Human Reference Atlas: ASCT+B Tables, 3D Reference Library & CCF User Interfaces

Katy Börner  |  @katycns
Victor H. Yngve Distinguished Professor of Intelligent Systems Engineering & Information Science
Luddy School of Informatics, Computing, and Engineering
Indiana University, Bloomington, IN

CFDE April Cross-Pollination Event
Virtual Event

April 6, 2021
HuBMAP

Vision
Catalyze the development of an open, global framework for comprehensively mapping the human body at cellular resolution.

Goals
1. Accelerate the development of the next generation of tools and techniques for constructing high resolution spatial tissue maps
2. Generate foundational 3D tissue maps
3. Establish an open data platform
4. Coordinate and collaborate with other funding agencies, programs, and the biomedical research community
5. Support projects that demonstrate the value of the resources developed by the program

https://commonfund.nih.gov/HuBMAP
HuBMAP Contributing Sites

- TMC University of Washington
  - Pacific Northwest National Lab
- RTI, TTD
  - Northwestern University
- TMC University of Iowa
- TTD Marquette University
- HIVE - Mapping, RTI
  - New York Genome Center
  - GE Global Research
  - University of Rochester
- HIVE - Tools, TTD, RTI, TMC
  - Harvard University, Medical School Broad Institute
  - Dana Farber Institute
  - Columbia University
  - Children's Hospital of Boston
- TMC, TTD
  - University of Connecticut
  - Yale University
- HIVE - IEC, HIVE - Tools, RTI, TMC
  - Carnegie Mellon University
  - Pittsburgh Supercomputing Center
  - University of Pittsburgh
  - National Disease Research Interchange
  - Children's Hospital of Philadelphia
  - University of Pennsylvania
  - Pennsylvania State University
- NIH Common Fund
- TMC
  University of Alabama, Birmingham
- TMC
  University of North Carolina, Chapel Hill
- TMC
  University of Florida
- TMC
  Texas Advanced Computing Center
- TMC, TTD, HIVE - TC
  - Stanford University
  - University of California, Santa Cruz
  - University of California San Diego
  - California Institute of Technology
  - City of Hope National Medical Center
- TMC
  University of North Carolina, Chapel Hill
- TMC
  University of Florida
- TMC
  Texas Advanced Computing Center
- TMC
  University of North Carolina, Chapel Hill
- TMC
  University of Florida
- TMC
  Texas Advanced Computing Center
- TMC
  University of North Carolina, Chapel Hill
- TMC
  University of Florida

Fig. 1 | The HubMAP consortium. The TMCs will collect tissue samples and generate spatially resolved, single-cell data. Groups involved in TTD and RTI initiatives will develop emerging and more developed technologies, respectively; in later years, these will be implemented at scale. Data from all groups will be rendered usable for the biomedical community by the HuBMAP integration, visualization and engagement (HIVE) teams. The groups will collaborate closely to iteratively refine the atlas as it is gradually realized.

**Fig. 2 | Key tissues and organs initially analysed by the consortium.**
Using innovative, production-grade ('shovel ready') technologies, HuBMAP TMCs will generate data for single-cell, three-dimensional maps of various human tissues. In parallel, TTD projects (and later RTI projects) will refine assays and analysis tools on a largely distinct set of human tissues. Samples from individuals of both sexes and different ages will be studied. The range of tissues will be expanded throughout the program.

**Single cell and ‘omics assays**
- Genomics
- Epigenomics
- Transcriptomics
- Proteomics
- Metabolomics

**Multiplexed spatial assays**
- Protein
- RNA
- Lipids / metabolites

**Map assembly and data query**
- Landmark A
- Landmark B
- Feature ID
- Reference coordinates

Fig. 3 | Map generation and assembly across cellular and spatial scales. HuBMAP aims to produce an atlas in which users can refer to a histological slide from a specific part of an organ and, in any given cell, understand its contents on multiple ‘omic levels—genomic, epigenomic, transcriptomic, proteomic, and/or metabolomic. To achieve these ends, centres will apply a combination of imaging, ‘omics and mass spectrometry techniques to specimens collected in a reproducible manner from specific sites in the body. These data will be then be integrated to arrive at a high-resolution, high-content three-dimensional map for any given tissue. To ensure inter-individual differences will not be confounded with collection heterogeneity, a robust CCF will be developed.
CCF ASCT+B Tables
CCF Requirements

The CCF must capture major **anatomical structures, cell types, and biomarkers** and their interrelations across **multiple levels of resolution**.

It should be **semantically explicit** (using existing ontologies, e.g., Uberon, CL) and **spatially explicit** (e.g., using 3D reference organs for registration and exploration).
ASCT+B Tables

Anatomical Structures, Cell Types, and Biomarkers (ASCT+B) tables aim to capture the partonomy of anatomical structures, cell types, and major biomarkers (e.g., gene, protein, lipid or metabolic markers).

<table>
<thead>
<tr>
<th>Structure/Region</th>
<th>Substructure/Subregion</th>
<th>Cell Type</th>
<th>Subset of Marker Genes</th>
</tr>
</thead>
<tbody>
<tr>
<td>Renal Corpuscle</td>
<td>Bowman’s Capsule</td>
<td>Parietal epithelial cell</td>
<td>CRB2*, CLDN1*</td>
</tr>
<tr>
<td></td>
<td>Glomerulus</td>
<td>Podocyte</td>
<td>NPHS2*, PODXL*, NPHS1*</td>
</tr>
<tr>
<td></td>
<td>Capillary Endothelial Cell</td>
<td></td>
<td>EHD3*, EMCN*, HECW2*, FLT1*, AQP1*</td>
</tr>
<tr>
<td></td>
<td>Mesangial Cell</td>
<td></td>
<td>POSTN*, PIEZO2*, ROBO1*, ITGAB8*</td>
</tr>
</tbody>
</table>

Partial ASCT+B Table from
Table 3: Cell types and associated markers from KMP Pilot 1 transcriptomic studies. Asterisk denotes genes detected by more than one technology. Italic, genes detected by a single technology.

<table>
<thead>
<tr>
<th>Structure/Region</th>
<th>Substructure/Subregion</th>
<th>Cell Type</th>
<th>Abbreviation</th>
<th>Subset of Marker Genes</th>
<th>Pertinent negative/comm. defects</th>
</tr>
</thead>
<tbody>
<tr>
<td>Bowman’s Capsule</td>
<td>Proximal Tubule</td>
<td>Proximal Tubule Epithelial Cell (general)</td>
<td>PT</td>
<td>CD2C, LFNB1, SLC47A1, SLC6A9</td>
<td>There is overlap among the segments</td>
</tr>
<tr>
<td>Glomeruli</td>
<td>Proximal Tubule</td>
<td>Proximal Tubule Epithelial Cell/Segment 1</td>
<td>PT-S1</td>
<td>SLC47A1, SLC6A9, TATFIP</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>Proximal Tubule Epithelial Cell/Segment 2</td>
<td>PT-S2</td>
<td>SLC24A12</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>Proximal Tubule Epithelial Cell/Segment 3</td>
<td>PT-S3</td>
<td>P0X3228, ATB7</td>
<td></td>
</tr>
<tr>
<td>Loop of Henle, Thin Limb</td>
<td>Unconforming Thick Limb Cell (general)</td>
<td>DTL</td>
<td>CD71, LFNB1, FNCT, SLC47A1, SLC6A9, CD2C</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Conforming Thick Limb Cell (general)</td>
<td>ATL</td>
<td>CD71, LFNB1, FNCT, SLC47A1, SLC6A9, CD2C</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Loop of Henle, Thick Limb</td>
<td>Thick Ascending Limb Cell (general)</td>
<td>TIL</td>
<td>SLC47A1, SLC6A9, CD2C</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Distal Convolutions</td>
<td>Urothelial Gland (general)</td>
<td>DCT</td>
<td>SLC47A1, SLC6A9</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>DCT Type 1 cell</td>
<td>DCT-1</td>
<td>SLC47A1, SLC6A9</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>DCT Type 2 cell</td>
<td>DCT-2</td>
<td>SLC47A1, SLC6A9, CD2C</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Connecting Tubule Cell (general)</td>
<td>CNT</td>
<td>SLC47A1, SLC6A9, TRPV5</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Connecting Tubule Cell/Principal Cell</td>
<td>CNT-PC</td>
<td>SLC47A1, SLC6A9, TRPV5</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Connecting Tubule Cell/Interstitiated Cell</td>
<td>CNT-IC</td>
<td>SLC47A1, SLC6A9</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Connecting Tubule Cell/IC-A Cell</td>
<td>CNT-IC-A</td>
<td>SLC47A1, TRPV5</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Connecting Tubule Cell/IC-B Cell</td>
<td>CNT-IC-B</td>
<td>SLC47A1, TRPV5</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Collecting Duct</td>
<td>Collecting duct (general)</td>
<td>CD</td>
<td>SLC47A1</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Collecting duct (general)</td>
<td>CD-PC</td>
<td>SLC47A1</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Collecting duct (general)</td>
<td>MEPC</td>
<td>SLC47A1</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

CCF ASCT+B Reporter UI

https://hubmapconsortium.github.io/ccf-asct-reporter/
Anatomical Structures (AS), Cell Types (CT), and Biomarkers (B) or ASCT+B tables aim to capture the partonomy of anatomical structures, cell types, and major biomarkers (e.g., gene, protein, lipid or metabolic markers).

### ASCT Table

<table>
<thead>
<tr>
<th>Structure/Region</th>
<th>Substructure/Subregion</th>
<th>Cell Type</th>
</tr>
</thead>
<tbody>
<tr>
<td>Renal Corpuscle</td>
<td>Bowman's capsule/mediobasal layer</td>
<td>Parietal epithelial cell</td>
</tr>
<tr>
<td></td>
<td>Bowman's capsule/visceral layer</td>
<td>Podocyte</td>
</tr>
<tr>
<td></td>
<td>Glomerular tuft</td>
<td>Capillary endothelial cell</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Mesangial cell</td>
</tr>
<tr>
<td>Tubules</td>
<td>Proximal tubule</td>
<td>Proximal tubule epithelial cell (general)</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Proximal convoluted tubule epithelial cell segment 1</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Proximal tubule epithelial cell segment 2</td>
</tr>
<tr>
<td></td>
<td>Loop of Henle, thin limb</td>
<td>Descending thin limb cell (general)</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Ascending thin limb cell (general)</td>
</tr>
<tr>
<td></td>
<td>Loop of Henle, thick limb</td>
<td>Thick ascending limb cell (general)</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Cortex-TAL cell</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Medulla-TAL cell</td>
</tr>
<tr>
<td></td>
<td></td>
<td>TAL-Macula densa cell</td>
</tr>
<tr>
<td>Distal convolution</td>
<td>Distal convoluted tubule cell (general)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>DCT Type 1 cell</td>
<td></td>
</tr>
<tr>
<td></td>
<td>DCT Type 2 cell</td>
<td></td>
</tr>
<tr>
<td>Connecting tubule</td>
<td>Connecting tubule cell (general)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>CNT-Principal cell</td>
<td></td>
</tr>
</tbody>
</table>

### Ontology

#### Anatomical Structures Partonomy
- Kidney
- Kidney capsule
- Cortex of kidney
- Outer cortex of kidney
- Renal medulla

#### Cell Types Ontology
- Connective tissue cell
- Pericyte cell
- Mesangial cell
- Extraglomerular mesangial cell
- Glomerular mesangial cell

### 3D Reference Object Library
Overview of CCF 3D Reference Models
ASCT+B Table Working Group

Lead by Katy Börner and Jim Gee; Ellen M Quardokus serves as Knowledge Manager

Meetings take place monthly to review and approve tables, formalize and unify table design language, discuss and expand table usage, see [WG Charter](#).

Upcoming meetings in 2021: April 7, May 5, 11a-noon ET.
Please [register](#) to receive invites and updates.
<table>
<thead>
<tr>
<th>TCGA</th>
<th>Allen Brain</th>
<th>BICCN</th>
<th>Gut Cell Atlas</th>
<th>GUDMAP</th>
<th>HCA</th>
<th>HTAN</th>
<th>LungMAP</th>
<th>SPARC</th>
<th>KPMP</th>
<th>RBK</th>
<th>Kidney</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>1</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>1</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>1</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>1</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>1</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>1</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>1</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>1</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>1</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>1</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
</tbody>
</table>

Table compiled for, during, and after the NIH-HCA Joint Meeting in March 2020, [https://hubmapconsortium.org/nihhca2020](https://hubmapconsortium.org/nihhca2020)
https://hubmapconsortium.github.io/ccf/pages/ccf-3d-reference-library.html (NLM VH organs)
https://www3.cs.stonybrook.edu/~ari/ (male colon)
CCF Registration User Interface (RUI)
ASCT+B Table Usage

ASCT+B tables guide **CCF Ontology** and **3D Reference Object Library** design that semantically name and spatially place tissue data from different donors into one CCF (i.e., mapping).

Tissue blocks are **registered** into the CCF using the Registration User Interface (RUI), and they can be **explored** via the Exploration User Interface (EUI).
Document the tissue extraction site by registering tissue blocks within a 3D reference organ.

*Image provided by Sanjay Jain, TMC-UCSD*
CCF Registration User Interface (RUI) v1.0.0

New Features:
• Organ carousel with 4 reference organs
• Support for tissue extraction sites
• Expanded ontology
• Semantic annotation via collision detection & manual annotation
• Support for non-HuBMAP usage

https://hubmap-ccf-ui.netlify.app/rui/
For the first HuBMAP portal release, 48 tissue blocks were registered.
Collision when Tissue Block hits Reference Organ

Tag Search behavior

Custom tag added to list
HuBMAP Upload Portal

HuBMAP Display ID Generator

Generate unique identifiers which will be used consortium wide to track sample and associate data with samples.

Source HuBMAP ID: TEST00005-RK

HuBMAP display id: TEST00005-RK

Type: Organ

Organ Type: Kidney (Right)

HUBMAP ID: HMB.204-1T71758

Description

Tissue Sample Type: FFPE block

Protocol 1

protocol ID: none

Protocol document: Choose a file

Generate IDs for multiple FFPE block samples

Example of sample for the HUBMAP project:

Lab IDs and sample locations can be assigned on the next screen after generating the upload IDs.

Metadata

Add Metadata

Image

Add Image

Make sure any uploaded images are do-identified

Generate ID

Cancel

HuBMAP Display ID Generator

Generate unique identifiers which will be used consortium wide to track sample and associate data with samples.

3 sample ids were generated: TEST0005-RK-6 through TEST0005-RK-8

Type: FFPE block

Assign Lab IDs and Sample Locations

Return to Search

Implied by the HIVE IEC
CCF Registration User Interface (RUI)

https://hubmapconsortium.github.io/ccf-ui/rui/
15 extraction sites by Kalyanam Shivkumar, UCLA (SPARC)
10 sites by Shin Lin, UW (HuBMAP)
Public private partnership panel with NIH, Google, Broad, Lilly and potentially Roche

Hacking the Kidney Hackathon

PARTICIPATION OPENS NOV 5TH, 10:00 AM EST

TOTAL PRIZE MONEY $60,000 TO BE AWARDED TO THE WINNING TEAMS!

OUR SPONSORS

Google Deloitte CAS Roche

Pistoia Alliance Maven Wave DEERFIELD

https://innovationdigi.com/hubmap-hackathon
CCF Exploration User Interface (EUI)
CCF Exploration User Interface (EUI)

https://portal.hubmapconsortium.org/ccf-eui
Register your data via https://hubmap-ccf-ui.netlify.app/rui/ so it can be spatially/semantically explored in EUI.
http://gehlenborglab.org/research/projects/vitessce/
Human Reference Atlas CCF: Checklist

In support of Common Coordinate Framework (CCF) design (see CCF Portal):
1. Make sure the Anatomical Structures, Cell Types, and Biomarkers (ASCT+B) that you use/submit are listed in the ASCT+B tables. The tables are authored and reviewed by an international team of anatomists, pathologists, physicians, and other experts, see this SOP.
2. Spatially register all tissue samples using the CCF Registration User Interface (RUI) in the Ingest Portal. End of October 2020, kidney, spleen, heart, colon registration are supported. For other organs, see SOP.
3. After submitting data, review data in the CCF Exploration User Interface and make sure spatial, semantic, and other metadata are correct.
4. For functional tissue unit (FTU) segmentation, submit a list of FTUs for your organ(s) and make sure FTU names and all relevant cell types (CT) are captured in the ASCT+B table. Use assays/biomarkers (B) that make it possible to identify FTUs—initially manually, later automatically. Submit tissue with 1000 FTUs manually identified FTUs.
5. In support of the Vasculature-based CCF, provide cell segmentation data for blood vessels and different cell types.

For questions, email infoccf@indiana.edu.
Visible Human MOOC (VHMOOC)
Goals
• Communicate tissue data acquisition and analysis,
• Demonstrate single-cell analysis and CCF mapping techniques, and
• Introduce major features of the HuBMAP portal.

Learning modules come with
• Videos (incl. interviews, tool demos)
• Hands-on exercises
• Self-quizzes

https://expand.iu.edu/browse/sice/cns/courses/hubmap-visible-human-mooc
1st HuBMAP Portal Release (Oct. 2020)

HuBMAP Overview
- Project Goals, Setup, and Ambitions

Tissue Data Acquisition and Analysis
- Behind the Scenes at Vanderbilt University

Biomolecular Data Harmonization
- An Introduction to Seurat

CCF Ontology, 3D Reference Objects, and User Interfaces
- Creating an Atlas of the Human Body

Portal Design and Usage
- Datasets and Software in the 1st HuBMAP Portal Release

Open Consent Your Data
- In Support of Research
2nd HuBMAP Portal Release (Dec. 2020)

**Ontologies 101**
- A gentle introduction on how to use ontologies to organize the world.

**Anatomical Structures, Cell Types, and Biomarkers (ASCT+B) Tables**
- What are ASCT+B tables and how they are used.

**Forthcoming**
- CODEX Data and Cell Segmentation by Gary Nolan
- Portal Design and Usage (Summer 2021 Update)
Learning Module Example:
CCF Ontology, 3D Reference Objects, and User Interfaces–Creating an Atlas of the Human Body

Videos

Registration User Interface (RUI)
- RUI Application
- RUI Intro Video

Exploration User Interface (EUI)
- EUI Application
- EUI Intro Video

NLM 3D
- Interview with Kristen Browne
Get Involved!
Contribute your expert experience and time.

**Author or Review ASCT+B Tables**

Anatomists, pathologists, biomolecular and other experts are invited to author, edit and/or review Anatomical Structures, Cell Types, and Biomarkers (ASCT+B) tables. Please register to participate.

**Explore 3D Reference Organs**

Download kidney or spleen objects from the HuBMAP Reference Object Library, explore them in a web-based 3D viewer, answer a simple question. Optional: Provide expert comments on the reference organs.

**Register Tissue Block via RUI**

Use the Registration User Interface (RUI) Prototype to spatially and semantically register three-dimensional tissue blocks within reference organs.

**Manually Annotate Human Tissue**

Learn how to visually identify functional tissue units in different organs, use human intelligence to annotate them in tissue samples. The resulting data will be used to train machine learning algorithms.
Explore 3D Reference Organs

Started: Aug 30, 2020 at 11:30pm

Quiz Instructions

Two 3D reference organs (kidney and spleen) have been made freely available as part of the 1st HuBMAP Portal Release.

The 3D reference objects files are provided in the GLB format, a binary form of the nested Graphics Library Transmission Format (https://www.khronos.org/gltf/). These files can be viewed and explored using free web browser, Babylon.js (https://sandbox.babylonjs.com). If you are a programmer, note that these files can also be accessed programatically via API-neutral runtime asset delivery of 3D scenes and models using the JSON standard.

To explore these 3D models in a web browser:

1. First, visit the Hubmap Github project source objects (https://github.com/hubmapconsortium/hubmap-ontology/tree/master/source_objects), and download the GLB file for left female kidney (VHF_Kidney_L_Low.glb, 96KB).
2. Next, visit the Babylon.js website and view the 3D kidney by dragging and dropping the GLB file into the browser.
3. In the Scene Explorer on left, click on + symbol to expand Nodes, root, VHF_Kidney_L_Low and other subtrees.

   Click on eye symbol to turn different parts of the 3D kidney model on/off. Click on square to turn on/off the bounding box (i.e., smallest 3D volume in which all object points lie) for each anatomical structure. To see inner structures, turn outer structures off.

While you explore the kidney, make sure to record the number of renal pyramids for the left female kidney, and report back your finding in the self-check quiz below.
Learning Module Example:
CCF Ontology, 3D Reference Objects, and User Interfaces—Creating an Atlas of the Human Body

Get Involved!
Contribute your expert experience and time.

Author or Review ASCT+B Tables
Anatomists, pathologists, biomolecular and other experts are invited to author, edit and/or review Anatomical Structures, Cell Types, and Biomarkers (ASCT+B) tables. Please register to participate.

Explore 3D Reference Organs
Download kidney or spleen objects from the HuBMAP Reference Object Library, explore them in a web-based 3D viewer, answer a simple question. Optional: Provide expert comments on the reference organs.

Register Tissue Block via RUI
Use the Registration User Interface (RUI) Prototype to spatially and semantically register three-dimensional tissue blocks within reference organs.

Manually Annotate Human Tissue
Learn how to visually identify functional tissue units in different organs, use human intelligence to annotate them in tissue samples. The resulting data will be used to train machine learning algorithms.
Register Tissue Block via RUI

Instructions

The Registration User Interface (RUI) Prototype is a tool developed for HubMAP that supports the registration of three-dimensional (3D) tissue blocks within 3D reference organs. Surgeons and others involved in the tissue procurement process can use the interface to size a virtual tissue block in three dimensions and then to position and rotate the 3D tissue block within a 3D reference organ so its placement mirrors the real-world tissue block extraction site.

The prototype RUI is freely available to use at: https://hubmapconsortium.github.io/ccf-3d-registration

Registration data can be saved in JSON format to support spatial search and browsing of tissue data in the Exploration User Interface (EUI).

![Kidney tissue block](image)

**Figure 1.** Example kidney tissue block

Please register the exemplary kidney tissue block, shown above, using the RUI using these steps (also shown in our tutorial):
Learning Module Example:
CCF Ontology, 3D Reference Objects, and User Interfaces—Creating an Atlas of the Human Body

Get Involved!
Contribute your expert experience and time.

Author or Review ASCT+B Tables
Anatomists, pathologists, biomolecular and other experts are invited to author, edit and/or review Anatomical Structures, Cell Types, and Biomarkers (ASCT+B) tables. Please register to participate.

Explore 3D Reference Organs
Download kidney or spleen objects from the HuBMAP Reference Object Library, explore them in a web-based 3D viewer, answer a simple question. Optional: Provide expert comments on the reference organs.

Register Tissue Block via RUI
Use the Registration User Interface (RUI) Prototype to spatially and semantically register three-dimensional tissue blocks within reference organs.

Manually Annotate Human Tissue
Learn how to visually identify functional tissue units in different organs, use human intelligence to annotate them in tissue samples. The resulting data will be used to train machine learning algorithms.
Manually Annotate Human Tissue

Unlimited Attempts

Details

Machine learning algorithms can be used to identify and count the number of functional tissue units (FTUs) present in a tissue section. For the kidney, we are interested in identifying and counting the number of glomeruli. Glomeruli have a ball-shaped structure and are composed of capillary blood vessels that filter waste products out of blood to form urine, see Fig. 1.

![Example of a renal glomeruli](image)

Figure 1. Example of a renal glomeruli

Machine learning algorithms benefit from training data, i.e., human annotations of tissue data that correctly identify glomeruli. For this assignment, please complete the following steps to annotate a kidney tissue sample to help generate machine learning training data and to measure and reduce variability in human annotation data.

1. Install QuPath ([https://qupath.github.io/](https://qupath.github.io/))
   - If your installed version is lower than 0.2, please update the QuPath to the latest version by visiting the website or by selecting "Help – Check for updates (web)" in the tool menu.
2. To open larger images, update the setting for larger memory in QuPath from
   - Navigate to help and select "Show setup options"
   - Change the maximum memory from the required 16GB to our recommendation of 32GB.
NEW Modules Released for XMas 2020

All Sections

Dear all, We are proud to release 2 new modules for XMas 2020: Ontologies 101 A gentle introduction on ho...

Posted on: Dec 18, 2020 at 9:17am

ASCT+B and RUI Onboarding Videos

All Sections

Hello everyone! As you may know, we have had a big amount of new teams joining HuBMAP recently, so we ...

Posted on: Nov 19, 2020 at 1:28pm

Azimuth: New App for Reference-Based Single-Cell Analysis Released

All Sections

The Satija Lab, the developers of Seurat (an R toolkit for single cell genomics), has released an exciting new w...

Posted on: Nov 19, 2020 at 11:31am

HuBMAP "Hacking the Kidney" Kaggle Competition is now live!

All Sections

Dear VHMOOC students, The Kaggle Competition titled HuBMAP: Hacking the Human Kidney is now live! V...

Posted on: Nov 19, 2020 at 10:47am

Welcome to the course!

All Sections

Dear Students, Welcome to the HuBMAP Visible Human MOOC, or VHMOOC! The course opened Tuesday, ...

Posted on: Sep 1, 2020 at 9am
HuBMAP Visible Human MOOC (VHMOOC)

Started Aug 4, 2020

GO TO CANVAS COURSE

You are enrolled.

Course Introduction

This 10-week course introduces the HuBMAP project which aims to create an open, global reference atlas of the human body at the cellular level. Among others, the course describes the compilation and coverage of HuBMAP data, demonstrates new single-cell analysis and mapping techniques, and introduces major features of the HuBMAP portal.

Delivered entirely online, all coursework can be completed asynchronously to fit busy schedules. If you have questions or experience issues during registration, please email cmoct@indiana.edu.

Learning Outcomes

- Theoretical and practical understanding of different single-cell tissue analysis techniques.
- Expertise in single-cell data harmonization used to federate data from different individuals analyzed using different technologies in diverse labs.
- Hands-on skills in the design and usage of semantic ontologies that describe human anatomy, cell types, and biomarkers (e.g., marker genes or proteins).
- Knowledge on the design and usage of a semantically annotated three-dimensional reference system for the healthy human body.
- An understanding of how the HuBMAP reference atlas might be used to understand human health but also to diagnose and treat diseases.

Module Topics Include

- HuBMAP Overview: Project Goals, Setup, and Ambitions
- Tissue Data Acquisition and Analysis
- Biomolecular Data Harmonization
- Ontology, 3D Reference Objects, and User Interfaces
- HuBMAP Portal Design and Usage

Meet the Instructors

Katy Besner, Victor H. Yergey
Endowed Professor of Engineering and Information Science, Founding Director of the Cyberinfrastructure for Network Science Center at Indiana University.

Ellen M. Quaas, Ph.D.
Staff in the Chemistry Department and research scientist, Cyberinfrastructure for Network Science Center, I UCC with expertise in molecular biology, microscopy, anatomy, and interdiscipinary communication.

Andreas Bueckle, Ph.D.
Candidate in Information Science, performing research on information visualization, specifically virtual and augmented reality.

https://expand.iu.edu/browse/sice/cns/courses/hubmap-visible-human-mooc
Thanks go to all the patients that agreed to volunteer healthy tissue and open use of their data.
Q&A