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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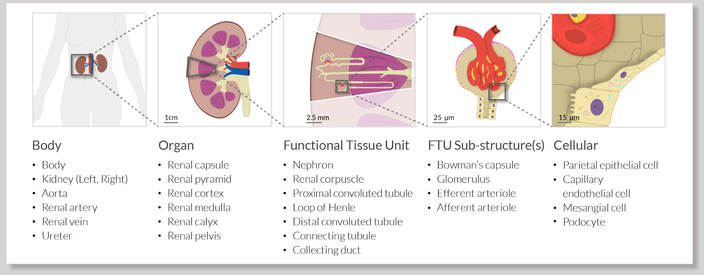
Abstract

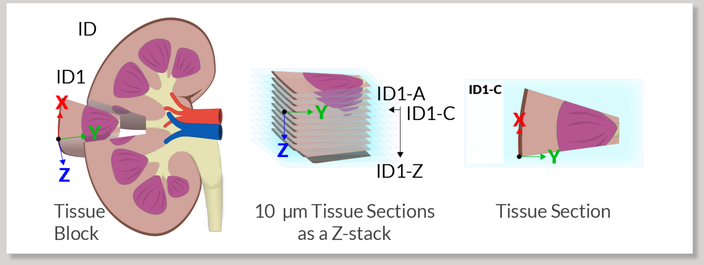
The ultimate goal of the HIVE Mapping effort is to develop a common coordinate framework (CCF) for the healthy human body. This framework will support cataloging different types of individual cells, understanding the functions of and relationships between those cell types, and modeling their individual and collective function. During the initial three years of HuBMAP, the MC-IU team has built many elements of the CCF. We co-organized the construction of ASCT+B Tables and implemented a CCF Ontology. We collaborated with NIAID at NIH on the design of a 3D Reference Object Library. Lastly, we developed three interactive user interfaces. The CCF ASCT+B Reporter supports the authoring and interactive review of ASCT+B Tables. The CCF Registration User Interface (RUI) supports uniform tissue data registration across organs and labs. The CCF Exploration User Interface (EUI) supports exploration of semantically and spatially explicit data—from the whole body to the single cell level, 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.



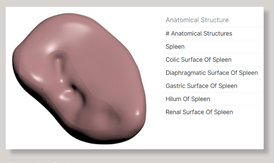
Semantic zoom from whole human body, to organ, to functional tissue units (FTUs), to FTU sub-structures, to single-cell level.



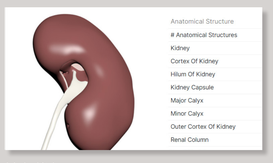
3-step spatial registration of single cells in relation to reference organs.

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.

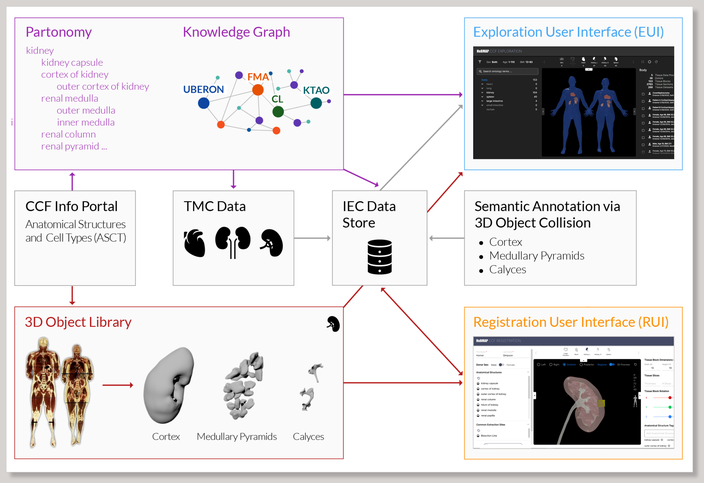


Female Spleen



Male Kidney

CCF Registration to CCF Exploration Workflow

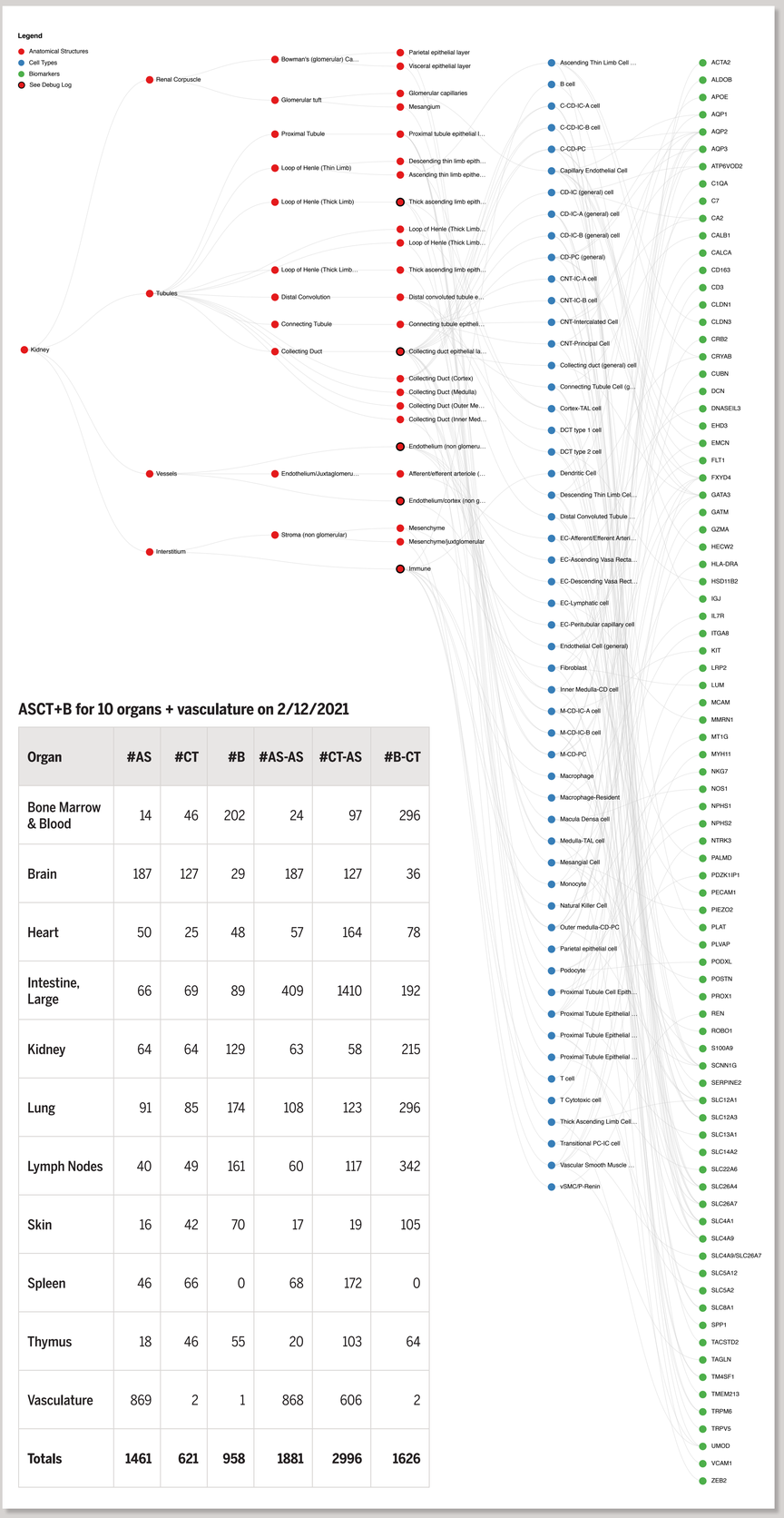


Overview of CCF Info Portal (left) which systematically captures CCF relevant information, CCF Ontology design (top left) and 3D Object Library construction (lower left), and CCF User Interfaces (right). Arrows indicate data flow.

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.

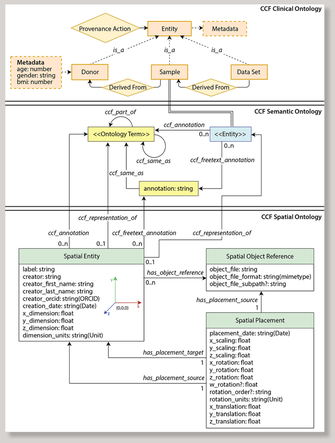


ASCT+B for 10 organs + vasculature on 2/12/2021

Organ	#AS	#CT	#B	#AS-AS	#CT-AS	#B-CT
Bone Marrow & Blood	14	46	202	24	97	296
Brain	187	127	29	187	127	36
Heart	50	25	48	57	164	78
Intestine, Large	66	69	89	409	1410	192
Kidney	64	64	129	63	58	215
Lung	91	85	174	108	123	296
Lymph Nodes	40	49	161	60	117	342
Skin	16	42	70	17	19	105
Spleen	46	66	0	68	172	0
Thymus	18	46	55	20	103	64
Vasculature	869	2	1	868	606	2
Totals	**1461**	**621**	**958**	**1881**	**2996**	**1626**

CCF Ontology

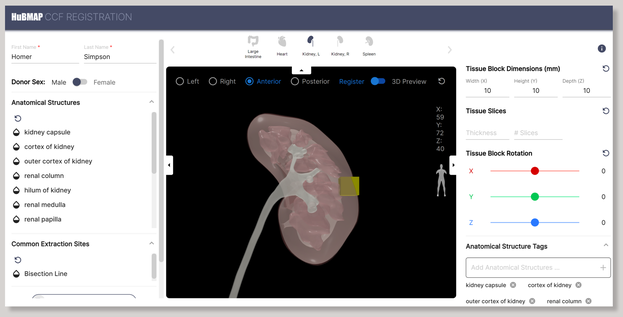
The CCF Knowledge Architecture has been defined as a formal ontology using Web Ontology Language 2 (OWL) to support compatibility and interlinkage with other ontologies.



CCF Knowledge Architecture, see https://hubmapconsortium.github.io/hubmap-ontology/ccf.owl

CCF Registration User Interface (RUI)

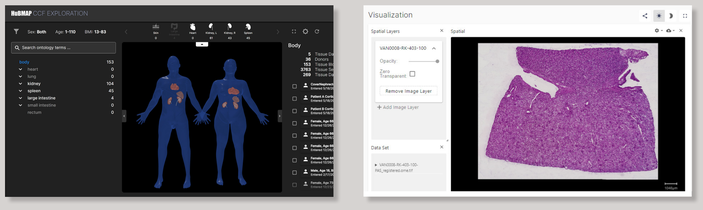
The RUI was designed for usage by experts that collect human tissue and need to document the tissue extraction site. It requires about 5 minutes of training time and 2 minutes for each tissue registration. Currently, the RUI supports gross anatomical tissue registration of tissue blocks. When biomolecular 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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