![Common Fund Data Ecosystem logo]

WRONG LINK! (SORRY) → November 1 Event

October Cross-Pollination Event

[A CFDE Cross-Pollination Event](#)

Tuesday, Oct 4, 2022 - 11am (PT) / 2pm (ET)
Where: https://zoom.us/j/99791103122?pwd=aGJ3OG8rRk4wVW00aDM3Rms3ZGRFZz09
Organizer: CFDE-CC CrossPollinationEvents+owner@groups.io

Post-Meeting Resources

Recordings:

Zoom Stream

Google Drive Download

Transcript:

https://drive.google.com/file/d/1DtDu83wBAuzZWafS9uEPFeepZdspKN4K/view?usp=sharing

Slides:

Anatomical Interoperation of Resources

A copy of the meeting chat is available at the bottom of this document.

Agenda

Announcements

- **Portal release**. New data! https://app.nih-cfde.org/

- **November meeting**. Please reserve your hotel room by **Friday October 7**.

  Meeting details and links at https://nih-cfde.github.io/2022-nov-meeting/

FAIR API Workspace Pilot
Presented by Katy Börner and Kristin Ardlie

Anatomical Interoperation of Resources
Presented by Bruce Herr and Jyl Boline

Hosted by Dr. Rayna Harris

Please review our Resources for Attendees for details on how to participate in this meeting.

Post-Meeting Resources

Chat:

11:03:02 From Avi Ma'ayan to Everyone:
　　　David Bowie…
11:03:11 From Nancy Ruschman to Everyone:
　　　+1
11:05:03 From Jeremy Walter (CFDE-CC) to Everyone:
　　　https://app.nih-cfde.org/
11:05:59 From Anne Deslattes Mays to Everyone:
　　　how do you see the RAS login?
11:06:41 From Jeremy Walter (CFDE-CC) to Everyone:
　　　https://nih-cfde.github.io/2022-nov-meeting/
11:08:17 From Anne Deslattes Mays to Everyone:
　　　I found the eRA Commons - a little slow but it comes up.
11:13:46 From Katy Borner to Everyone:
　　　Pilot site: https://hubmapconsortium.github.io/ccf-gtex-pilot/
11:14:57 From Shankar Subramaniam to Everyone:
　　　Katy, thanks for the intro to this GTex-HubMap alliance. In addition to the ontologies, don't you need a cytoanatomical map to map the cell specific gene expression? if the expression is at the tissue level we will still need an anatomical map. How much of this do we have? And how individual-specific will such an anatomical atlas be? Looking at the scRNA data on the aorta example, don't we still need a microanatomical atlas?

11:16:32 From Bruce Herr to Everyone:
    https://hubmapconsortium.github.io/ccf-ui/rui/
11:20:50 From George Papanicolaou to Everyone:
    This is really cool.
11:24:58 From Katy Borner to Everyone:
    GTEx Training as part of the HuBMAP Visible Human MOOC (VHMOOC)
    https://expand.iu.edu/browse/sice/cns/courses/hubmap-visible-human-mooc
11:25:32 From Anne Deslattes Mays to Everyone:
    I see that you are using heroku - is there a link to the technical document that outlines the architecture for this site
11:27:24 From Bruce Herr to Everyone:
    Heroku is not used so much anymore (staging only). Our solution uses GitHub Actions to test, build, and deploy to GitHub Pages and AWS AppRunner (+ a Docker container). Also publish to NPM and PyPi for our CCF-API libraries.
11:27:59 From Bruce Herr to Everyone:
    Database is an in-memory triplestore (N3.js)
11:28:32 From Katy Borner to Everyone:
    Here is more info on CCF Ontology: Specimen, Biological Structure, and Spatial Ontologies in Support of a Human Reference Atlas
    https://biorxiv.org/cgi/content/short/2022.09.08.507220v1 -- all comments/questions welcome.
11:28:33 From Anne Deslattes Mays to Everyone:
    How are cell-types defined? Is it by surface markers? Is it possible to search by surface markers?
11:30:02 From Anne Deslattes Mays to Everyone:
    Thank you @Bruce -- is the documentation of the architecture ? Is it all on GitHub ? Are you able to share the GitHub with the GitHub actions ?
11:31:03 From Bruce Herr to Everyone:
    I'm drawing a blank on a good doc describing our software architecture. All code is on GitHub here: https://github.com/hubmapconsortium/ccf-ui
11:31:50 From Bruce Herr to Everyone:
    CCF-API has interactive documentation of the routes/methods available here: https://ccf-api.hubmapconsortium.org/#/
11:32:10 From Bruce Herr to Everyone:
    (including a SPARQL endpoint for custom queries)
11:33:00 From Shankar Subramaniam to Everyone:
    To clarify my question further, the anatomical atlas/map is at best at the millimeter level, which gene expression from tissue blocks covers a much smaller region. Will the celltype population/heterogeneity seen at the tissue block level reflect the anatomical region? Will you not need spatial transcriptomics and perhaps broad sampling of the tissue block to see if the cell population distribution from one small region is conserved across the microanatomy? We know for e.g. in brain this is not the case. I don't know enough anatomy to provide any meaningful suggestion, but please educate me now or later one on one.
11:35:31 From Shankar Subramaniam to Everyone:
    Thank you Katy. we can talk off line. I like this very much, but have more questions. thanks.
11:35:41 From Jyl Boline to Everyone:
    Can you post the link to the paper you mentioned again please?
11:35:44 From Anne Deslattes Mays to Everyone:
    How are celltypes defined? Is it by cell surface markers?

11:36:35 From Rayna Harris to Everyone:
    paper: Pilot site: https://hubmapconsortium.github.io/ccf-gtex-pilot/
11:36:48 From Rayna Harris to Everyone:
    https://biorxiv.org/cgi/content/short/2022.09.08.507220v1
11:36:56 From Jyl Boline to Everyone:
    Thanks!
11:37:58 From Anne Deslattes Mays to Everyone:
    If it would be possible is to put the markers used for the characterization
11:38:25 From Anne Deslattes Mays to Everyone:
    just document it so that it is known - so that if new data comes in
11:44:53 From Katy Borner to Everyone:
    @Anne More info on ASCT+B Tables is at
https://hubmapconsortium.github.io/ccf/pages/ccf-anatomical-structures.html
11:45:46 From Katy Borner to Everyone:
    Also see https://www.nature.com/articles/s41556-021-00788-6
11:47:12 From Katy Borner to Everyone:
    The ASCT+B Working Group meet every first Wed of the month, 11a ET. Register at
https://iu.co1.qualtrics.com/jfe/form/SV_bpaBhIr8XfdiNRH to get meeting invites and access
to slides/recordings from last 30 meetings.
11:48:14 From Anne Deslattes Mays to Everyone:
    thanks @katy
11:50:36 From Bruce Herr to Everyone:
    https://hubmapconsortium.github.io/ccf-sparc-pilot/
11:53:24 From Katy Borner to Everyone:
    CCF 3D Organ Library:
https://hubmapconsortium.github.io/ccf/pages/ccf-3d-reference-library.html
11:58:28 From Shankar Subramaniam to Everyone:
    going forward (perhaps decade or so), we will have spatial transcriptomics that will
have the resolution to map the cells better.