10X GENOMICS

Biology at True Resolution

2018 ASHG CONFERENCE GUIDE

Visit us at booth #635

10X GENOMICS WORKSHOP

Biology at True Resolution: Enabling a Comprehensive View of Genomics

WEDNESDAY, OCTOBER 17 | 12:30 PM – 1:45 PM | ROOM 30 C-D, UPPER LEVEL

Learn how researchers are using groundbreaking technology from 10x Genomics to reveal insights into cellular systems and human genetics:

- Understand genomic diversity
- Reveal genomic heterogeneity
- Profile the chromatin landscape of thousands of individual nuclei
- Perform high resolution genetic screening and enhanced single cell phenotyping of complex cell populations

MOLLY GASPERINI
Graduate Student
University of Washington

JIMMIE YE, PHD
Assistant Professor
University of California, San Francisco

COLABS PRESENTATIONS

Getting Started with Single Cell Transcriptomics

WEDNESDAY, OCTOBER 17 | 4:00 PM – 4:30 PM | COLABS THEATER | BOOTH #241

Understand the considerations for experimental design, sample preparation, and downstream data analysis for single cell gene expression experiments.

Accelerating Biology: New Product Innovations from 10x Genomics

THURSDAY, OCTOBER 18 | 10:30 AM – 11:00 AM | COLABS THEATER | BOOTH #241

Meet our latest innovations, each transforming our understanding of biology from DNA, RNA to epigenetics, cell by cell.

Unraveling Multiple Dimensions of Cellular Heterogeneity

THURSDAY, OCTOBER 18 | 1:45 PM – 2:15 PM | COLABS THEATER | BOOTH #241

Learn how to examine cellular heterogeneity and analyze the complexity of biological systems, both within a population and over time, all at the single cell level.

Visualization of Multiple Single Cell Genomic Datatypes

FRIDAY, OCTOBER 19 | 1:45 PM – 2:15 PM | COLABS THEATER | BOOTH #241

Deepen your understanding of complex cell populations with our easy to use software and visualization tools.

SCIENTIFIC SESSIONS

Understanding Tumor Heterogeneity from Single Cell Sequencing of Genomes, Transcriptomes and Epigenomes

WEDNESDAY, OCTOBER 17 | 10:30 AM – 12:30 PM | BALLROOM 20A - UPPER LEVEL

CONCURRENT INVITED SESSION I

Xinying Zheng 10X GENOMICS

Elham Azizi, Memorial Sloan Kettering Cancer Center

What are We Missing? Identification of Previously Underappreciated Mendelian Variants

THURSDAY, OCTOBER 18 | 11:00 AM – 12:30 PM | BALLROOM 20A - UPPER LEVEL

CONCURRENT PLATFORM SESSION E

Daniel Koboldt, Nationwide Children's Hospital

Zeynep Coban Akdemir, Baylor College of Medicine

Single Cell Approaches to Reveal Disease Biology

THURSDAY, OCTOBER 18 | 11:00 AM – 12:30 PM | BALLROOM 20BC - UPPER LEVEL

CONCURRENT PLATFORM SESSION E

Kimberly Aldinger, Seattle Children's Research Institute

Manolis Kellis, Massachusetts Institute of Technology

Increasing Functional Resolution Through Single Cell Analysis

SATURDAY, OCTOBER 20 | 9:45 AM – 11:15 AM | ROOM 6B - UPPER LEVEL

CONCURRENT PLATFORM SESSION H

Nick Banovich, Translational Genomics Research Institute

Mingyao Li, University of Pennsylvania

POSTERS

Wednesday, October 17th

2:00 PM – 3:00 PM
A novel next generation sequencing based genetic test platform for congenital adrenal hyperplasia due to CYP21A2 defects
Qizong Lao | #2877
NIH

2:00 PM – 3:00 PM
Haplotype resolved analysis and improved genome coverage with Linked-Reads
Stephen Williams | #385
10X GENOMICS

2:00 PM – 3:00 PM
Classification of prostate cancer patients as indolent or aggressive using machine learning approach
Tarun karthik kumar Mamidi | #825
Louisiana State University

2:00 PM – 3:00 PM
Characterizing tumor heterogeneity at single cell level
Claudia Catalanotti | #903
10X GENOMICS

3:00 PM – 4:00 PM
SAMPLOT: Rapid structural variant visualization for short, long, linked, and phased reads
Ryan Layer | #1446
University of Colorado, Boulder

3:00 PM – 4:00 PM
A public benchmarking resource of 194,731 CNV calls generated from a combination of short reads, linked long reads and true long read technologies
Xiao Chen | #1638
Illumina

3:00 PM – 4:00 PM
Single nuclei RNA-seq to decipher hypothalamic transcriptional response to chronic topiramate administration
Kathy Ushakov | #2202
Boston Children's Hospital

3:00 PM – 4:00 PM
Using linked-read sequencing to resolve pathogenic mutations and overcome pseudogene interference in PKD1 for autosomal dominant polycystic kidney disease testing
Charlly Kao | #2874
Children's Hospital of Philadelphia

3:00 PM – 4:00 PM
Classification of cell type from single-cell RNA sequencing data by deep neural networks
Carolyn Lou | #3534
University of Pennsylvania

3:00 PM – 4:00 PM
Detecting inversion polymorphisms at population scale with linked read sequencing
Christopher Whelan | #394
Broad Institute

3:00 PM – 4:00 PM
New methods for discovery and interpretation of allelic diversity in human genomes
Robert Fulton | #442
Washington University in St. Louis

3:00 PM – 4:00 PM
Gene regulation and cell-cell communication underlying intra-tumoral heterogeneity in HCC liver cancer
Bojan Losic | #852
Icahn Institute for Genomics and Multiscale Biology

3:00 PM – 4:00 PM
Genetic heterogeneity profiling by single cell RNA sequencing
Zilu Zhou | #894
University of Pennsylvania

3:00 PM – 4:00 PM
A comprehensive cross-platform comparison of single-cell RNA sequencing using reference samples
Charles Wang | #924
Loma Linda University

POSTERS

Thursday, October 18th

2:00 PM – 3:00 PM
Imputation of single-cell gene expression with an autoencoder neural network
Rui Li | #1687
University of Idaho

2:00 PM – 3:00 PM
Single cell sequencing of iPSC neural cells from Down syndrome patients uncovers perturbed cell differentiation
Joakim Klar | #1747
Science for Life Laboratory

2:00 PM – 3:00 PM
Supporting single-cell RNA-seq at scale in the genomics platform at the Broad Institute
Cole Walsh | #1783
Broad Institute

2:00 PM – 3:00 PM
Single cell analysis of Alzheimer's disease
Manolis Kellis | #1897
Massachusetts Institute of Technology

2:00 PM – 3:00 PM
Combining single-cell RNA and DNA sequencing analysis to measure genomic instability at individual clone resolution in gastric cancer
Sue Grimes | #817
Stanford University

2:00 PM – 3:00 PM
Linked read technology enables disambiguation of structural variants to PMS2 and PMS2CL
Jeroen Van den Akker | #919
Color Genomics, Inc.

3:00 PM – 4:00 PM
LinkedSV: Detection of mosaic structural variants from linked-read sequencing
Li Fang | #1486
Children's Hospital of Philadelphia

3:00 PM – 4:00 PM
Detection of structural variants using linked-reads with novel algorithms
Ian Fiddes | #1564
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3:00 PM – 4:00 PM
How well can you detect structural variants: towards a standard framework to benchmark human structural variation
Justin Zook | #1648
National Institute of Standards and Technology

3:00 PM – 4:00 PM
Cell-type specific differential gene expression in post-mortem snRNA-seq of the depressed brain
Malosree Maitra | #1744
Douglas Institute

3:00 PM – 4:00 PM
High-throughput single nuclei RNA-seq from limited amounts of frozen human and mouse tissues
Anugraha Raman | #1780
Ludwig Institute for Cancer Research

3:00 PM – 4:00 PM
Studies of liver tissue identifies functional gene regulatory elements associated to gene expression, type 2 diabetes and other metabolic diseases
Claes Wadelius | #2188
Science for Life Laboratory

3:00 PM – 4:00 PM
De novo human genome assemblies reveal novel sequences in diverse populations
Karen Wong | #440
University of California, San Francisco

POSTERS

Friday, October 19th

2:00 PM – 3:00 PM
Single-nucleus RNA-sequencing of human subcutaneous adipose tissue reveals a heterogeneous population of 12 cell types
Marcus Alvarez | #1709
University of California, Los Angeles

2:00 PM – 3:00 PM
Single-cell RNA-sequencing of bulk peripheral blood mononuclear cells from idiopathic multicentric Castleman disease (iMCD) reveals leukocyte heterogeneity underlying disease pathology
Michael Gonzalez | #2279
The Children's Hospital of Philadelphia

2:00 PM – 3:00 PM
Building human reference genomes for Africa
Martin Pollard | #2771
Wellcome Sanger Institute

2:00 PM – 3:00 PM
Beyond the exome: Identification of novel mutational signatures and oncogenic dependencies in the non-coding genome of multiple myeloma
Cody Ashby | #899
University of Arkansas for Medical Sciences

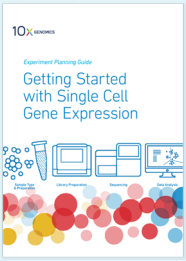
3:00 PM – 4:00 PM
Single cell transcriptomes of sickle cell disease PBMC identifies markers of disease severity in distinct cell populations
Samuel Lessard | #1004
Bioverativ

3:00 PM – 4:00 PM
Precise breakpoint detection of balanced and unbalanced structural variation in whole genome sequencing data using haplotype blocks created by linked-reads
Jeroen Knijnenburg | #2990
Leiden University Medical Center

LEARN MORE

Getting Started Guide

Whether you have questions about how to design your experiments, optimize parameters, or identify the computational/analytical tools necessary to best analyze your single cell gene expression data, this guide has you covered. Take full advantage of the rich information enabled by single cell transcriptomic technology by downloading the getting started guide today!



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