

NCI Informatics Technology for Cancer Research (ITCR) Annual Meeting 2019

Natural History Museum Utah, Rio Tinto Center, 301 Wakara Way, Salt Lake City, UT 84108

Lodges at Deer Valley, of 2900 Deer Valley Drive East, Building 45, Park City, UT 84060

Tuesday, May 28 – Friday, May 31, 2019

Day 1 – Tuesday, May 28, Natural History Museum of Utah

- 5:30pm** “Drinks with the Dinosaurs”
6:00pm Dinner in The Canyon
7:00pm Conference Welcome, Dr. Juli Klemm, NCI, and Dr. Gabor Marth, University of Utah
7:05pm Opening Address, Dr. Mary Beckerle, CEO, Huntsman Cancer Institute
7:30pm Keynote Speaker, Dr. Elaine Mardis, Co-Executive Director, Institute for Genomic Medicine, Nationwide Children’s Hospital
8:30pm Buses will transport attendees to Deer Valley

Day 2 – Wednesday, May 29, Lodges at Deer Valley

- 7:00am** Buffet Breakfast, Brass Tag and Spruce A&B, The Lodges
8:30am Welcoming Remarks, Evergreen Room
Gabor Marth, University of Utah
Juli Klemm, National Cancer Institute

Session 1: Clinical Cancer Informatics, 8:50am – 10:10am, Evergreen Room

Session Chair: Betsy Hsu

8:50	Ken Kawamoto, University of Utah <ul style="list-style-type: none">Using Standards-Based Clinical Decision Support Algorithms to Identify and Manage Patients who Meet Evidence-Based Criteria for Genetic Evaluation of Familial Cancer
9:10	David Hanauer, University of Michigan <ul style="list-style-type: none">EMERSE: The Electronic Medical Record Search Engine
9:30	Jeremy Warner, Vanderbilt University <ul style="list-style-type: none">HemOnc: A New Standard Vocabulary for Chemotherapy Regimen Representation in the OMOP Common Data Model
9:50	GQ Zhang, The University of Texas Health Science Center at Houston <ul style="list-style-type: none">An Ontology-driven Faceted Query Engine for the Kentucky Cancer Registry

10:10am – 10:40am Break, Evergreen Foyer, The Lodges

Lightning Talks 1: 10:40am – 11:30am, Evergreen Room (5 min each)

Chair: Juli Klemm

Paul Fitzgerald, GE Research: <i>Introducing a New Open-Source Tool: XCIST (X-ray-based Cancer Imaging Simulation Toolkit)</i>
Clifford Meyer, Dana-Farber Cancer Institute / Harvard School of Public Health: <i>Cistrome Data Browser: Expanded Datasets and New Tools for Gene Regulatory Analysis</i>
Paul Marjoram, University of Southern California: <i>Conservation and Functional-Characterization of Tumor Methylation Sites</i>
Andrew Janowczyk, Case Western Reserve University: <i>HistoQC: A Quality Control Pipeline for Digital Pathology Slides</i>
Joshua Campbell, Boston University School of Medicine: <i>Enhanced Deconvolution and Prediction of Mutational Signatures</i>

Fuyong Xing, University of Colorado Anschutz Medical Campus: <i>Deep Pixel-to-pixel Learning for Single-stage Nucleus Recognition in Digital Pathology Images</i>
Gordon Harris, Massachusetts General Hospital: <i>Precision Imaging Metrics: All-in-One Cloud-Hosted Quantitative Imaging Assessment and Workflow Management System for Cancer Centers</i>
Trinity Urban, Massachusetts General Hospital: <i>Crowds Cure Cancer: Crowd-Sourcing Ground-Truth Measurements on Publicly Available Imaging Data</i>
Xiaodong Wu, University of Iowa: <i>What Does AI See? Deep Segmentation Networks Discover Biomarkers for Lung Cancer Survival</i>
Anjishnu Banerjee, Medical College of Wisconsin: <i>Stochastic Covariance Functions for Understanding the Histology and Improving Detection in Solid Tumors</i>

**NCI Program Presentations: 11:30am – 12:00pm, Evergreen Room
NCI Staff**

11:30	Tanja Davidsen, NCI CBIIT <ul style="list-style-type: none"> • <i>NCI Cancer Research Data Commons Overview</i>
11:45	Tony Dickherber, NCI CSSI <ul style="list-style-type: none"> • <i>Coordination with Cancer Moonshot and Other NCI Programs</i>

12:00pm – 1:30pm, Lunch in Brass Tag and Spruce A&B, The Lodges

**Session 2: Cancer Genomics 1, 1:30pm – 3:30pm, Evergreen Room
Session Chair: David Miller**

1:30	Tim Griffin, University of Minnesota <ul style="list-style-type: none"> • <i>A Resource for Complete Proteogenomic Informatics in Cancer Research: Built on ITCR Tools</i>
1:50	Brian Haas, Broad Institute <ul style="list-style-type: none"> • <i>Latest Developments in the Trinity Cancer Transcriptome Analysis Toolkit</i>
2:10	Evan Johnson, Boston University <ul style="list-style-type: none"> • <i>Interactive Single Cell RNA-Seq Analysis with the Single Cell Toolkit (SCTK)</i>
2:30	Ravi Madduri, University of Chicago <ul style="list-style-type: none"> • <i>Applying ConVarCal, A High Performance Consensus Variant Calling, For Discovery of Prevalence of Inherited Mutations in Breast Cancer Predisposition Genes among Uganda and Cameroon Women</i>
2:50	Giuseppe Narzisi, New York Genome Center <ul style="list-style-type: none"> • <i>Somatic Variant Analysis of Linked-Reads Sequencing Data with Lancet</i>
3:10	Li Song, Dana-Farber Cancer Institute <ul style="list-style-type: none"> • <i>Bioinformatics Technology to Characterize Tumor Infiltrating Immune Repositories</i>

3:30pm – 5:30pm Free time for relaxing, hiking, socializing

**Lightning Talks 2: 5:30pm – 6:30pm, Evergreen Room (5 min each)
Chair: Mervi Heiskanen**

Simina Boca, Georgetown University Medical Center: <i>CDGnet: Cancer Drug Gene Network</i>
Hayley Dingerdissen, the George Washington University: <i>OncoMX: A Web Resource for Exploring Integrated Cancer Biomarker Data in the Context of Mutation, Differential Expression, Evolutionarily Conserved Expression Patterns, and Automatically Mined Literature Evidence</i>
Ian Holmes, University of California at Berkeley: <i>The JBrowse Cancer Genome Browser</i>
Min Jin Ha, University of Texas MD Anderson Cancer Center: <i>Personalized Integrated Network Modeling of the Cancer Proteome Atlas</i>

Martin Morgan, Roswell Park Comprehensive Cancer Center: <i>Cancer Genomics: Integrative and Scalable Solutions in R / Bioconductor</i>
Kristen Naegle, University of Virginia: <i>Inferring Kinase Activity Profiles from Phosphoproteomic Data</i>
Li-Xuan Qin, Memorial Sloan Kettering Cancer Center: <i>Statistical Evaluation and Selection of Normalization Methods for microRNA Sequencing Data in Cancer Biomarker Studies</i>
Michael Reich, University of California, San Diego: <i>GenePattern Notebooks for Cancer Research</i>
Ei-Wen Yang, University of California, Los Angeles: <i>Allele-Specific Binding of RNA-Binding Proteins Reveals Functional Genetic Variants in the RNA</i>
Tahsin Kurc, Stony Brook University: <i>Actionable Pathomics</i>
Linda Shapiro, University of Washington: <i>A Unified Machine Learning Package for Cancer Diagnosis</i>
Dinler Antunes, Rice University: <i>Conformational Sampling of Large Ligands Made Possible by a Parallelized Incremental Meta-Docking Approach</i>

6:45pm – 8:00pm, Dinner at SnowPark Lodge

8:00pm – 9:30pm, Poster Session I with wine/cocktails/dessert, SnowPark Lodge

Day 3 – Thursday, May 30, Lodges at Deer Valley

7:00am – 8:30am Buffet Breakfast, Brass Tag and Spruce A&B, The Lodges

Session 3: Cancer Genomics 2, 8:30am – 10:10am, Evergreen Room

Session Chair: Jerry Li

8:30	Yi Qiao, University of Utah <ul style="list-style-type: none">• <i>scBayes: A Computational Method to Study Tumor Subclone-Specific Gene Expression and Chromatin Accessibility Using Single Cell RNA Sequencing and Single Cell ATAC Sequencing in Combination of Bulk DNA Sequencing</i>
8:50	Ethan Cerami, Dana Farber Cancer Institute <ul style="list-style-type: none">• <i>The cBioPortal for Cancer Genomics</i>
9:10	Jeremy Goecks, Oregon Health and Science University <ul style="list-style-type: none">• <i>Galaxy Workflows for the Human Tumor Atlas Network</i>
9:30	Rachel Karchin, Johns Hopkins University <ul style="list-style-type: none">• <i>Informatics Tools for High-Throughput Analysis of Cancer Mutations</i>
9:50	Han Liang, The University of Texas MD Anderson Cancer Center <ul style="list-style-type: none">• <i>Systematic Identification of Cancer Therapeutic Liabilities Through Adaptive Functional Proteomics</i>

10:10am – 10:40am Break, Evergreen Foyer, The Lodges

Session 4: Cancer Imaging Informatics, 10:40am – 12:00pm, Evergreen Room

Session Chair: Yantian Zhang

10:40	Corey Arnold, University of California, Los Angeles <ul style="list-style-type: none">• <i>Classifying Prostate Cancer from Multiparametric Magnetic Resonance Imaging and Whole Slide Histology Imaging using Machine Learning</i>
11:00	Hugo Aerts, Harvard-DFCI <ul style="list-style-type: none">• <i>ModelHub.AI: Dissemination Platform for Deep Learning Algorithms</i>
11:20	Despina Kontos and Christos Davatzikos, University of Pennsylvania <ul style="list-style-type: none">• <i>The Cancer Imaging Phenomics Toolkit (CaPTk)</i>
11:40	Ashish Sharma, Emory University <ul style="list-style-type: none">• <i>PRISM – Platforms for Quantitative Imaging Informatics in Precision Medicine</i>

12:00pm – 1:30pm Lunch, Brass Tag and Spruce A&B, The Lodges

Session 5: Resource Management Technologies, 1:30pm – 3:10pm, Evergreen Room

Session Chair: Jacek Capala

1:30	David Gutman, Emory University <ul style="list-style-type: none">• <i>The Digital Slide Archive 2.0: MultiChannel Image Support and Dockerized Algorithm Support</i>
1:50	Dexter Pratt, University of California, San Diego <ul style="list-style-type: none">• <i>NDEx in 2019: Workflows and Application Integration</i>
2:10	Joseph Perl, SLAC National Accelerator Laboratory <ul style="list-style-type: none">• <i>The TOPAS Tool for Particle Simulation, a Monte Carlo Simulation Tool for Physics, Biology and Clinical Research</i>
2:30	Nathalie Conte, EMBL-EBI <ul style="list-style-type: none">• <i>Implementing Novel Functionality for PDX Finder Through Collaborations with ITCR and Other Community Resources</i>
2:50	Lee Cooper, Emory University <ul style="list-style-type: none">• <i>Cell Detection and Classification in Hematopathology</i>

3:10pm – 3:40pm Break, Evergreen Foyer, The Lodges

Session 6: Cancer Genomics 3, 3:40pm – 5:20pm, Evergreen Room

Session Chair: George Redmond

3:40	Obi Griffith, Washington University School of Medicine <ul style="list-style-type: none">• <i>Aggregating Evidence to Determine the Clinical Significance of Cancer Variants in the CIViC</i>
4:00	Shobana Sekar, Mayo Clinic <ul style="list-style-type: none">• <i>Application of CNVnator to Analyze Copy Number Alterations in Cancer</i>
4:20	Vincent Carey, Harvard Medical School <ul style="list-style-type: none">• <i>Opening Apps and Notebooks for Cloud-Scale Cancer Genomics with Bioconductor</i>
4:40	Kai Tan, University of Pennsylvania <ul style="list-style-type: none">• <i>Diverse Noncoding Mutations Contribute to Deregulation of Cis-Regulatory Landscape in Pediatric Cancers</i>
5:00	Anthony Castanza, University of California, San Diego <ul style="list-style-type: none">• <i>MSigDB 7 and Beyond, a Scalable Resource for Transcriptome Interpretation</i>

5:20pm – 6:30pm Break before dinner

6:30pm – 8:00pm Dinner at SnowPark Lodge

8:00pm – 9:30pm Poster Session II wine/cocktails/dessert at SnowPark Lodge

Day 3 – Friday, May 31, Lodges at Deer Valley

**7:30am – 8:30am Buffet Breakfast, Brass Tag and Spruce A&B
Announce poster prizes**

Conference ends, attendants depart

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