

Day 1 (September 15th) QBI workshop on multiplex image analysis and computational pathology

Time	Tentative talk/topic	Speaker
	Day 1 AM session 1	
8:00 - 9:00 AM	On-site registration opens	
9:00 - 9:30 AM	Nuclear segmentation and phenotyping pipelines (tentative)	David Van Valen Lab, Caltech
9:30 - 10:00 AM	Tissue multiplexing is more messier or merrier - introduction and start of the art	Sripad Ram, Pfizer Inc
10:00 - 10:30 AM	Contributed talk 1	
10:30 - 11:15 AM	AM coffee break	
	Day 1 AM session 2 - mxIF data analysis and insights	
11:15 - 11:45 AM	Spatial analysis of multiplex datasets - overview and applications	Saumaditya Pyne, UC Santa Barbara
11:45 AM - 12:15 PM	Deciphering cell-to-cell spatial relationships for pathology using spatialQPFs	Xiao Li, Roche
12:15 - 1:00 PM	Panel discussion: Foundation models vs bespoke pipelines for spatial proteomics	
1:00 - 2:00 PM	Lunch break	
	Day 1 PM session 1	
2:00 - 2:30 PM	DeepLIF - deep learning inferred immunofluorescence	Saad Nadeem, MSKCC
2:30 - 3:00 PM	Contributed talk 2	
3:00 - 3:30 PM	Contributed talk 3	
	Panel discussion	
3:30 - 4:15 PM	Panel discussion: Standardization vs innovation: are we slowing the field down	
4:00 - 4:45 PM	PM coffee break	
	Day 1 PM session 2 - software features demo session	
4:45 - 5:15 PM	QuPath demo (tentative)	Sara McArdle, La Jolla Institute of Immunology
5:15 - 5:30 PM	Short talk 1	
5:30 - 5:45 PM	Short talk 2	
5:45 - 6:00 PM	Short talk 3	
6:00 - 8:00 PM	Day 1 dinner	

Day 2 (September 16th) QBI workshop on multiplex image analysis and computational pathology

Time	Tentative talk/topic	Speaker
	Day 2 AM session 1 - Novel multiplexing approaches	
9:00 - 9:30 AM	Chromogenic multiplexing for clinical applications	Daniel Bauer, Roche
9:30 - 10:00 AM	Contributed talk 4	
10:00 - 10:30 AM	Contributed talk 5	
10:30 - 11:15 AM	AM coffee break	
	Day 2 AM session 2 - multimodel data analysis 1	
11:15 - 11:45 AM	AI tools for spatial proteomics data analysis	Rujia Li, Stanford University
11:45 AM - 12:15 PM	Topological tools for spatial proteomics	Chao Chen, Stonybrook university
12:15 - 12:45 PM	Contributed talk 6	
12:45 - 1:00 PM	Short talk 4	
1:00 - 2:00 PM	Lunch break	
	Day 1 PM session 1 - multimodel data analysis 2	
2:00 - 2:30 PM	Characterizing cell-type spatial relationships in spatially resolved omics data	Rafael dos Santos Peixoto, Johns Hopkins University
2:30 - 3:00 PM	Contributed talk 7	
3:00 - 3:30 PM	Contributed talk 8	
3:30 - 4:15 PM	PM coffee break	
4:15 - 5:00 PM	Panel discussion: Are we overinterpreting spatial patterns?" (Biology vs. artifacts debate)	
5:00 - 6:00 PM	Evening reception + poster viewing session	
6:00 - 8:00 PM	Day 2 dinner	