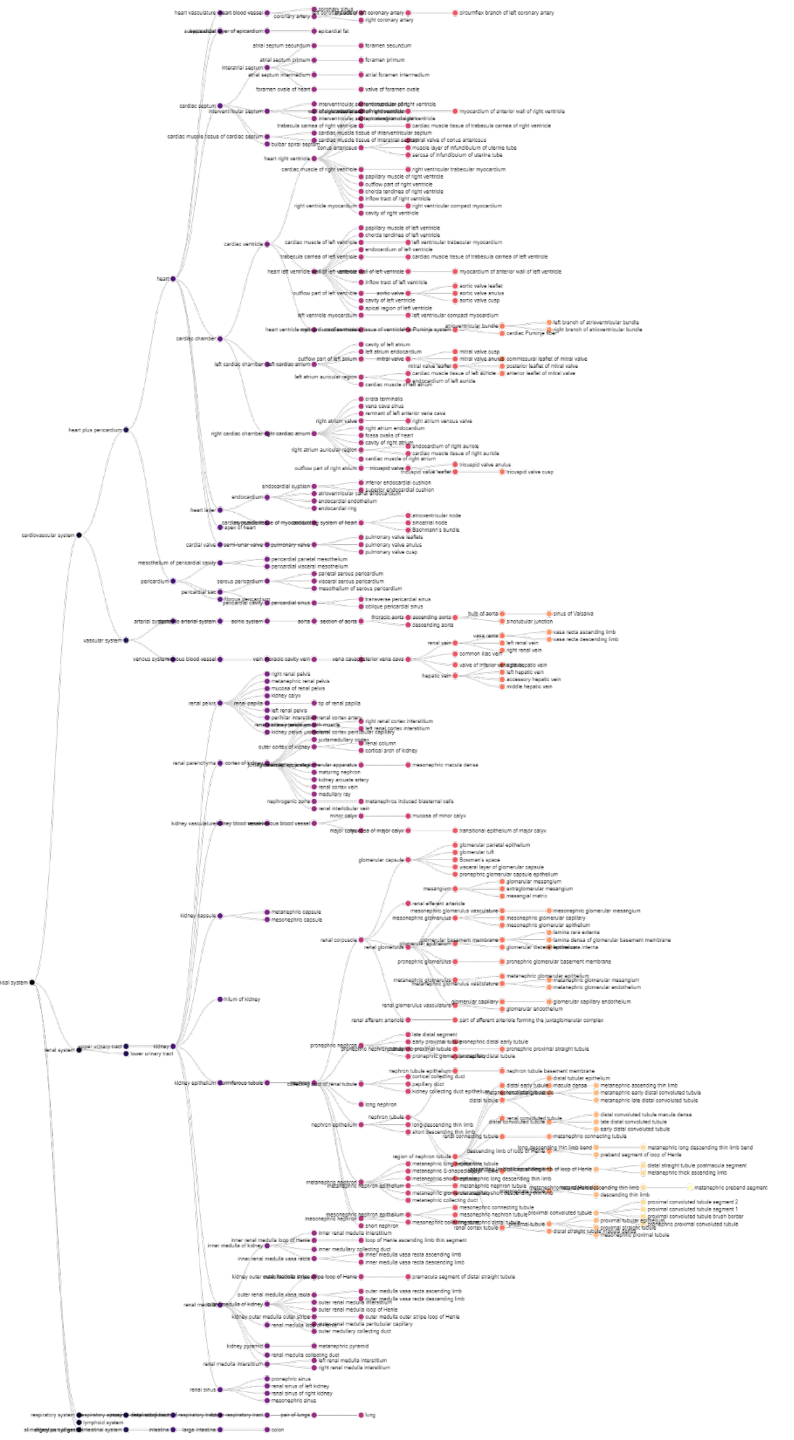
- Basic Formal Ontology (BFO)
- Information Artifact Ontology (IAO)
- Ontology of units of Measure (OM)
- Provenance, Authoring and Versioning ontology (PAV)
- VIVO (Identifying researchers)

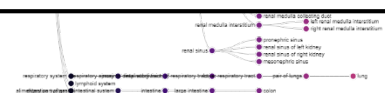
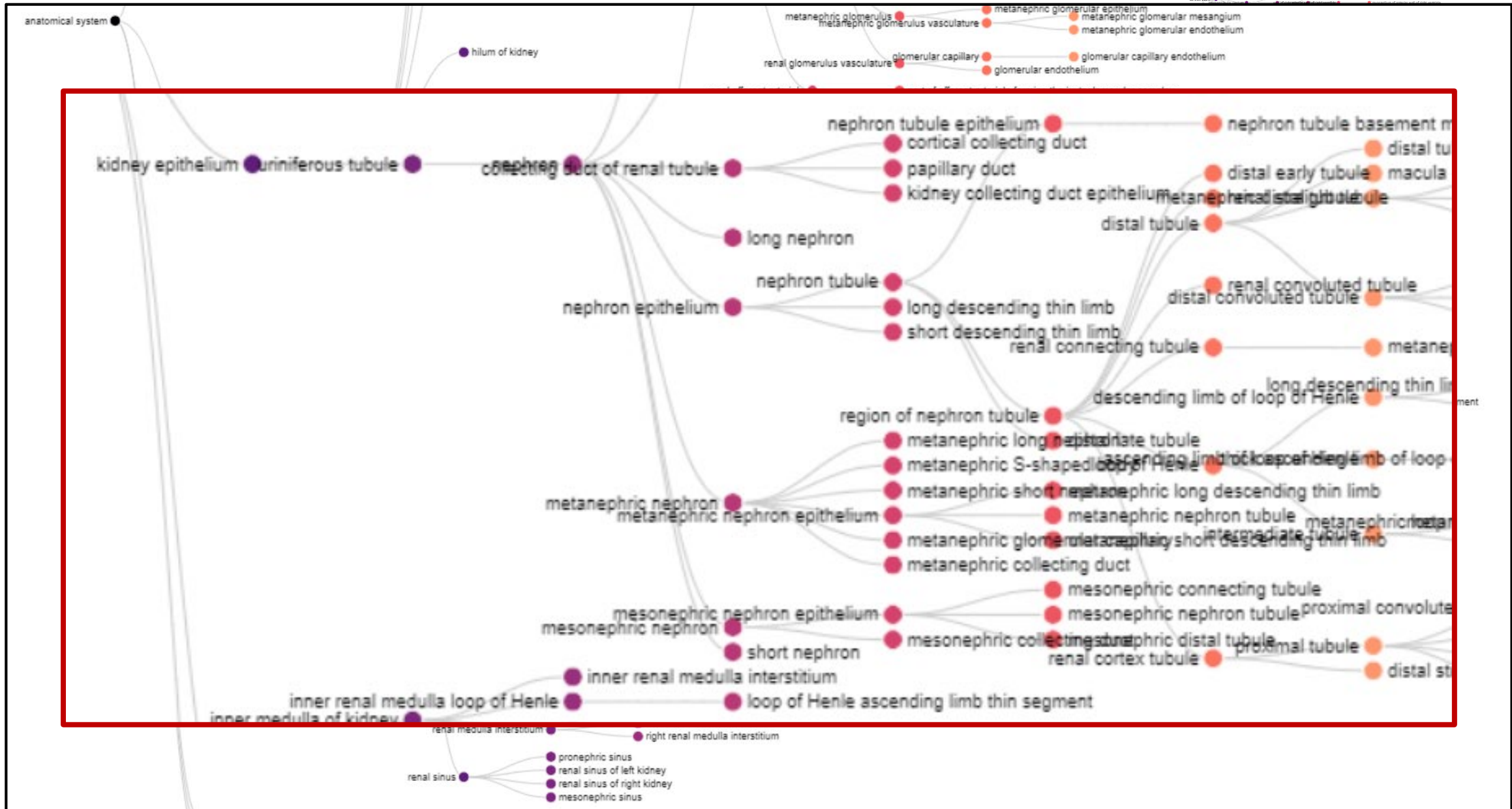
MeSH and NCI Thesaurus

Ontology

Current CCF Ontology:

- Use 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](#)





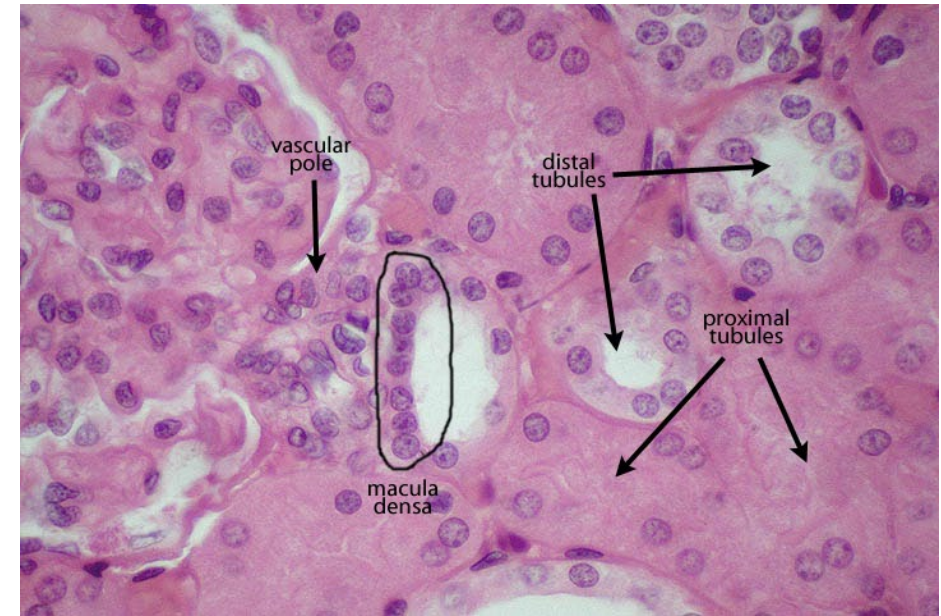
Data Formats

IU CCF Initial (v0.5.0) Image Formats

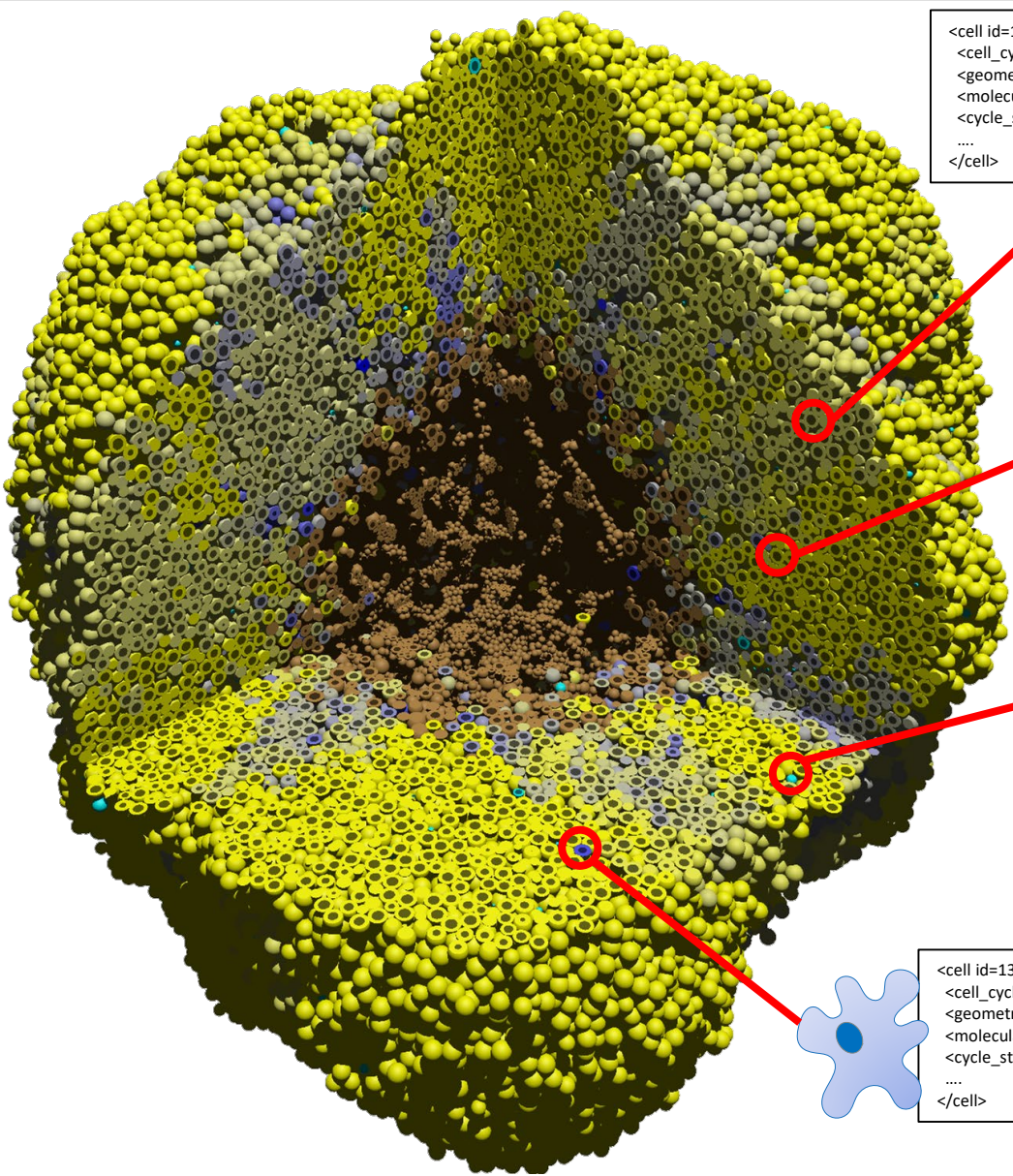
- **Basic image**: OME-Tiff
 - 2D to 4D data (includes movies)
 - more than three “color channels”
 - More flexible “color” data format (int, float, etc.)
- **Regions of images**: SVG with annotations
(aligned with a particular OME-Tiff)
- **Volumetric** (e.g., computed tomography, MR, ultrasound, ...)
 - Data normally represented as volumes or surfaces

More data

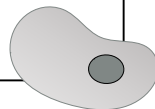
- RNAseq and other OMICS data
 - Challenges in:
 - Data formatting and visual representation of spatial data
 - Extracting *knowledge* from complex, often noisy data
 - Harmonizing data sets from different platforms
 - Validating and benchmarking
- Extracted information
 - Segmented cells and structures
 - SVG overlays
 - e.g., cell apical surfaces, glomerulus podocyte, renal corpuscle, Bowman's space, ...
 - Vectorized annotations (e.g., as in MultiCellDS – see below)
 - Multiplexed and massively multichannel imaging (e.g., MALDI)
 - Associate vectors of measurements with segmented structures
 - Additional ontology-driven annotations for the structures
 - e.g., cell type and state by Cell Ontology ...
 - Cell morphometric annotations ...



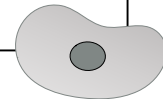
Vectorized annotations of extracted cell features: a step from data towards knowledge



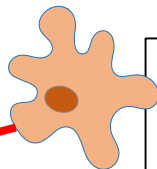
```
<cell id=137 type="renal carcinoma">  
<cell_cycle />  
<geometric_properties />  
<molecular_properties />  
<cycle_state/>  
....  
</cell>
```



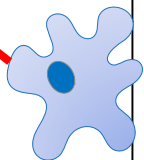
```
<cell id=137 type="epithelial tubal">  
<cell_cycle />  
<geometric_properties />  
<molecular_properties />  
<cycle_state/>  
....  
</cell>
```



```
<cell id=139 type="podocyte">  
<cell_cycle />  
<geometric_properties />  
<molecular_properties />  
<cycle_state/>  
....  
</cell>
```



```
<cell id=138 type="fibroblast">  
<cell_cycle />  
<geometric_properties />  
<molecular_properties />  
<cycle_state/>  
....  
</cell>
```



```
><cellular_information>  
><cell_populations>  
>><cell_population type="individual">  
>>><custom>  
>>>><simplified_data type="matlab" source="BioFVM">  
>>>>><filename>output00000540_cells.mat/</filename>  
>>>></simplified_data>  
>>>><simplified_data type="matlab" source="PhysiCell">  
>>>>><labels>  
>>>>>><label index="0" size="1">ID</label>  
>>>>>><label index="1" size="3">position</label>  
>>>>>><label index="4" size="1">total_volume</label>  
>>>>>><label index="5" size="1">cell_type</label>  
>>>>>><label index="6" size="1">cycle_model</label>  
>>>>>><label index="7" size="1">current_phase</label>  
>>>>>><label index="8" size="1">elapsed_time_in_phase</label>  
>>>>>><label index="9" size="1">nuclear_volume</label>  
>>>>>><label index="10" size="1">cytoplasmic_volume</label>  
>>>>>><label index="11" size="1">fluid_fraction</label>  
>>>>>><label index="12" size="1">calcified_fraction</label>  
>>>>>><label index="13" size="3">orientation</label>  
>>>>>><label index="16" size="1">polarity</label>  
>>>>>><label index="17" size="1">migration_speed</label>  
>>>>>><label index="18" size="3">motility_vector</label>  
>>>>>><label index="21" size="1">migration_bias</label>  
>>>>>><label index="22" size="3">motility_bias_direction</label>  
>>>>>><label index="25" size="1">persistence_time</label>  
>>>>>><label index="26" size="1">motility_reserved</label>  
>>>>>><label index="27" size="1">oncoprotein</label>  
>>>>>><label index="28" size="1">elastic_coefficient</label>  
>>>>>><label index="29" size="1">kill_rate</label>  
>>>>>><label index="30" size="1">attachment_lifetime</label>  
>>>>>><label index="31" size="1">attachment_rate</label>  
>>>>></labels>  
>>>>><filename>output00000540_cells_physicell.mat/</filename>  
>>>></simplified_data>  
>>></custom>  
>></cell_population>  
></cell_populations>  
></cellular_information>
```

Bonus 1: Can represent domain expert knowledge via expert-defined features.

Bonus 2: Extracted features could be *directly imported* into computational models.

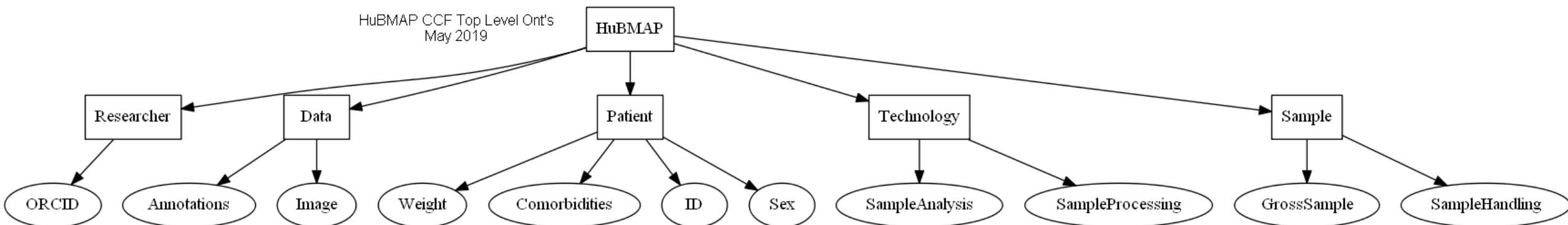
Metadata

Some Key Types of Metadata:

- Biological (patient specific data)
 - May include patient differentia such as disease state
- Technological (analysis tools; MS, immunohistochemical, RNAseq, ...)
 - Where possible, respect and reuse any technology domain-specific standards, ontologies, etc.
 - Will often include the biological results (e.g., gene expression levels)
- Interpretive
 - Summary of findings, e.g., conversion of gene expression lists into list of highly impacted pathways
 - Algorithms and software used in interpretation and analysis
- Provenance
 - Who processed and analyzed samples
 - Points of contact (to answer questions on the samples and analyses)
 - Can be important for QC and account
- Use metadata
 - Licenses, citation information,

Many data and metadata types and files

- Patient
- Sample
- Analysis Technology
- Results
- Researcher
- ...



Example: Metadata for Similar Large-Scale Data & Imaging Projects

GUDMAP:

GUDMAP/RBK Resources Search Create Dashboards (requires login) Help Feedback Log In

Gene Export Permalink

Present

Show Details

Imaging Data

Present Not Present

Show Details

Array Data

Scored Expression

Assay Type

Anchor Gene

Marker Gene

Search 25 items per page

Clear All Species: Homo sapi... Any Data: Pres... Imaging Data: Pres...

Displaying 25 of 70 Records

View	Gene ID ↑↓	NCBI Symbol ↑↓	Species ↑↓	Description ↑↓	Expression Score ↑↓	Array Data ↑↓	Imaging Data
	58	ACTA1	Homo sapiens	actin, alpha 1, skeletal muscle			Fetal 10wk Fetal 10wk Fetal 13wk Fetal 14wk
							Fetal 11wk
							Fetal 16wk

RID: Persistent citable resource identifier
Imaging Data
Genes
Species
Stage
Anatomical Sources
Assay Type
Preparation
Principle Investigator . . .

Kidney Tissue Atlas Ontology from KPMP

Human cell Atlas, SPARC (informed by BIDS)

Structured Datasets (like BIDS) provide...

- A convention for organizing data files into folders
- A set of descriptive files that contain information on subjects, experimental information, data set descriptions
- A set of naming conventions for files
- A means to extend the core structure to accommodate most data acquisitions

Top Level Folders (Dataset)

subjects
samples
protocol
docs
code
derivatives
sourcedata

Challenge: Inconsistent metadata specifications

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

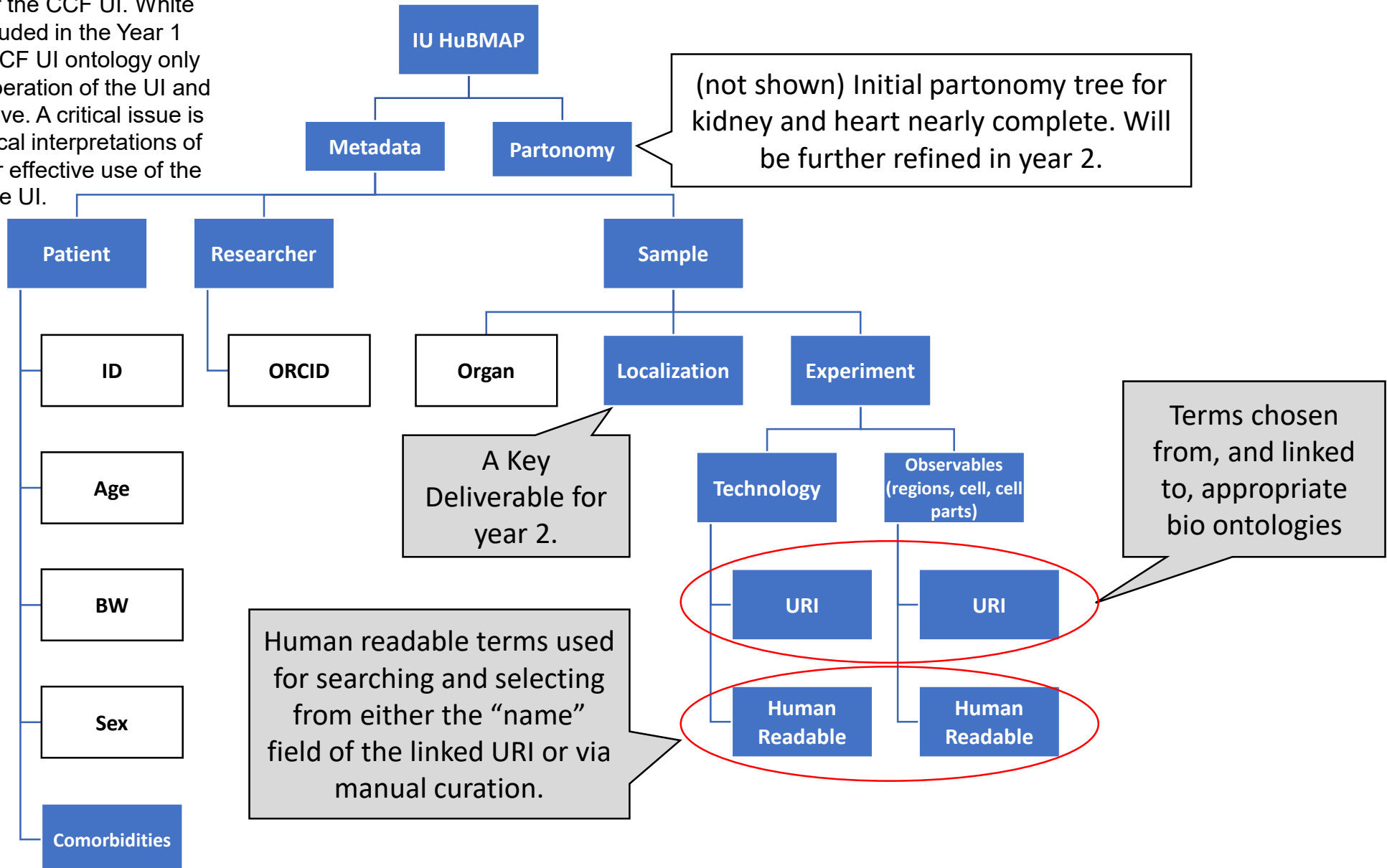
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32	Donor	History of cancer		,cancer_oth_ostxt			varchar(50)			1	50	
33	Details	//History of hyper		hypertension			smallint	lkup_histhype_dur				

AMIS (absolute minimal information solution)

Figure 2: Partial AMIS ontology for the CCF UI. White boxes indicate metadata terms included in the Year 1 metadata ontology. Note that the CCF UI ontology only covers the CCF data needed for operation of the UI and that is reflected in the ontology above. A critical issue is that human understandable biological interpretations of the various data sets is required for effective use of the image datasets by end users via the UI.



IU CCF Initial (v0.5.0) Patient Metadata

Column Header	Data Type	Comments
HuBMAP Sample ID	string	<i>assigned by PSE/IEC</i>
HuBMAP Patient Number	string	
Source Sample ID	string	<i>assigned by clinical unit, deidentified.</i>
Source Patient Number	string	
Procedure ID	string	
Procedure Date	formatted date	
Species	Human (STY:T016)	<i>required, though always human</i>
Age	decimal years	
Sex	M/F/u (SNOMED extended with "unkown")	
Race		<i>Race, ethnicity, strain</i>
Height	meter	
Weight	killogram	
BMI	float (calculated locally from height and weight)	
Comorbidities and other clinical classifications	MEDRA, SNOMED CT or MeSH terms	
Type of Procedure	MEDRA, SNOMED CT or MeSH terms	
Indications for Procedure	MEDRA, SNOMED CT or MeSH terms	
Laterality	MEDRA, SNOMED CT or MeSH terms	
Tissue Type	MEDRA, SNOMED CT or MeSH terms	
Anatomical Landmark	MEDRA, SNOMED CT or MeSH terms	
Displacement from Landmark	Affine transformation matrix	

Next?

Discussion Points

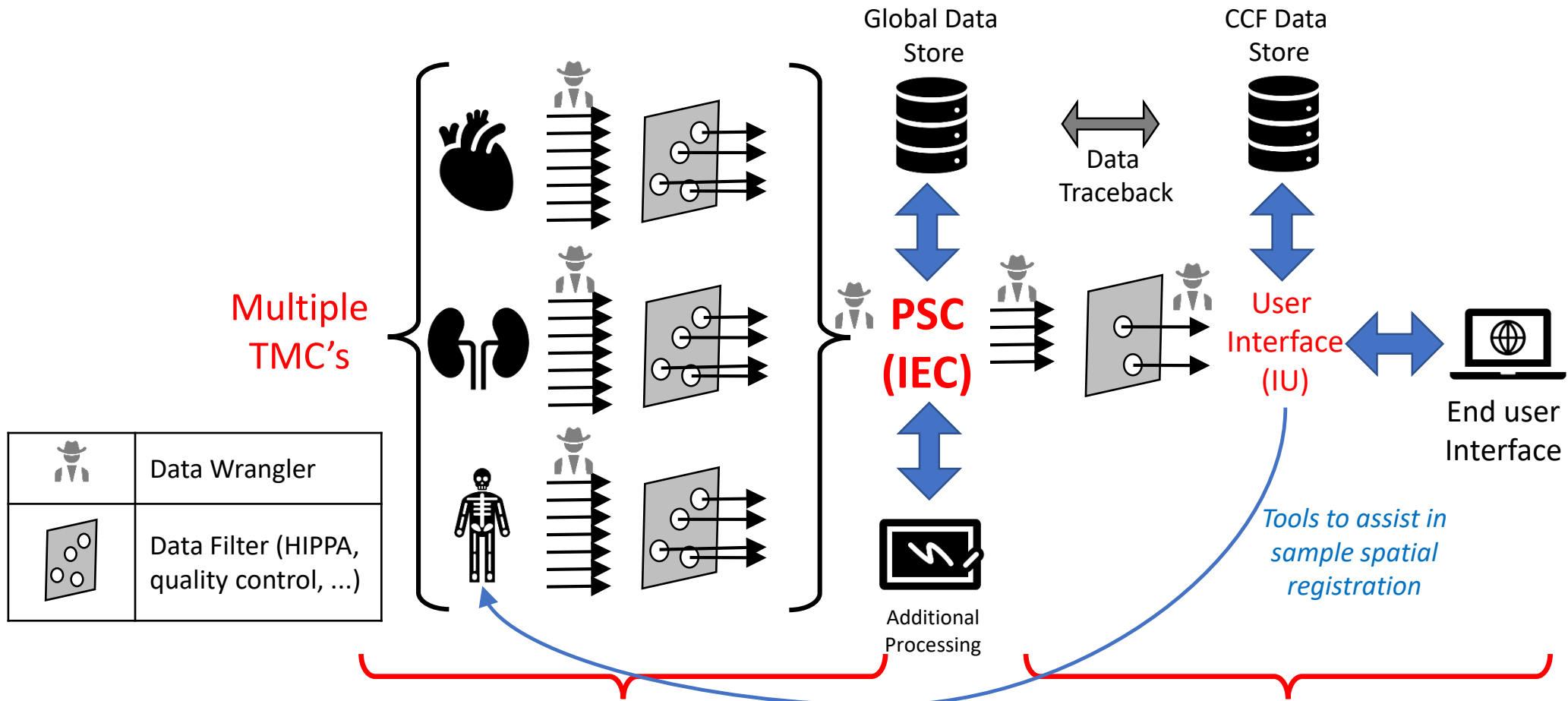
- **Year 2 Plans**

- Finalize metadata formats with input from the TMCs
- Unify data formats across TMCs' technologies
- Work closely with the CCF IU team to ensure data content and formatting is compatible with the needs and goals of the user interface.
- Work closely with TMCs to insure all anatomical scales are represented with ontology terms

- **Other TMC needs?**

- Are there unmet needs?
- Any "must have" features or terms to describe your data?

Extra reference materials



- 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


What is an ontology?

An ontology is a particular view of reality that encompasses a defined set of objects, processes and relationships within that reality.

“Ontological Commitment”



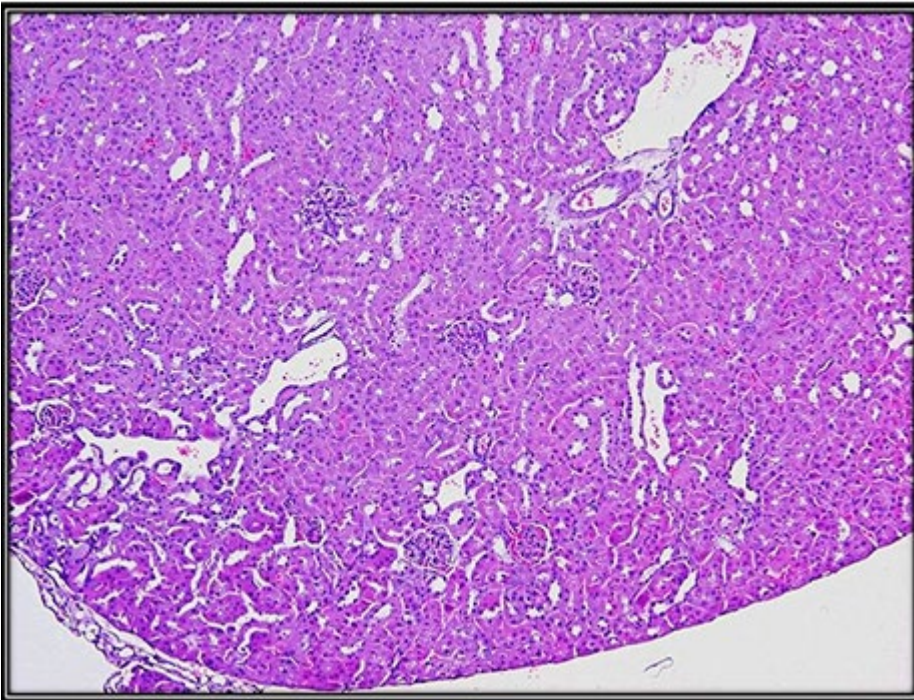
Controlled Vocabulary	Hierarchy of Terms (isA)	Full Ontology
Cell Hepatocyte Leukocyte	1. Cell a. Hepatocyte b. Leukocyte	1. Cell a. Hepatocyte b. Leukocyte
Organ Heart Liver	2. Organ a. Heart b. Liver	2. Organ a. Heart b. Liver



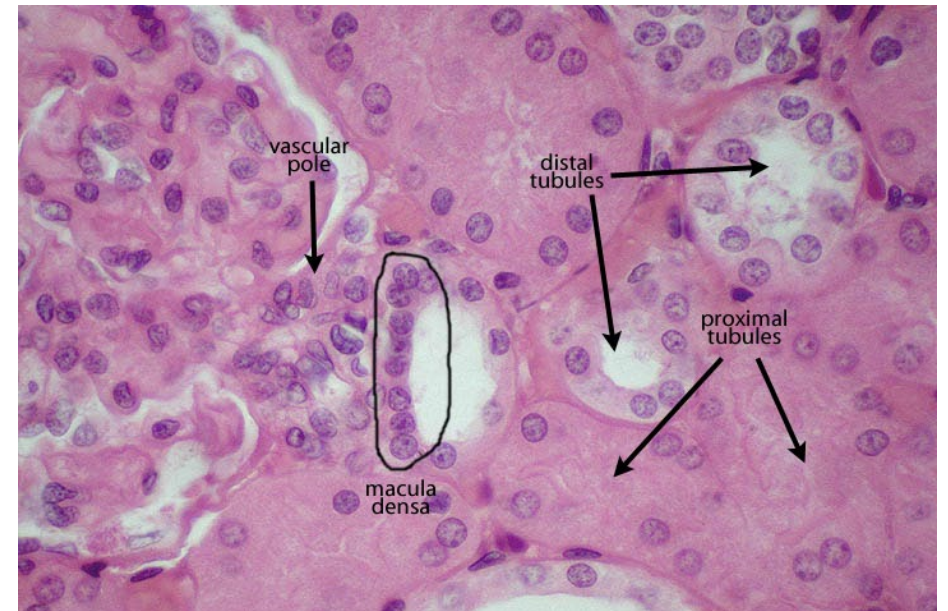
adjacentTo, containedIn, derivesFrom,
definedBy, participatesIn, contributesTo,
downStreamOf, ...

Annotating Images and Images containing identified (not just identifiable) things

In the H&E stained kidney image below what regions (e.g., nephron, tubule, ...), cell types, cell states etc. are present? Regions must be annotated, presumably by the TMCs. It is not enough to simply say this image contains cell types X, Y and Z in cell states 1, 2, and 3:



This image has been annotated (though the regions aren't very clear):

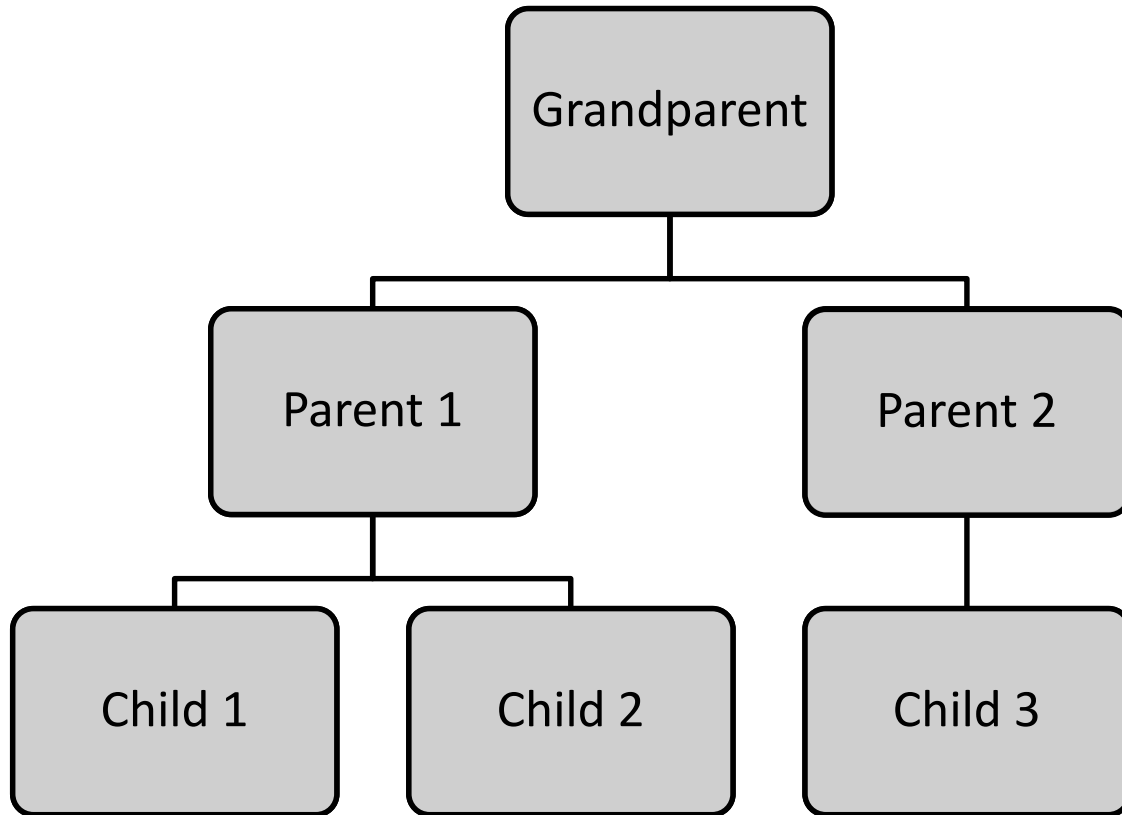


Solution: Multiple Slim Ontologies

- Gene Ontology (GO) is a massive ontology. Researchers didn't need the entire ontology, but only a subset of it.
- GO users create "slim" versions of GO:
 - Subsets that contained the terms needed along with the necessary ancestor and children terms
 - Can better illuminate the science of what is going on rather than being overwhelmed by too much information
- Terms in the main ontology can receive "slim" annotations, indicating their use in the corresponding "slim" ontology

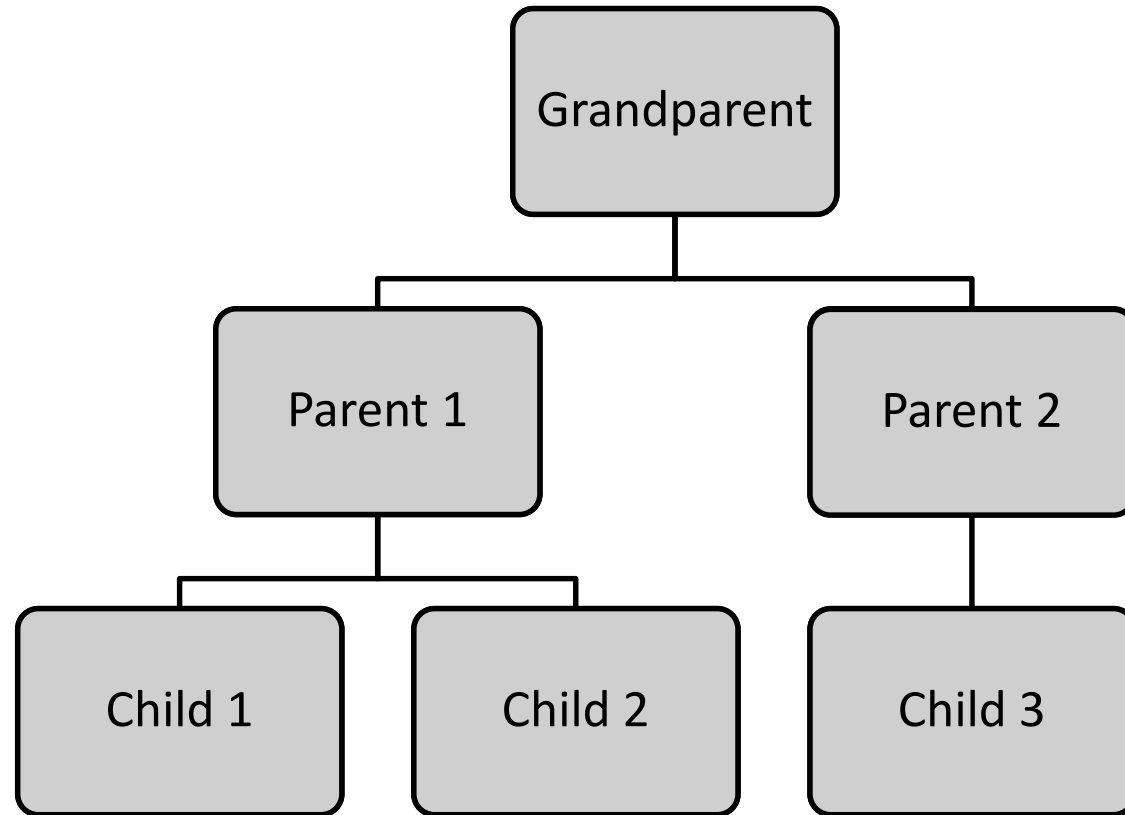
Multiple Slim Ontologies to Main HuBMAP/CCF Ontology

- Instead of creating a single ontology file, we have software create the ontology based on the needed terms.
- We can ensure that we obtain all appropriate parent/child nodes are included



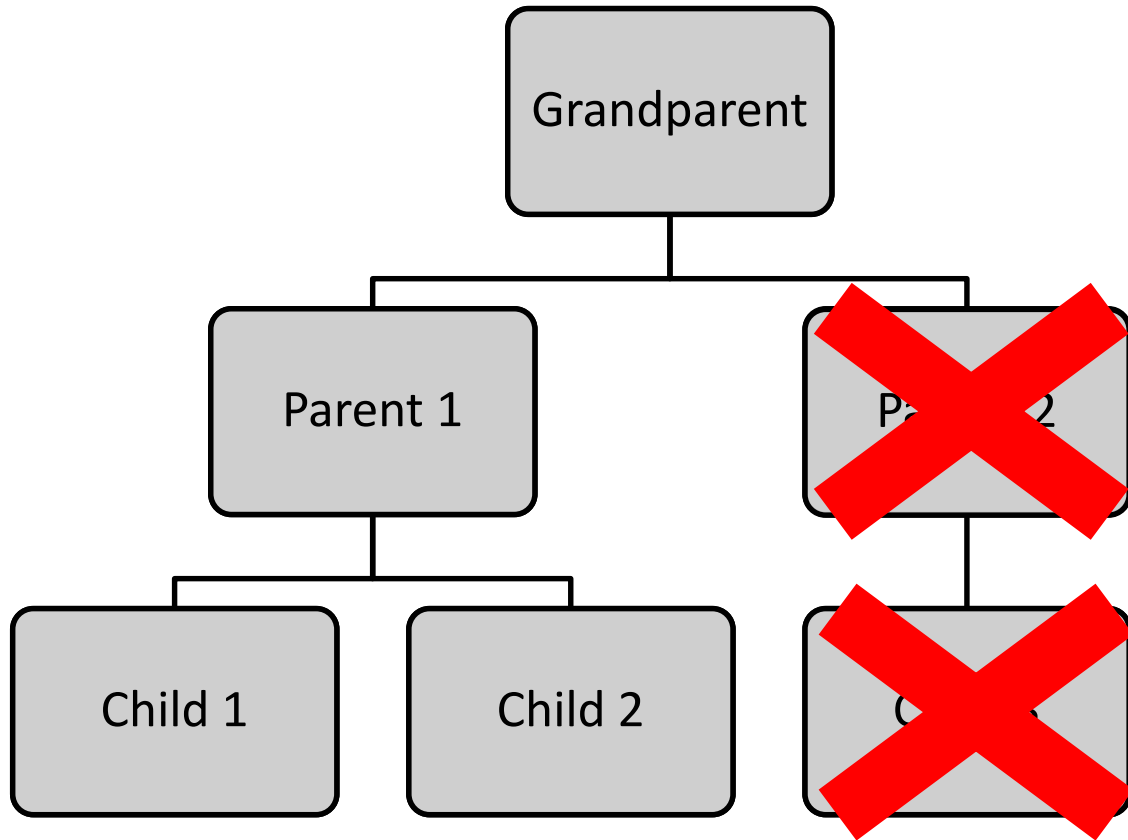
Multiple Slim Ontologies to Main HuBMAP/CCF Ontology

- We could specify for the main file we want nodes Parent 1 (from Ontology A) and Parent 2 (from Ontology B) and all their descendent nodes.
- We could specify we want nodes Children 1, 2, and 3 and all of their ancestor nodes.
- We could do a mix and still get the ontology.



Multiple Slim Ontologies to Main HuBMAP/CCF Ontology

- When viewing the ontology, we can easily eliminate extraneous terms for UI/navigation (e.g. eliminate Parent 2)
- When in a specific part of the body, certain terms could just disappear (e.g. eliminate Parent 2 and descendants)
- With a graph library, very easy to remove nodes or branches.



Pros/Cons of Multiple Slim Ontologies

Pros

- Ensures that we have the correct biology in the base ontology.
 - Lots of work already done by using pre-existing ontologies
- Can have slim ontologies for each zoom level, organ, or system
- As the base ontologies continue to update, new information propagates in
- Easy to add additional ontologies through crosswalks
- Elimination of some of the hand editing of ontologies

Cons

- Need to specify which versions of the input ontologies we are using
- Tracking of slim ontologies could become burdensome
- Lack of hand editing could make slim ontologies harder to use
- Hand editing could be replaced with code, but then additional coding effort is necessary
- Most of these cons are easily surmountable by using GitHub and using a triplestore repository like LungMAP did for its ontology

Dimensions of CCF Ontology

- Overall anatomical location
 - Heart aorta
- Cell line/type location
 - Endothelial cells
- Chemical location
 - Areas for positive staining for H&E
- Real data will have to be mapped into/annotated with the ontologies
- Some of this data will need to come from the experimental protocols (possible semantic integration with protocols.io ?) and some will likely come from Machine Learning