





Spatial Transcriptomics Workshop

Featuring BIL, HuBMAP Data Giotto, Harpy & Sparrow Tools

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Brain Image Library

<u>Mission:</u> National public resource enabling researchers to deposit, analyze, mine, share and interact with optical microscopy datasets of the brain.



- No depositor size limitations
- Professional curation
- Help desk support
- Network bottleneck/analysis assistance for depositors transferring large datasets
- DOI Issuance for datasets through DataCite membership
- Landing pages for datasets
- LTO Tape for disaster recovery of data
- LTO tape (7/8/9) capable for import of large datasets

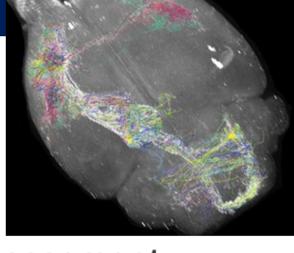
Providing Access

Analysis Ecosystem

- Scalable Architecture
- Data available on PSC's HPC and Al Resources for computational analysis without downloading data
- Frequently used community open-source and commercial software tools available

Web Resources

- Metadata API with web searchable interface + File SDK
- Visualization Resources:
 - Neuroglancer (3d Datasets)
 - o OpenSeaDragon (2d Datasets)
 - Napari plug-in



Engagement

Workshops

- Data Submission Workshops
- Spatial Transcriptomics Workshop for BICAN & BICAN Orientation
- CFDE Reproducible Workflow Workshop

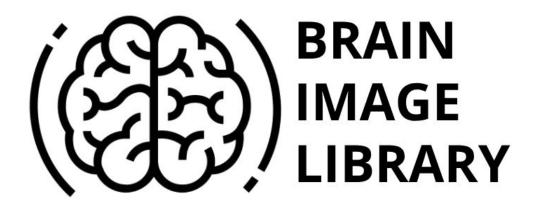
Meetings

- Society for Neuroscience
- BRAIN Investigators
- Annual Biomedical Research Conference for Minoritized Scientists (ABRCMS)

Newsletter

The BIL Bulletin

BIL Workshop Team









Alex Ropelewski



Alan Watson



Iván Cao-Berg



Dominic Bordelon



Mariah Kenney



Alison McWilliams

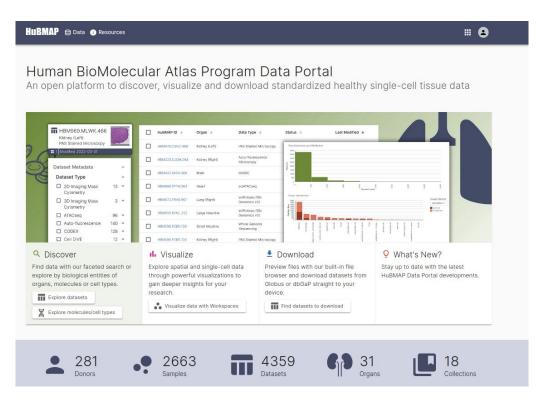


Luke Tuite



Iana Vasylieva

HuBMAP

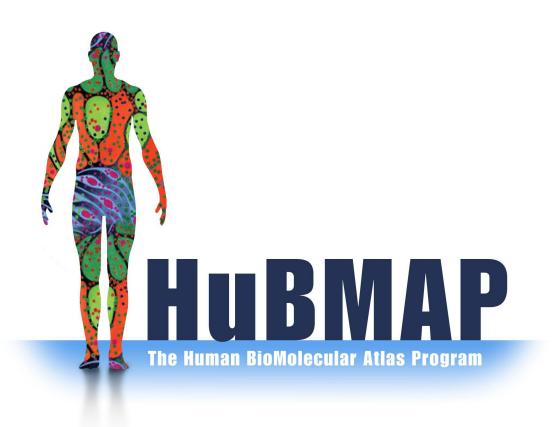


The HuBMAP Data Sharing Portal.

The Human Biomolecular Atlas Program (HuBMAP) is dedicated towards mapping the human body at the single-cell level.

- 42 contributing sites
 - HuBMAP Integration, Visualization, and Engagement (HIVE) group
 - Includes the Infrastructure and Engagement Component (IEC) - HuBMAP's "data core"
 - Tissue Mapping Centers (TMCs)
 - Transformative Technology Developers (TTDs)
- TMCs work with a variety of experimental assays on tissue samples from 31 organs throughout the human body

HuBMAP Workshop Team











Phil Blood

Alex Ropelewski



Alison McWilliams

Dominic Bordelon

Iván Cao-Berg

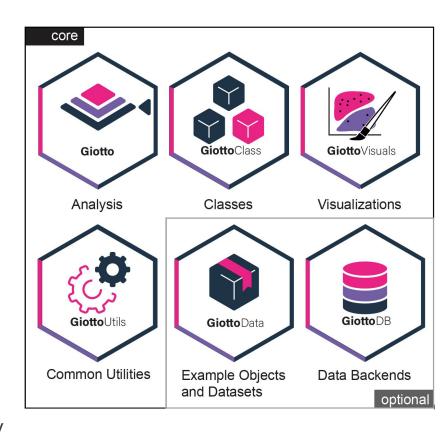
Brendan Honick

Juan Muerto

Giotto



Giotto Suite provides tools to process, analyze and visualize spatial multi-omics data at all scales and multiple resolutions. The underlying framework is generalizable to virtually all current and emerging spatial technologies. Our Giotto Suite prototype pipeline is generally applicable on various different datasets, such as those created by



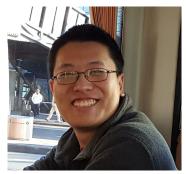
state-of-the-art spatial technologies, including in situ hybridization, sequencing, and imaging-based multiplexing/proteomics.

Giotto Team











Ruben Dries

Guo-Cheng Yuan

Jiaji George Chen

Joselyn Chávez

Dries & Yuan lab members providing additional support on Slack:

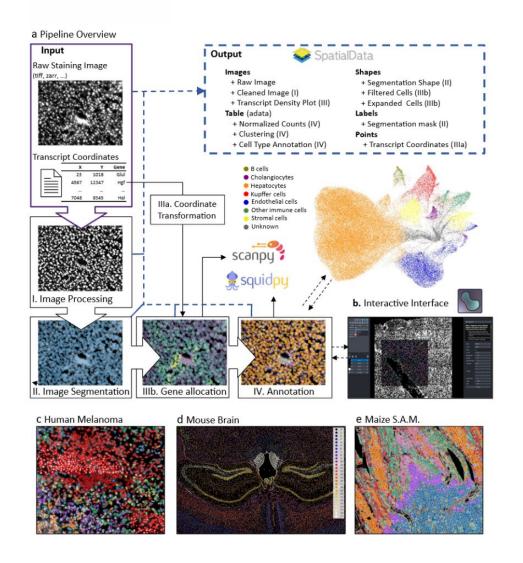
Jeffrey Sheridan

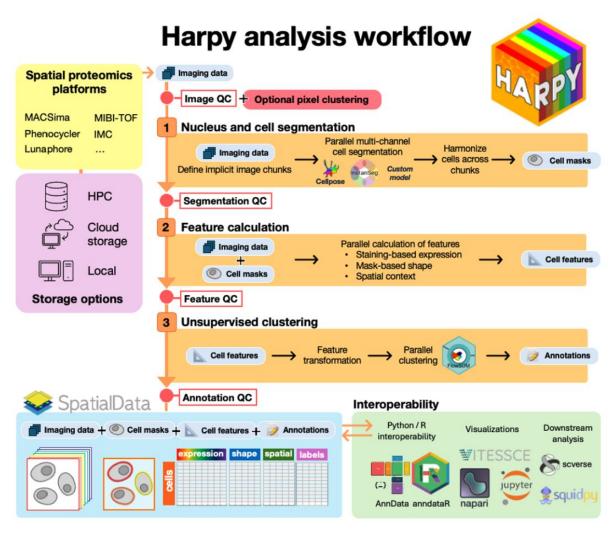
Veronica Jarzabek

Crystal Shin

Harpy/SPArrOW







Harpy/SPArrOW Team

SCIENCE MEETS LIFE

VIB-UGent Center for Inflammation Research

SaeysLab

Lotte Pollaris Benjamin Rombaut Ruth Seurinck

Sofie Van Gassen

•••

Yvan Saeys

VIB Spatial Catalyst

Arne Defauw

Frank Vernaillen

Julien Mortier

Elina Kuznecova

Fleur Parmentier

Evelien Van Hamme









Agenda - Today

Time (EDT)	Topic
11:00 - 12:00	 Optional: Pre-Workshop Office Hours Join if you have any questions about accounts and resource access
12:00 - 12:15	Welcome and Introduction
12:15 - 1:00	Introduction to Spatial Technologies
1:00 - 2:00	 Spatial Data Introduction to Spatial Data in the Brain Image Library Introduction to Spatial Data in HuBMAP
2:00 - 2:15	Break
2:15 - 3:15	Accessing Spatial Data at the Brain Image Library • Using the Data Analysis Ecosystem
3:15 - 4:15	Accessing Spatial Data Through HuBMAP

Workshop Agenda

Day	Topics
Monday	 Intro to Spatial Technologies Spatial Data in BIL and HuBMAP Using PSC Computational Platforms
Tuesday	 Intro to Giotto Exploring 3D MERFISH data from BIL Finding genes Integration with scRNAseq data
Wednesday	 Giotto data import and pre-processing Spatial data alignment Multimodal integration & analysis Multi sample integration
Thursday	 High level intro SPArrOW. Hands on Intro SpatialData. Hands on Intro SPArrOW. Run SPArrOW on Xenium data from HubMap.
Friday	 High level intro Harpy. Hands on into Harpy. FlowSom clustering with Harpy. Run Harpy on Phenocycler data.