# NIH-HCA 2020 Joint Meeting

Home | Pre-Meeting Webinars and Schedule | Meeting Agenda | Breakout Summaries

## Agenda

| Day 1: March 30, 2020 | |
|---|---|
| 9:30 -9:35 | Opening |
| 9:35 - 10:05 | COVID-19 Collaborations |
| 10:05 - 10:30 | Day 1 Opening Plenary |
| 10: 30 - 11:15 | Breakout Session #1, Part 1 |
| 11:15 - 11:30 | Welcoming Remarks: NIH Director Francis Collins |
| 11:30 - 11:45 | Break |
| 11:45 - 1:00 | Breakout Session #1, Part 2 |
| 1:00 - 1:45 | Lunch Break |
| 1:45 - 1:50 | Plenary |
| 1:50 - 2:50 | Breakout Session #2, Part 1 |
| 2:50 - 3:05 | Break |

| Day 2: March 31, 2020 | |
|---|---|
| 10:00 - 10:15 | Day 2 Opening Plenary |
| 10:15 - 11:00 | Breakout Session #3, Part 1 |
| 11:00 - 11:15 | Break |
| 11:15 - 12:30 | Breakout Session 3, Part #2 |
| 12:30 - 1:15 | Lunch Break |
| 1:15 - 1:20 | Plenary Session |
| 1:20 - 2:05 | Breakout Session #4, Part 1 |
| 2:05 - 2:20 | Break |
| 2:20 - 3:35 | Breakout Session #4, Part 2 |
| 3:35 - 4:30 | Day 2 Closing Plenary |

| Day 1: March 30, 2020 | |
|---|---|
| 3:05 - 4:05 | Breakout Session #2, Part 2 |
| 4:05 - 4:30 | Day 1 Closing Plenary |

Breakout Sessions

**Breakout #1, Monday morning** | **Breakout #2, Monday afternoon** | **Breakout #3, Tuesday morning** | **Breakout #4, Tuesday afternoon**

| Clinical Metadata | Data Architecture and Integration | Temporal Analysis: Development and Pediatric | Multiplex Molecular Profiling Tools | Spatial Profiling Tools |
|---|---|---|---|---|
| a. **What is the scope of "clinical" metadata?** Developing a roadmap of establishing "clinical" metadata | a. **Common interfaces** There are several different cell atlas'ing initiatives which are all building portals and storage solutions for their data. What common interfaces are needed to minimize any access barriers across multiple projects | a. **Organ-based or anatomical unit-based atlas** How do we achieve V1 development atlas | a. **Imaging-based techniques** Imaging-based techniques at all scales for multimodal molecular profiling | a. **Antibody-based imaging methods** e.g., staining using fluorochromes, metal-chelates, etc., in an antibody-based manner |
| b. **Core clinical metadata** How do we achieve core clinical metadata standards across diverse tissue types, tissue collection methods, and tissue collection sites. (sample level vs patient level)? | b. **Data Storage and Data Movement** | b. **Engaging developmental biology community** Expertise in developmental biology | b. **Single-cell sequencing-based techniques** Spanning the Central Dogma | b. **Imaging-based transcriptomics methods** e.g., multiplexed FISH and in situ sequencing methods |
| c. **Levels of Metadata** How to manage the clinical metadata data outside of the core? | c. **Data format standards** | c. **What biology can we learn from development atlas** What are important questions? | | c. **Sequencing-based spatial measurements** (e.g. ST) |
| d. **Review process for Clinical Metadata** The process to gain consensus | d. **Authentication for access** | d. **Relevance of development to pediatric and adult health/disease** | | d. **Multi-omic spatial data and integratio** |

| Clinical Metadata | Data Architecture and Integration | Temporal Analysis: Development and Pediatric | Multiplex Molecular Profiling Tools | Spatial Profiling Tools |
|---|---|---|---|---|
| e. **Sample ID Naming Conventions** Naming conventions to account for patient or subject, multiple samples per subject, many time points (longitudinal studies) and spatial attributes | | e. **Ethics relating to development atlas** | | |
| | | f. **Age resolution for pediatric and development atlas** | | |

*Return to Home.*