

2018 Single-cell Genomic Data Analytics Symposium
August 6, 2018 – Palmer Commons, Great Lakes Rooms

Please join us for the Single-cell Genomic Data Analytics Symposium. The event will highlight U-M researchers whose work is on the leading edge of innovation and discovery. This symposium is organized by the Michigan Center for Single-Cell Genomic Data Analytics, and sponsored by the Michigan Institute for Data Science. Please register at <https://midas.umich.edu/2018-single-cell/>.

SYMPOSIUM SCHEDULE

8:00 – 8:30 A.M. COFFEE & LIGHT BREAKFAST

8:30-8:45 A.M. WELCOME REMARKS

Steve Kunkel, PhD, Senior Associate Dean for Research, Endowed Professor in Pathology Research, U-M Medical School

8:45-10:15 A.M.

Dana Pe'er, PhD, Chair, Computational and Systems Biology, Sloan Kettering Institute, MSKCC.
"Having fun with single cell RNA-seq, trajectories in health and disease" (30)

Clay Scott, PhD, Professor of Electrical Engineering & Computer Science and Statistics, U-M
"Cluster-Preserving Dimensionality Reduction" (20)

Xiang Zhou, PhD, Assistant Professor of Biostatistics, CCMB Affiliated Faculty, U-M
"Variability-preserving imputation for accurate gene expression recovery in single cell RNA sequencing studies" (20)

Justin Colacino, PhD, John G. Searle Assistant Professor of Environmental Health Sciences, Assistant Professor of Nutritional Sciences, U-M
"Single Cell Profiling to Understand the Role of Stem Cells in Breast Cancer Disparities"(20)

10:15 A.M. COFFEE BREAK

10:30 – 12:50 noon.

Peter Kharchenko, PhD, Assistant Professor of Biomedical Informatics, Harvard Medical School
"Analysis of transcriptional dynamics with single-cell data"(30)

Anna Gilbert, PhD, Herman Goldstine Collegiate Professor of Mathematics, Affiliations with Electrical Engineering and Computer Science, U-M
"Feature selection and dimension reduction for (sparse) scRNA-seq data" (20)

Joshua Welch, PhD, Assistant Professor, Department of Computational Medicine & Bioinformatics; Assistant Professor, Electrical Engineering & Computer Science, U-M
"Comparing and Contrasting Highly Heterogeneous Single Cell Datasets" (20)

Gil Omenn, PhD, Harold T. Shapiro Distinguished University Professor; Director, Center for Computational Medicine and Bioinformatics, U-M
"Analytic pipeline for full-length single-cell RNA sequencing data acquired by Fluidigm Polaris platform"(20)

12:00 – 1:00 P.M. BOX LUNCH & NETWORKING

1:00-2:10 P.M.

Emma Lundberg, PhD, Visiting Associate Professor, Stanford University; Associate Professor, KTH Royal Institute of Technology

"Dissecting the Spatiotemporal Subcellular Distribution of the Human Proteome" (30)

Sue Hammoud, PhD, Assistant Professor of Human Genetics, Assistant Professor of Obstetrics and Gynecology, Assistant Professor of Urology, U-M

"Single-cell RNA-seq analysis of the adult and neonatal testis uncovers a potential reserve somatic cell progenitor" (20)

Jun Li, PhD, Professor Human Genetics, Professor & Associate Chair for Research, Department of Computational Medicine and Bioinformatics, U-M

"Assessing transcriptional diversity in single cells using adjusted Gini index" (20)

2:10 P.M. COFFEE BREAK

2:30-4:00 P.M.

Christina Kendzierski, PhD, Professor, Department of Biostatistics & Medical Informatics, University of Wisconsin Madison

"Statistical Methods for Single-Cell RNA Seq" (30)

Johann Gagnon-Bartsch, PhD, Assistant Professor of Statistics, Affiliated with MIDAS, U-M

"Endogenous Single Cell Controls" (20)

Max Wicha, PhD, Madeline and Sidney Forbes Professor of Oncology, Director, Forbes Institute for Cancer Discovery, Professor of Internal Medicine, CCMB Affiliated Faculty, U-M

"Heterogeneity of breast cancer stem cells at single-cell resolution" (20)

Lana Garmire, PhD, Associate Professor of Computational Medicine and Bioinformatics, U-M

"Using Single Nucleotide Variations in Single-Cell RNA-Seq to Identify Subpopulations" (20)

4:00 P.M. – 4:30 P.M. Discussions and Closing Remarks