NCI Informatics Technology for Cancer Research (ITCR) Annual Meeting 2018

Natcher Conference Center | 9000 Rockville Pike, Building 45 | Bethesda, MD 20894
Wednesday, May 23 – Thursday, May 24, 2018

Agenda

Day 1 – Wednesday, May 23 (Ruth L. Kirschstein Auditorium and Balcony C)

8:30am   **NCI Welcome and Overview -** Tony Kerlavage and Juli Klemm, CBIIT

Imaging Session 1: 8:40 am – 10:10 am

8:40	**Tools to Analyze Morphology and Spatially Mapped Molecular Data** Joel Saltz, *Stony Brook University*
8:55	**Quantitative Image Informatics for Cancer Research** Andrey Fedorov, *Brigham and Women's Hospital and Harvard Medical School*
9:10	**Cancer Imaging Phenomics Software Suite: Application to Brain and Breast Cancer** Christos Davatzikos, *University of Pennsylvania*
9:25	**Quantitative Radiomics System Decoding the Tumor Phenotype** John Quackenbush, *Dana-Farber Cancer Institute*
9:40	**Integrative Imaging Informatics for Cancer Research** Daniel Marcus and Richard Wahl, *Washington University in St. Louis*
9:55	**Pathology Image Informatics for Visualization, Analysis and Management** Metin Gurcan, *Wake Forest School of Medicine*

10:10 am – 10:25 am - Break

10:25	**Lightning Talks:** New ITCR Grantees

Somatic Variant Calling and Phasing using Colored de Bruijn Graphs in Heterogeneous Tumors Giuseppe Narzisi, *New York Genome Center*
Bioinformatics Technology to Characterize Tumor Infiltrating Immune Repertoires Shirley Liu, *Dana Farber Cancer Institute*
Tools for Annotating Mutations in the 3D Cancer Genome Kai Tan, *Children's Hospital of Philadelphia*
Informatics Tools for Quantitative Digital Pathology Profiling and Integrated Prognosis Modeling Lee Cooper, *Emory University*
The TOPAS Tool for Particle Simulation, a Monte Carlo Simulation Tool for Physics, Biology and Clinical Research Bruce Faddegon, *University of California, San Francisco*
Detection of Somatic, Subclonal, and Mosaic CNVs from Sequencing Alexej Abyzov, *Mayo Clinic Rochester*

Day 1 – Wednesday, May 23, Continued

Supporting and Evolving Gene Set Enrichment Analysis and the Molecular Signatures Database for Cancer Research Helga Thorvaldsdottir, *University of California, San Diego*
Database and Tools for Functional Inference and Mechanistic Insight for Cancer Research Jie Liang, *University of Illinois at Chicago*

Omics Session 1: 11:05 am – 12:05 pm

11:05	**Trinity: Transcriptome Assembly for Genetic and Functional Analysis of Cancer** Brian Haas, *Broad Institute*
11:20	**Developing the JBrowse Genome Browser to Visualize Structural Variants and Cancer Genomics Data** Ian Holmes, *University of California, Berkeley*
11:35	**Informatics Tools for Single Nucleotide Analysis of Cancer RNA-Seq** Xinshu Grace Xiao, *University of California, Los Angeles*
11:50	**Building Protected Data Sharing Networks to Advance Cancer Risk Assessment and Treatment** Ian Foster, *University of Chicago*

12:05 pm – 2:00 pm Lunch, Posters and Demonstrations

Tool Demonstrations: 12:30 pm – 1:50 pm

	Demo Session 1: Auditorium Chair: Jerry Li, NCI DCB	Demo Session 2: Balcony C Chair: Yantian Zhang, NCI DCTD
12:30	**Cancer-Related Analysis of Variants (CRAVAT/MuPIT)** Mike Ryan, *In Silico Solutions*	**The Cancer Imaging Archive (TCIA)** Fred Prior, *University of Arkansas*
12:50	**The Network Data Exchange (NDEx)** Trey Ideker and Dexter Pratt, *University of California, San Diego*	**3D Slicer** Andrey Fedorov, *Brigham and Women's Hospital and Harvard Medical School*
1:10	**GenePattern Notebooks** Michael Reich, *University of California, San Diego*	**Lesion Tracker Web Image Viewer** Gordon Harris, *Massachusetts General Hospital*
1:30	**Clinical Interpretation of Variants in Cancer (CIViC)** Malachi Griffith, *Washington University in St. Louis*	**Cancer Imaging Phenomics Toolkit (CaPTk)** Christos Davatzikos, *University of Pennsylvania*

Breakout Sessions 2:00 pm – 3:00 pm

	Breakout Session 1: Auditorium	Breakout Session 2: Balcony C
2:00	**A Network-Based Approach for Personalized Treatment of Multiple Myeloma** Alessandro Lagana, *Icahn School of Medicine at Mount Sinai*	**Developing Enabling PET-CT Image Analysis Tools for Predicting Response in Radiation Cancer Therapy** Xiaodong Wu, *University of Iowa*
2:10	**Integrative Genomic Framework for Dissecting Regulatory Mechanisms Underlying Hepatocellular Carcinoma** Nathalie Pochet, *Brigham and Women's Hospital*	**Structure-Based Selection of Tumor Antigens for T-Cell Based Immunotherapy** Dinler Antunes, *Rice University*

Day 1 – Wednesday, May 23, Continued

2:20	**Algorithms for Literature-Guided Multi-Platform Identification of Cancer Subtypes** Dongjun Chung and Linda Kelemen, *Medical University of South Carolina*	**CGDnet: Cancer Gene Drug Network: Using patient-specific drug-gene networks for recommending targeted cancer therapies** Simina Boca, *Georgetown University*
2:30	**Accelerating Cancer Genomics with Cloud-Scale Bioconductor** Vincent Carey, *Brigham and Women's Hospital*	**An Integrative Analysis Toolkit for Single Cell RNA-Seq in Cancer Research** William Evan Johnson, *Boston University*
2:45	**Integration of Comprehensive Cancer Mutation and Expression-Associated Data for Biomarker Evaluation and Discovery** Daniel Crichton, *Jet Propulsion Laboratory* and Raja Mazumder, *George Washington University*	

3:00 pm – 3:15 pm - Break

Imaging/Clinical Session 2: 3:15 pm – 5:15 pm

3:15	**Advanced Development and Dissemination of EMERSE for Cancer Phenotyping from Medical Records** David Hanauer, *University of Michigan*
3:30	**Cancer Deep Phenotyping Extraction from Electronic Medical Records** Guergana Savova, *Boston Children's Hospital* and *Harvard Medical School*
3:45	**Advancing Cancer Pharmacoepidemiology Research Through EHRs and Informatics** Jeremy Warner, *Vanderbilt University*
4:00	**Scalable Clinical Decision Support for Individualized Cancer Risk Management** Guilherme Del Fiol and Kensaku Kawamoto, *University of Utah*
4:15	**Informatics Tools for Tumor Heterogeneity in Multiplexed Fluorescence Images** S. Chakra Chennubhotla and Brion Sarachan, *University of Pittsburgh* and *GE Global Research*
4:30	**Extensible Open-Source Zero-Footprint Web Viewer for Oncologic Imaging Research** Gordon Harris, *Massachusetts General Hospital*
4:45	**Open Source Diffusion MRI Technology for Brain Cancer Research** Lauren Jean O`Donnell, *Brigham and Women's Hospital and Harvard Medical School*
5:00	**The PDX Integrator – Re-purposing KOMP2 Informatics to Widely Disseminate Data from Patient Derived Xenografts and Electronic Access to Mouse Tumor Data** Terry Meehan, *European Molecular Biology Laboratory*

5:15 pm – 5:20 pm   Day 1 Wrap-Up: Juli Klemm, NCI CBIIT

Day 2 – Thursday, May 24 (Ruth L. Kirschstein Auditorium and Balcony C)

8:25 am   Announcements: Juli Klemm, NCI CBIIT

Omics Session 2: 8:30 am – 10:15 am

8:30	**Computational Framework for Single-Cell Genomics of Tumors** Alexander Krasnitz, *Cold Spring Harbor Laboratory*

Day 2 – Thursday, May 24, Continued

8:45	**NDEx – The Network Data Exchange, A Network Commons for Biologists** Trey Ideker and Dexter Pratt, *University of California, San Diego*
9:00	**Next Generation Clustered Heat Maps for Fluent, Interactive Exploration of Omic Data** John Weinstein and Bradley Broom, *University of Texas - MD Anderson Cancer Center*
9:15	**UCSC Xena – Platform for Functional Genomics Visualization and Analysis** Jing Zhu, *University of California, Santa Cruz*
9:30	**The cBioPortal for Cancer Genomics** Ethan Cerami, *Dana Farber Cancer Institute*
9:45	**Informatics Links between Histological Features and Genetics in Cancer** Kun Huang, *Indiana University*
10:00	**Cancer Genomics: Integrative and Scalable Solutions in R/Bioconductor** Levi Waldron, *City University of New York*

10:15 am – 10:30 am - Break

10:30	**Plenary Talk:** NCI Director, Dr. Norman E. Sharpless
11:00	**Lightning Talks**: Investigators Developing Data Compression Methods Funded by BD2K Targeted Software Development Program

MMTF-Spark: Interactive, Scalable, and Reproducible Datamining of 3D Macromolecular Structures Peter Rose, *University of California, San Diego*
Task-based Compression of Pathology Images Ali Bilgin, *University of Arizona*
Integrated Querying of Biological Network Databases Mehmet Koyuturk, *Case Western Reserve University*
Multiomics Data Compression Mikel Hernaez, *University of Illinois, Urbana-Champaign*

11:30 am – 1:30 pm Lunch, Posters and Demonstrations

Tool Demonstrations: 12:00 pm – 1:20 pm		
	Demo Session 3: Auditorium Chair: Leah Mechanic, NCI DCCPS	Demo Session 4: Balcony C Chair: Natalie Abrams, NCI DCP
12:00	**Integrative Genomics Viewer (IGV)** Jim Robinson and Helga Thorvaldsdottir, *University of California, San Diego*	**The Cancer Proteome Atlas (TCPA)** Han Liang, *University of Texas - MD Anderson Cancer Center*
12:20	**Next Generation Clustered Heat Maps** Bradley Broom, *University of Texas - MD Anderson Cancer Center*	**Text Information Extraction System (TIES/TCRN)** Michael Becich, *University of Pittsburgh*
12:40	**UCSC Xena** Mary Goldman, *University of California, Santa Cruz*	**Pathology Imaging Informatics Platform (PIIP)** Anant Madabhushi, *Case Western Reserve University*
1:00	**cBioPortal for Cancer Genomics** Nikolaus Schultz, *Memorial Sloan Kettering Cancer Center*	**Trinity Cancer Transcriptome Analysis Toolkit (CTAT)** Aviv Regev, *Broad Institute*

Imaging Session 3: 1:30 pm – 2:15 pm

Day 2 – Thursday, May 24, Continued

1:30	**Informatics Tools for Optimized Imaging Biomarkers for Cancer Research and Discovery** Jayashree Kalpathy-Cramer, *Massachusetts General Hospital*
1:45	**Advanced Development of an Open-Source Platform for Web-Based Integrative Digital Image Analysis in Cancer** David Andrew Gutman and Lee Cooper, *Emory University*
2:00	**TCIA Sustainment and Scalability – Platforms for Quantitative Imaging Informatics in Precision Medicine** Ashish Sharma, *Emory University*

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Omics/Clinical Session 3: 2:15 pm – 4:30 pm

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2:15	**Monitoring Tumor Subclonal Heterogeneity Over Time and Space** Gabor Marth, *University of Utah*
2:30	**A Galaxy-Based Multi-Omic Informatics Hub for Cancer Researchers** Timothy Griffin and Pratik Jagtap, *University of Minnesota*

2:45 pm – 3:00 pm - Break

3:00	**Informatics Tools for High-Throughput Analysis of Cancer Mutations** Rachel Karchin, *Johns Hopkins University*
3:15	**The Cancer Proteome Atlas, TCPA: An Integrated Bioinformatics Resource for Functional Cancer Proteomic Data** Han Liang and Gordon Mills, *University of Texas - MD Anderson Cancer Center*
3:30	**The Integrative Genomics Viewer (IGV): Visualization Supporting Cancer Research** Jim Robinson, *University of California, San Diego*
3:45	**GenePattern Notebooks for Cancer Research** Michael Reich, *University of California, San Diego*
4:00	**Advanced Development of TIES Enhancing Access to Tissue for Cancer Research** Michael Becich, *University of Pittsburgh*
4:15	**Development of Informatics Resources for Interpretation of Clinically Actionable Variants in Cancer** Obi Griffith, *Washington University in St. Louis*

4:30 pm – 4:45 pm   Meeting Wrap-Up: Juli Klemm, NCI CBIIT