The Human Body Atlas: High-Resolution, Functional Mapping of Voxel, Vector, and Meta Datasets

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HuBMAP The Human BioMolecular Atlas Program

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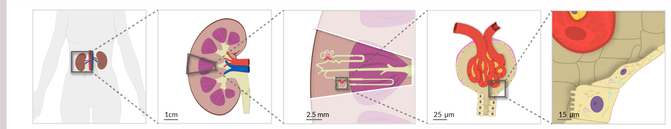
Abstract

The ultimate goal of the HIVE Mapping effort is to develop a common coordinate framework (CCF) for the healthy human body that supports the cataloguing of different types of individual cells within anatomical structures, understanding the function and relationships between those cell types, and modeling their individual and collective function. In order to exploit human and machine intelligence, different visual interfaces are implemented in support of CCF data generation, exploration, and communication. The CCF and the interactive data visualizations are multi-level and multi-scale. They support the registration and exploration of diverse types of data—from single cell to whole body. In the initial two years, MC-IU ran user needs analyses with stakeholders, compiled an initial CCF ontology and associated 3D object library, developed novel CCF registration and exploration UIs, and explored using the vasculature as a coordinate system to map all cells in the human body, see https://hubmapconsortium.github.io/ccf.

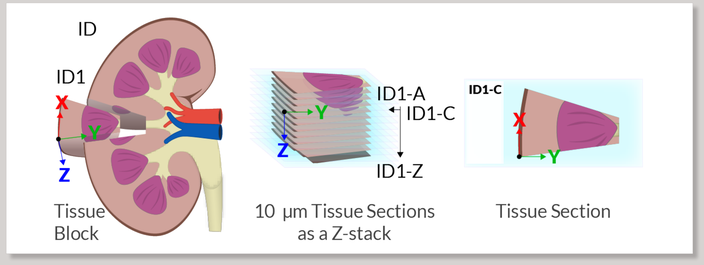
Common Coordinate Framework

A common coordinate framework (CCF) is a conceptual and computational framework for the storage, analysis, and (visual) exploration of spatially and semantically indexed data—across individuals, technologies, labs.



Body	Organ	Functional Tissue Unit	FTU Sub-structure(s)	Cellular
• Body • Kidney (Left, Right) • Aorta • Renal artery • Renal vein • Ureter	• Renal capsule • Renal pyramid • Renal cortex • Renal medulla • Renal calyx • Renal pelvis	• Nephron • Renal corpuscle • Proximal convoluted tubule • Loop of Henle • Distal convoluted tubule • Connecting tubule • Collecting duct	• Bowman's capsule • Glomerulus • Efferent arteriole • Afferent arteriole	• Parietal epithelial cell • Capillary endothelial cell • Mesangial cell • Podocyte

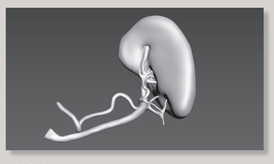
Semantic zoom from whole human body, to organ, to functional tissue units (FTUs), to FTU sub-structures, to single-cell level.



3-step spatial registration of single cells in relation to reference organs.

CCF 3D Object Library

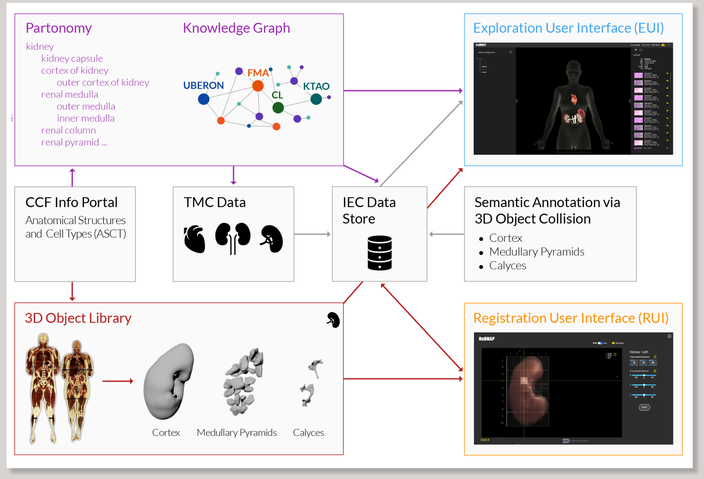
In collaboration with Kristen Browne at National Institute of Allergy and Infectious Diseases (NIAID), NIH we are developing a library of anatomically correct human organ models using data from NLM's Visible Human (VH) dataset.



VH Spleen

VH Kidney

CCF Registration to CCF Exploration Workflow

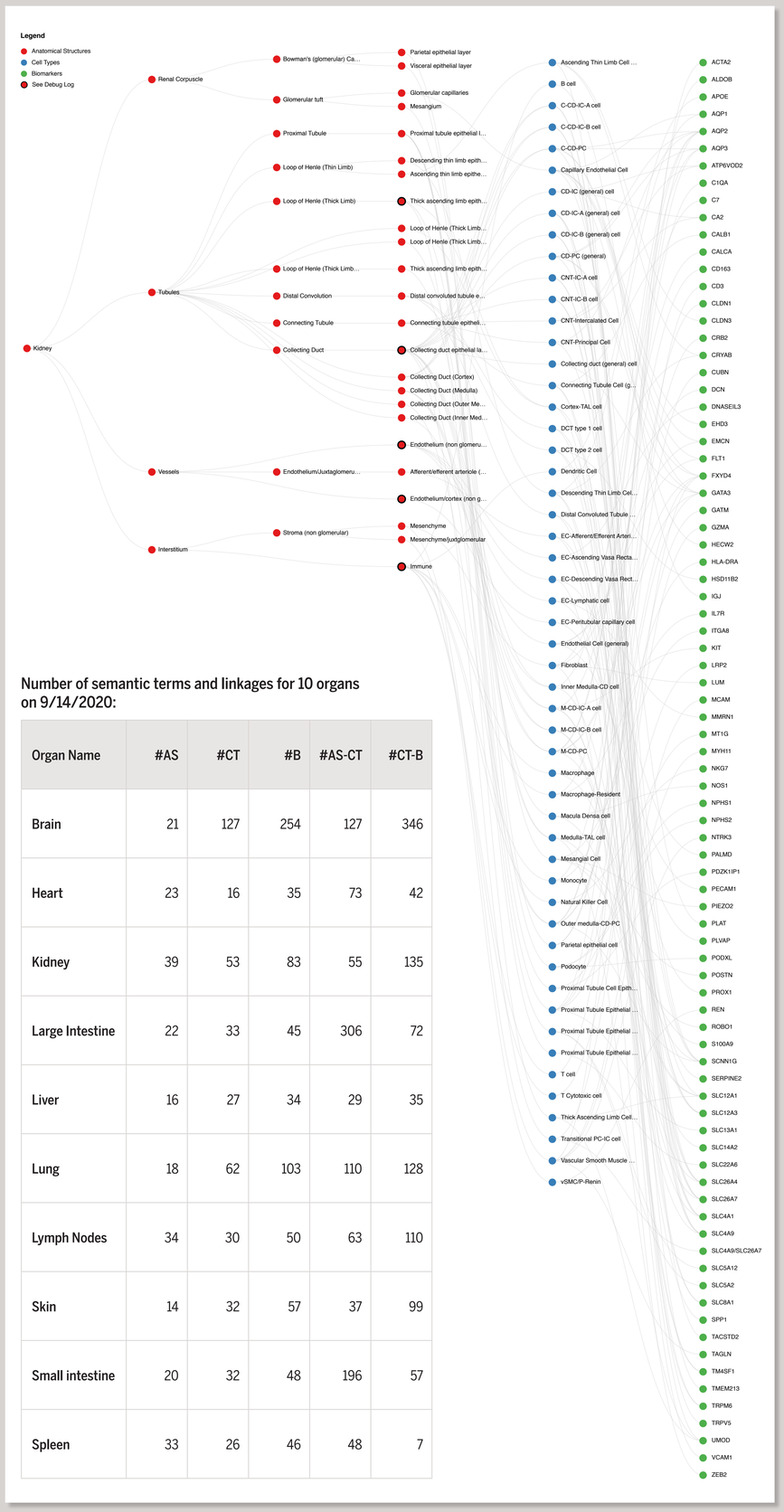


Overview of CCF Info Portal (left) which systematically captures CCF relevant information, CCF Ontology design (top left) and 3D Object Library construction (lower left), and CCF User Interfaces (right). Arrows indicate data flow.

ASCT+B Tables

Anatomical Structures, Cell Types, plus Biomarkers (ASCT+B) tables aim to capture the nested part_of structure of anatomical human body parts, the typology of cells, and biomarkers used to identify cell types (e.g., gene, protein, lipid or metabolic markers). The tables are authored and reviewed by an international team of anatomists, pathologists, physicians, and other experts.

The CCF ASCT+B Reporter makes it possible to explore tables visually—per organ or across all organs in support of table authoring and review. It combines two different types of Angular visualizations: A partonomy tree of anatomical structures and bimodal networks that link anatomical structures to cell types and cell types to biomarkers.

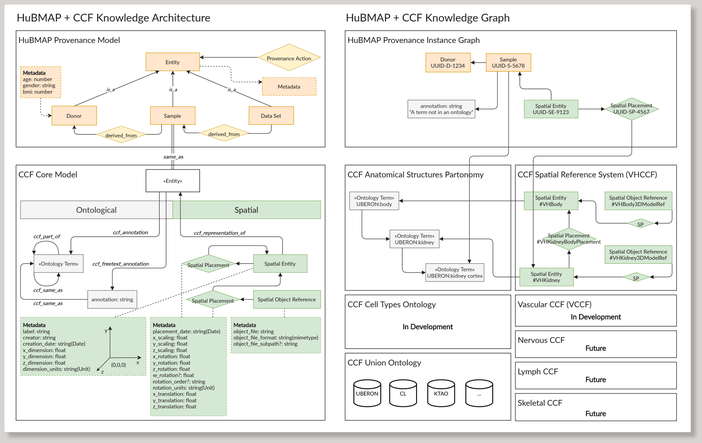


Number of semantic terms and linkages for 10 organs on 9/14/2020:

Organ Name	#AS	#CT	#B	#AS-CT	#CT-B
Brain	21	127	254	127	346
Heart	23	16	35	73	42
Kidney	39	53	83	55	135
Large Intestine	22	33	45	306	72
Liver	16	27	34	29	35
Lung	18	62	103	110	128
Lymph Nodes	34	30	50	63	110
Skin	14	32	57	37	99
Small intestine	20	32	48	196	57
Spleen	33	26	46	48	7

CCF Ontology

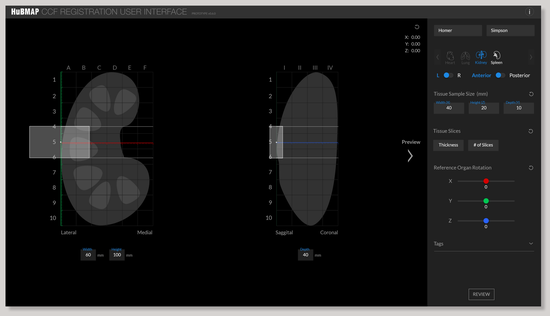
The CCF Core Model has been defined as a formal ontology using Web Ontology Language 2 (OWL) to support compatibility and interlinkage with other ontologies.



CCF Core Model, see https://hubmapconsortium.github.io/hubmap-ontology/ccf.owl

CCF Registration User Interface (RUI)

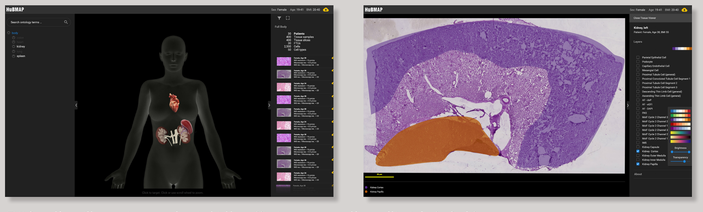
The RUI was designed for usage by experts that collect human tissue and need to document the tissue extraction site. It requires about 5 minutes of training time and 2 minutes for each tissue registration. Currently, the RUI supports gross anatomical tissue registration of tissue blocks. When biomolecular data becomes available, it will be extended to support placement based on biomolecular markers and patterns.



RUI functionality can be examined at https://hubmapconsortium.github.io/ccf-3d-registration

CCF Exploration User Interface (EUI)

The EUI makes it possible to explore 2D/3D tissue data semantically and spatially across multiple scales. Spatial data generated by the RUI is used to position tissue blocks. Cell segmentation algorithm results will soon support cell position and cell type exploration. Semantic and spatial search, browsing, filtering, and details on demand are supported.



EUI functionality can be examined at https://hubmapconsortium.github.io/ccf-ui/

Publications

- Griffin M. Weber, Yingnan Ju, Katy Börner. Considerations for Using the Vasculature as a Coordinate System to Map All the Cells in the Human Body. *Frontiers in Cardiovascular Medicine*. 7 (29): doi: 10.3389/fcvm.2020.00029
- Michael P. Snyder et al., 2019. The Human Body at Cellular Resolution: The NIH Human Biomolecular Atlas Program. *Nature*. 574: 187-192. doi: 10.1038/s41586-019-1629-x.
- Börner K, Quardokus EM, Herr II, BW, Cross LE, Record EG, Ju Y, Bueckle A, Sluka JP, Silverstein J, Browne K, Jain S, Wasserfall CH, Jorgensen ML, Spraggins JM, Patterson NH, Weber GM. 2020. Construction and Usage of a Human Body Common Coordinate Framework Comprising Clinical, Semantic, and Spatial Ontologies. https://arxiv.org/abs/2007.14474.

Acknowledgements

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