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.

https://ccfws.cns.iu.edu
Please use #hubmapccf
Organizers

Katy Börner
MC-IU
Indiana University

Jeffrey Spraggins
TMC-Vanderbilt
Vanderbilt University

Sanjay Jain
TMC-UCSD
Washington University, St. Louis

Local Organizers

Lisel Record
MC-IU
Indiana University

Matt Martindale
MC-IU
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Acknowledgements

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Agenda

All times are in Eastern Daylight Time (UTC-4)

9:00am  Welcome by Organizers and Richard Conroy, NIH
9:05am  Brief Introductions by Participants
9:30am  HuBMAP Overview by Organizers
10:00am Metadata
  Paul Macklin et al., IU; Kidney Metadata and Ontology Design (HuBMAP)
  Bernard de Bono, U of Auckland; Kidney Anatomical Knowledge and Metadata (SPARC)
10:40am Coffee Break
11:10am Metadata
  Jonathan Himmelfarb, U of Washington; The Kidney Precision Medicine Project Overview of KPMP Metadata (KPMP)
11:30am Ontologies
  Jonathan Silverstein, U Pitt; Graphing UMLS (HuBMAP)
  Yongqun "Oliver" He, U Michigan Medical School; Integrative Ontology Development to Support Precision Medicine and Molecular Atlas Research (KPMP)
  Olivier Bodenreider, NLM/NIH; Anatomical Ontologies: How many of them do we need?
12:30pm Catered Lunch
Agenda

All times are in Eastern Daylight Time (UTC-4)

1:30pm  Anatomical Mapping

Zorina Galis, NIH/NHLBI; Using the Vasculature for CCF (NIH)
Simon Watkins & Alan Watson, U Pitt; Ribbon Scanning Confocal for High-Speed High-Resolution Volume Imaging
Seth Winfree, IU School of Medicine; Bi-directional Interrogation of Image Volumes and Segmented Cells With 3D Tissue Cytometry

2:30pm  Coffee Break

3:00pm  CCF User Interfaces

Katy Börner, IU; Multi-Level, Multi-Modal CCF UI for Data Providers and Users (HuBMAP)
Becky Steck, U Mich; KPMP’s User-Centered Approach to User Interfaces and Data Visualization (KPMP)
Peter Hunter, U of Auckland; 3D Scaffolds (SPARC)

4:00pm  Discussion of challenges and (collaboration) opportunities

5:00pm  Adjourn

5:30pm  Dinner at FARMbloomington Restaurant
Due to federal funding policy, participants will be responsible for their individual dinner expenses.
Agenda

All times are in Eastern Daylight Time (UTC-4)

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Olivier Bodenreider, NLM/NIH; Anatomical Ontologies: How many of them do we need?

12:30pm  Catered Lunch
CCF Challenges and Opportunities

Collected from participant registration data and during the CCF WS, see https://ccfws.cns.iu.edu
Please feel free to add!

Challenges

CCF Metadata

- Lack of guidance from the NIH
- Balancing between too little and too much information
- The usual, ease of access, search quality, data manipulation, etc.
- Different approaches to the data because of different methodologies
- Human variability is quite diverse by organ. Brain efforts have been able to register datasets to specific cells but many organs won’t be able to attain this. I need fast registration of all datasets so they can be explored in a portal.
- Standardising metadata between diverse groups into a model that is sufficiently detailed to capture relevant data but also flexible enough to meet all user needs
- Within HuBMAP, there will soon exist data by 5 TMCs, using 25 different assay types, for 9+ organs. Protocols and workflows are evolving.

CCF Ontologies

- The lack of understanding of what an ontology is, how it is created and what it can do.
- Ability to effectively translate integrate and share across the many expertise domains that are needed for HuBMAP.
- How to utilize both spatial and “mother-daughter” relationships
- Identifying existing or creating ontologies that sufficiently cover from acquisition of whole

https://tinyurl.com/ccfws-feedback
Vision:
Catalyze the development of an open, global framework for comprehensively mapping the human body at a cellular resolution.

https://commonfund.nih.gov/HuBMAP
HuBMAP 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
HuBMAP Consortium

Based upon new imaging and biomolecular sequencing technologies, multiple national and international efforts are underway to more comprehensively understand human cells. The Human BioMolecular Atlas Program (HuBMAP) is a consortium composed of diverse research teams funded by the National Institutes of Health (https://commonfund.nih.gov/HuBMAP). HuBMAP is committed to developing the next generation of molecular analysis technologies, computational tools, and to generate foundational tissue maps in order to accelerate the construction of an atlas of the human body for the understanding the relationship between tissue organization and function. HuBMAP values secure, open sharing, and collaboration with other consortia and the wider research community.

https://hubmapconsortium.org
In FY18, 1x Infrastructure, 2x Tools & 2x Mapping OT2 awards.

In FY18, 5x U54 Centers funded for 4 years.

In FY18, 1x Collaboration OT2 award.

In FY18, 4x UG3 / UH3 phased awards for 2+2 years.

In FY19, 4-8 UH3 awards to accelerate technology implementation.

Will come later in the program
Temporal Bar Graph of HuBMAP Project
MC-IU within HuBMAP (https://hubmapconsortium.org)
03/25/2019

Zhang, Kun
Cai, Long
Caprioli, Richard
Satija, Rahul
Nystrom, Nicholas
Mabee, Paula
Mabee, Paula
Gehlenborg, Nils
Borner, Katy
Bar-Joseph, Ziv
Cai, Long
Snyder, Michael
Yin, Peng
Laskin, Julia
Harbury, Pehr
Atkinson, Mark

Legend
Area size: FY Total Cost by IC
Label: PI (Contact)
Maximum = $ 650,000
Minimum = $ 15,000

How To Read This Visualization
This temporal bar graph visualization shows total funding by NIH center or institute (IC) for the period from 2018 to 2022, indicating contact principal investigator (PI) of funded projects. Maximum and minimum total costs per project are given in the legend. Bars are colored by project types.
Geospatial Layout of HuBMAP Teams
MC-IU within HuBMAP (http://hubmapconsortium.org)
04/16/2019

Legend
Label: Experts
Color: Role

How To Read This Visualization
This geospatial map shows the collaboration network of 134 experts. Principal investigators (PIs) are placed at their exact geolocation. Team members are placed nearby and are linked to PIs. Nodes and edges are colored according to their roles.
Bimodal Network of Experts and Working Groups
MC-IU within HuBMAP (https://hubmapconsortium.org)
04/09/2019

Legend
Label: Experts
- Working Groups
Color: Team Type
- Nodes and Edges
  - WG: WGs
  - TMC: TMC
  - HIVE: HIVE
  - NIH: NIH
  - TTD: TTD
  - CC: CC

How To Read This Visualization
This bimodal network represents a network between five working groups and 126 experts of those groups. Nodes and edges are colored according to the team type that expert belongs to. Working group nodes are sized by the total number of experts in the group.
Bimodal Network of PI (Contacts) and NIH Projects
MC-IU within HuBMAP (https://hubmapconsortium.org)
04/22/2019

Legend
Label: PI (Contacts)  NIH Projects
Maximum = 71,882,084
Minimum = 3,065,740

How To Read This Visualization
This bimodal network represents a network between six NIH projects and 73 PI (Contacts). Nodes and edges are colored according to the Funding Institute & Center that project of PI (Contact) is financed from. NIH project’s node sizes based on award amount.
Mapping the Human Body at Cellular Resolution—
The NIH Common Fund Human BioMolecular Atlas Program
Mapping the Human Body at Cellular Resolution—
The NIH Common Fund Human BioMolecular Atlas Program
Mapping the Human Body at Cellular Resolution—
The NIH Common Fund Human BioMolecular Atlas Program
Summary of Sample Data

Upload Files To HuBMAP
Transfer files to HuBMAP using Globus file transfer service where you'll be able to monitor the status of your upload

Download Files From HuBMAP
Search for, select and download files from HuBMAP