# 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

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

### 10:10 am – 10:25 am - Break

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

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

# Day 1 – Wednesday, May 23, Continued

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

## Omics Session 1: 11:05 am – 12:05 pm

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| 11:05 | **Trinity: Transcriptome Assembly for Genetic and Functional Analysis of Cancer**<br>Brian Haas, *Broad Institute* |
| 11:20 | **Developing the JBrowse Genome Browser to Visualize Structural Variants and Cancer Genomics Data**<br>Ian Holmes, *University of California, Berkeley* |
| 11:35 | **Informatics Tools for Single Nucleotide Analysis of Cancer RNA-Seq**<br>Xinshu Grace Xiao, *University of California, Los Angeles* |
| 11:50 | **Building Protected Data Sharing Networks to Advance Cancer Risk Assessment and Treatment**<br>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<br>Chair: Jerry Li, NCI DCB | Demo Session 2: Balcony C<br>Chair: Yantian Zhang, NCI DCTD |
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| 12:30 | **Cancer-Related Analysis of Variants (CRAVAT/MuPIT)**<br>Mike Ryan, *In Silico Solutions* | **The Cancer Imaging Archive (TCIA)**<br>Fred Prior, *University of Arkansas* |
| 12:50 | **The Network Data Exchange (NDEx)**<br>Trey Ideker and Dexter Pratt, *University of California, San Diego* | **3D Slicer**<br>Andrey Fedorov, *Brigham and Women's Hospital and Harvard Medical School* |
| 1:10 | **GenePattern Notebooks**<br>Michael Reich, *University of California, San Diego* | **Lesion Tracker Web Image Viewer**<br>Gordon Harris, *Massachusetts General Hospital* |
| 1:30 | **Clinical Interpretation of Variants in Cancer (CIViC)**<br>Malachi Griffith, *Washington University in St. Louis* | **Cancer Imaging Phenomics Toolkit (CaPTk)**<br>Christos Davatzikos, *University of Pennsylvania* |

## Breakout Sessions 2:00 pm – 3:00 pm

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

## Day 1 – Wednesday, May 23, Continued

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| 2:20 | **Algorithms for Literature-Guided Multi-Platform Identification of Cancer Subtypes**<br>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**<br>Simina Boca, *Georgetown University* |
| 2:30 | **Accelerating Cancer Genomics with Cloud-Scale Bioconductor**<br>Vincent Carey, *Brigham and Women's Hospital* | | **An Integrative Analysis Toolkit for Single Cell RNA-Seq in Cancer Research**<br>William Evan Johnson, *Boston University* |
| 2:45 | **Integration of Comprehensive Cancer Mutation and Expression-Associated Data for Biomarker Evaluation and Discovery**<br>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**

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| 3:15 | **Advanced Development and Dissemination of EMERSE for Cancer Phenotyping from Medical Records**<br>David Hanauer, *University of Michigan* |
| 3:30 | **Cancer Deep Phenotyping Extraction from Electronic Medical Records**<br>Guergana Savova, *Boston Children's Hospital* and *Harvard Medical School* |
| 3:45 | **Advancing Cancer Pharmacoepidemiology Research Through EHRs and Informatics**<br>Jeremy Warner, *Vanderbilt University* |
| 4:00 | **Scalable Clinical Decision Support for Individualized Cancer Risk Management**<br>Guilherme Del Fiol and Kensaku Kawamoto, *University of Utah* |
| 4:15 | **Informatics Tools for Tumor Heterogeneity in Multiplexed Fluorescence Images**<br>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**<br>Gordon Harris, *Massachusetts General Hospital* |
| 4:45 | **Open Source Diffusion MRI Technology for Brain Cancer Research**<br>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**<br>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**

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

## Day 2 – Thursday, May 24, Continued

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

### 10:15 am – 10:30 am - Break

| 10:30 | **Plenary Talk:** NCI Director, Dr. Norman E. Sharpless |
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| 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**<br>Peter Rose, *University of California, San Diego* |
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| **Task-based Compression of Pathology Images**<br>Ali Bilgin, *University of Arizona* |
| **Integrated Querying of Biological Network Databases**<br>Mehmet Koyuturk, *Case Western Reserve University* |
| **Multiomics Data Compression**<br>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<br>Chair: Leah Mechanic, NCI DCCPS | Demo Session 4: Balcony C<br>Chair: Natalie Abrams, NCI DCP |
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| 12:00 | **Integrative Genomics Viewer (IGV)**<br>Jim Robinson and Helga Thorvaldsdottir, *University of California, San Diego* | **The Cancer Proteome Atlas (TCPA)**<br>Han Liang, *University of Texas - MD Anderson Cancer Center* |
| 12:20 | **Next Generation Clustered Heat Maps**<br>Bradley Broom, *University of Texas - MD Anderson Cancer Center* | **Text Information Extraction System (TIES/TCRN)**<br>Michael Becich, *University of Pittsburgh* |
| 12:40 | **UCSC Xena**<br>Mary Goldman, *University of California, Santa Cruz* | **Pathology Imaging Informatics Platform (PIIP)**<br>Anant Madabhushi, *Case Western Reserve University* |
| 1:00 | **cBioPortal for Cancer Genomics**<br>Nikolaus Schultz, *Memorial Sloan Kettering Cancer Center* | **Trinity Cancer Transcriptome Analysis Toolkit (CTAT)**<br>Aviv Regev, *Broad Institute* |

### Imaging Session 3: 1:30 pm – 2:15 pm

## Day 2 – Thursday, May 24, Continued

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

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

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

### 2:45 pm – 3:00 pm - Break

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

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