



30th Anniversary AACR Special Conference

Convergence: Artificial Intelligence, Big Data and Prediction in Cancer

October 14-17, 2018 | Newport, RI



Poster Session A

Monday, October 15, 2018

5:30-7:30 p.m.

A01 BRISK: An Artificial Intelligent Decision Support Tool for Precision Risk Assessment of Breast Cancer. Tiancheng He, Informatics Development Department, Houston Methodist Hospital, Houston, Texas, USA

A02 Classification of electronic medical records of breast cancer and melanoma patients into clinical episodes. Chen Lin, Boston Children's Hospital, Boston, MA, USA

A03 Combining natural language processing with machine-learning models for detecting progression of disease in radiology report of cancer patients. Lior Gazit, Memorial Sloan-Kettering Cancer Center, New York City, NY, USA

A04 Deep Learning in Genetic Biomarker Discovery in Glioblastoma. Kelvin Wong, Houston Methodist Cancer Center, Houston, TX, USA

A05 DeepAbstractor: A scalable deep learning framework for automated information extraction from free-text Pathology Reports. Georgia Tourassi, Oak Ridge National Laboratory, Oak Ridge, TN, US

A06 Dimensionality reduction methods applied to DNA sequencing data for enhanced interpretability and cohort selection. Will Manidis, Foundation Medicine, Cambridge, MA, USA

A07 Response Algorithm for Drug positioning and Rescue (RADR): Lantern Pharma's Artificial Intelligence based integrative machine learning approach for drug positioning and rescue. Umesh Kathad, Lantern Pharma Inc, Dallas, Texas, United States

A08 Targeting the disordered p27Kip1 protein with small molecules using artificial intelligence enabled multi-scale simulations. Arvind Ramanathan, Oak Ridge National Laboratory, Oak Ridge, TN, USA

A09 Towards A Thinking Microscope for Cancer Research and Diagnosis: Deep Learning for Automated Analysis of Cellular and Tissue Images. Lei Huang, Houston Methodist Cancer Center and Research Institute, Houston, Texas, USA

A10 Bioconductor:Cancer -- Genome-scale data science for precision oncology. Vincent Carey, Channing Division of Network Medicine, Brigham and Women's Hospital, Boston, MA, USA

A11 DeepMT: Predict original primary tumor types for metastasis cancer samples from integrated multi-omics integration data using deep learning methods and its application on metastatic breast cancer. Enze Liu, Indiana University school of informatics and computing, Indianapolis, IN, USA

A12 Degrees of diabetes and risk of pancreatic cancer. Christie Jeon, Cedars-Sinai Medical Center, Los Angeles, CA, U.S.A.



30th Anniversary AACR Special Conference

Convergence: Artificial Intelligence, Big Data and Prediction in Cancer

October 14-17, 2018 | Newport, RI



Poster Session A

Monday, October 15, 2018

5:30-7:30 p.m.

- A13 De-identified Aggregate Electronic Health Record Data as Resource for Understanding Pediatric Leukemia Patient Trajectories.** Mark Hoffman, Children's Mercy Hospital, Kansas City, MO, USA
- A14 Genetic differences between primary and metastatic tumors from cross-institutional data.** Julie Wu, Vanderbilt University Medical Center, Nashville, TN, USA
- A15 Incidence and mortality rates of suicide in cancer related patients: A population-based analysis.** Muhammed Elfaituri, University of Tripoli, Tripoli, Libya
- A16 Leveraging heterogeneous clinical data to construct patient and population level trajectories and visualizations for precision cancer surveillance.** Donna Rivera, National Cancer Institute, Rockville, MD, USA
- A17 Life without KRAS: profiling the KRAS-dependent kinome to identify novel therapeutic vulnerabilities in pancreatic cancer.** J. Nathaniel Diehl, University of North Carolina, Chapel Hill, NC, United States
- A18 Multi-omics analysis reveals hallmarks of Immune-tolerance in breast cancer.** Meenakshi Anurag, Baylor College of Medicine, Houston, Texas, US
- A19 Optimal extent of resection for glioblastoma according to site, extension, and size: a population-based study in the temozolomide era.** Yi-Jun Kim, Seoul National University Hospital, Seoul, Korea, republic of
- A21 Re-runnable, open-source software pipeline for reproducible radiomics and deep learning.** Aditya Apte, Memorial Sloan Kettering Cancer Center, New York, NY, USA
- A22 Signatures of T-cell dysfunction and exclusion predict cancer immunotherapy response.** Peng Jiang, Dana Farber Cancer Institute, Boston, MA, USA
- A23 Linking clinical molecular profiles of tumors to the electronic medical record.** Debajyoti Datta, University of California San Francisco, San Francisco, CA, USA
- A24 Oncology model fidelity score differentiates human from mouse.** Debajyoti Datta, University of California San Francisco, San Francisco, CA, USA
- A25 A Novel *In Silico* Approach to Identify Gene Signatures Associated with Recurrent Cancer.** Kirsten Wohlers, Cornell University, Ithaca, New York, USA
- A26 Cancer drug response and drug synergy in public-domain high-throughput cell-line studies.** Michael Fonstein, Argonne National Laboratory, Argonne, IL, USA



30th Anniversary AACR Special Conference

Convergence: Artificial Intelligence, Big Data and Prediction in Cancer

October 14-17, 2018 | Newport, RI



Poster Session A

Monday, October 15, 2018

5:30-7:30 p.m.

A27 Correcting image segmentation via a spatially-aware clustering algorithm. Sandhya Prabhakaran, Memorial Sloan Kettering Cancer Centre, New York City, NY, US

A28 Crowd-sourced advancement of computational drug synergy predictions for Oncology. Jonathan Dry, AstraZeneca, Waltham, MA, USA

A29 Deep learning to predict of the impact of variants on 3D genome organization. Tuan Trieu, Weill Cornell Medicine, New York, USA

A30 Development and calibration of patient-specific tumor growth model for predicting the response of hepatocellular carcinoma. Ernesto A B F Lima, Institute for Computational Engineering and Sciences, The University of Texas at Austin, Austin, TX, USA

A31 Distribution-based measures of tumor heterogeneity are sensitive to mutation calling and lack strong clinical predictive power. Javad Noorbakhsh, The Jackson Laboratory for Genomic Medicine, Farmington, CT, USA

A33 Expression variation analysis for tumor heterogeneity in single-cell RNA-sequencing data. Emily Davis, Johns Hopkins University School of Medicine, Baltimore, MD, USA

A34 Fuzzy C-Means clustering to dissect proteogenomics-based lung squamous cancer subtypes. Steven Eschrich, Moffitt Cancer Center, Tampa, FL, US

A35 Genome-wide identification of genetic interactions in human cells using CRISPR/Cas9. Maximilian Billmann, Department of Computer Science and Engineering, University of Minnesota-Twin Cities, Minneapolis, MN, USA

A36 Heterogeneous network-based analysis for characterizing drug response and biological targets. Maryam Pouryahya, Memorial Sloan Kettering Cancer Center, New York, NY, US

A37 Hidden Markov models lead to higher resolution maps of mutation signature activity in cancer. Mark Leiserson, University of Maryland, College Park, MD, USA

A38 Identification of relevant alterations in cancer using topological data analysis. Pablo Camara, Perelman School of Medicine, University of Pennsylvania, Philadelphia, PA, USA

A39 Identifying genetic interactions that drive aggressive prostate cancer using an ensemble of penalized cox regression models. Teemu Laajala, University of Turku, Turku, Finland

A40 Improving the assessment of immunogenic mutational burden as a predictor of checkpoint blockade treatment efficacy. Zeynep Kosaloglu-Yalcin, La Jolla Institute for Allergy and Immunology, La Jolla, CA, USA



30th Anniversary AACR Special Conference

Convergence: Artificial Intelligence, Big Data and Prediction in Cancer

October 14-17, 2018 | Newport, RI



Poster Session A

Monday, October 15, 2018

5:30-7:30 p.m.

A41 Integrating proteome-scale interaction modeling, phenotypic experiments, and machine learning to discover cell-specific networks and synthesize network targeting molecules for cancer cell specific lethality and immunotherapy. Gaurav Chopra, Purdue University, West Lafayette, IN, USA

A42 Metabolic deregulation in prostate cancer. Sriganesh Srihari, MaxwellPlus+, The University of Queensland, Brisbane, Queensland, Australia

A43 Model-based analysis of positive selection using cancer somatic mutations. Siming Zhao, Univ. of Chicago, Chicago, IL, USA

A44 Modeling cell line-specific recruitment of signaling proteins to the insulin-like growth factor 1 receptor. Keesha Erickson, Los Alamos National Lab, Los Alamos, New Mexico, USA

A46 Prediction of selective genetic vulnerabilities from large-scale functional screens in cancer cells. Benedikt Rauscher, German Cancer Research Center (DKFZ), Heidelberg, Germany

A47 Systematic network-based analysis reveals novel molecular subtypes conserved in multiple pancreatic cancer cohorts and at the single cell level. Pasquale Laise, Columbia University, New York, New York, United States

A48 The modular tumor checkpoint landscape of human cancer. Evan Paull, Columbia University, New York, NY, USA

A49 Topological Data Analysis for breast tumor molecular classification and prognosis. James Mathews, Department of Medical Physics, Memorial Sloan-Kettering Cancer Center, New York, NY, USA

A50 Uncovering hidden effects in single cell RNA-sequencing data using Manifold Enhancement of Latent Dimensions (MELD). Daniel Burkhardt, Yale University, New Haven, CT, USA

A51 Early onset Colorectal Cancer shows higher susceptibility to common genetic risk factors. Alexi Archambault, New York University, New York, NY, United States

A52 Precision medicine in lung cancer: towards predicting recurrence for early stage disease. Donald Johann, UAMS, Little Rock, Arkansas, USA

A53 Predictive modeling of cancer-type in Li-Fraumeni syndrome. Valli Subasri, Peter Gilgan Centre for Research and Learning, Toronto, ON, Canada

A55 A Statistical Approach to Identify Environmental and Demographic Causes of Cancer Incidences Across US Counties. Kaushik Shivakumar, The Harker School, San Jose, CA, USA



30th Anniversary AACR Special Conference

Convergence: Artificial Intelligence, Big Data and Prediction in Cancer

October 14-17, 2018 | Newport, RI



Poster Session A

Monday, October 15, 2018

5:30-7:30 p.m.

A56 Hyperspectral Cell Sociology Analysis of Histological Specimens. Calum MacAulay, British Columbia Cancer Agency, Vancouver, BC, Canada

A57 Assessing Tumor Pseudo Progression for Translation Research in Immuno Cancer Therapy using AI enabled Informatics Platform. Madhuri Gadekar, Indx Technology, Inc, Cupertino, CA, USA

A58 iCore as an AI Platform to determine tumor pseudo progression in immunotherapy translational research. Madhuri Gadekar, Indx Technology, Inc, Cupertino, CA, USA

A59 Defining transcriptional programs and cellular states. Kwat Huwate Yeema, Moores Cancer Center, University of California, San Diego, La Jolla, CA, United States