30th Anniversary AACR Special Conference

Convergence: Artificial Intelligence, Big Data and Prediction in Cancer

October 14-17, 2018 | Newport, RI

AACR American Association for Cancer Research

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.

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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 Wohlars, 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

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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

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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

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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

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Poster Session B

Tuesday, October 16, 2018
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B01 Discovery of cancer immune molecular subtypes by multi 'omics tensor matrix factorization. Aedin Culhane, Dana-Farber Cancer Institute, Boston, MA, USA

B02 An integrative genetic epidemiologic approach to analysis of multiomics data identifies low and medium risk susceptibility genes for breast cancer. Roxana Moslehi, University at Albany, SUNY, Albany, NY, USA

B03 Analysis of the genomic landscape of appendiceal neoplasms identifies GNAS and TP53 mutation as prognostic biomarkers. John Paul Shen, University of Texas MD Anderson Cancer Center, Houston, TX, USA

B04 Focal DNA copy number variation-driven gene expression prognostic signatures reveal distinct risk sub-types and pathways within low- and high- genetic grade breast carcinoma forms. Vladimir Kuznetsov, SUNY Upstate Medical University, Syracuse, NY, US

B05 Peripheral blood lymphocyte markers of DNA damage correlate with chemoradiation response in patients with locally advanced rectal cancer. Sanjeevani Arora, Fox Chase Cancer Center, Philadelphia, PA, USA

B06 Understanding inherited cancer risk alleles through omics-informed genetic analyses. Oana A Zeleznik, Channing Division of Network Medicine, Brigham and Women's Hospital and Harvard Medical School, Boston, MA, USA

B07 Mammogram-derived texture features and risk of breast cancer. Oana A Zeleznik, Channing Division of Network Medicine, Brigham and Women's Hospital and Harvard Medical School, Boston, MA, USA

B08 Applying Machine Learning Techniques to Drug Response in Colorectal Patient Derived Organoids.. Erin Spiller, Lawrence J. Ellison Institute for Transformative Medicine of USC, Los Angeles, CA, US

B09 Capturing individual differences in tumor growth and response through image-based, predictive mechanistic models in the pre-clinical and clinical settings. David Hormuth, The University of Texas at Austin, Austin, TX, USA

B10 Incorporating breast anatomy in radiomic machine learning for breast cancer risk estimation with digital mammograms. Aimilia Gastounioti, University of Pennsylvania, Philadelphia, PA, United States

B11 Objective risk stratification of prostate cancer using machine learning and radiomics applied to mpMRI images. Bino Varghese, University of Southern California, Los Angeles, CA, USA

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B12 ROLE OF FDG-PET/CT IN THE MANAGEMENT OF PEDIATRIC BURKITT LYMPHOMA. Ahmed Abdelsalam, Children Cancer Hospital Egypt, Cairo, Egypt

B13 An Unsupervised Learning Approach to Identifying Cancer Recurrence Using Longitudinal Radiology Reports. James Christian, Oak Ridge National Laboratory, Oak Ridge, TN, USA

B14 Applying Machine Learning Approaches to "BIG" Social Environmental Data in Cancer Studies: Comparisons, Challenges, and Considerations. Shannon Lynch, Fox Chase Cancer Center, Philadelphia, PA, USA

B15 Applying machine learning models of drug activity across studies to identify predictive and predictable cell line datasets. Fangfang Xia, Argonne National Laboratory, Argonne, IL, USA

**B16 Bayesian network model of multiple myeloma patients
based on pharmaceutical records.** Jaroslaw Zola, University of Buffalo, Buffalo, NY, USA

B17 Breast Cancer Risk Prediction Using Neural Networks. Zoe Guan, Harvard T.H. Chan School of Public Health, Boston, MA, US

B18 Combining machine learning with flow cytometry immunophenotyping of myeloid and lymphoid cell populations to identify subjects with prostate cancer (PCa) from benign prostate hyperplasia (BPH). George Dominguez, Anixa Biosciences, San Jose, CA, USA

B19 Computed tomography textures machine learning classifiers predict response to immunotherapy in patients with lung cancer. Harini Veeraraghavan, Memorial Sloan Kettering Cancer Center, New York, NY, USA

B20 Deep machine learning is feasible for volumetric quantification and longitudinal assessment of lung tumor volume changes on CT and MR images from radiotherapy and immunotherapy. Harini Veeraraghavan, Memorial Sloan Kettering Cancer Center, New York, NY, USA

B21 Comparison of Classical Machine Learning and Convolution Neural Nets for the Differentiation of Malignant from Benign Sub 1.1 cm Lung Nodules in CT Scans. Calum MacAulay, British Columbia Cancer Agency, Vancouver, BC, Canada

B22 Coupling Machine Learning with Empirical Bayes Estimates from Mixed-Effects Modeling for High-throughput and Efficient Feature Selection for Longitudinal Disease Dynamic data with High-dimensional Prognostic Biomarkers. Xiang Li, Janssen R&D, Raritan, NJ, USA

B23 Deep neural networks to predict drug response using integrated genome-wide molecular profiles of pediatric tumors. Aparna Gorthi, University of Texas Health at San Antonio, San Antonio, Texas, USA

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B25 Discovering single-cell tumor sub-populations via Random Matrix Theory and Unsupervised Machine Learning Algorithms. Mykola Bordyuh, Columbia University, New York, NY, USA

B26 Identification of the involvement of adipocytes in nivolumab (anti-PD1) response in ipilimumab (anti-CTLA4) resistant melanoma patients using a machine learning model of the immune system. Yair Benita, CytoReason, Tel Aviv, Israel

B27 Improved Microsatellite Instability Detection on Next-Generation Sequencing Data Utilizing Deep Multiple Instance Learning. John Ziegler, Memorial Sloan Kettering Cancer Center, New York, New York, United States of America

B28 Leveraging machine learning to predict prostate cancer diagnosis and diagnosis date using International Classification of Diseases (ICD) codes with gradient boosted decision trees. Ahmad Halwani, Huntsman Cancer Institute, University of Utah, Salt Lake City, UT, USA

B29 Machine learning approach for detection of osteosarcoma exosome-associated biomarkers. Ali Khammanivong, University of Minnesota, Minneapolis, MN, US

B31 Machine learning to design genetic models of radiation-induced complications in prostate cancer patients following radiotherapy. Jung Hun Oh, Memorial Sloan Kettering Cancer Center, New York, NY, USA

B32 Malignant and benign classification in power Doppler breast ultrasound imaging. Wei-Chung Shia, Cancer Research Center, Department of Research, Changhua Christian Hospital, Changhua, Taiwan

B33 More accurate prediction of epitope presentation in tumors for cancer vaccines based on large datasets of HLA-associated epitopes. Siranush Sarkizova, Harvard University, Cambridge, MA, USA

B34 Moving Toward Real-Time Diagnostics using Brain-Inspired Hyperdimensional Computing. Mohsen Imani, UC San Diego, La Jolla, California, San Diego

B35 National Cancer Institute-Department of Energy Collaborations: Extending Frontiers of Predictive Oncology and Computing. Emily Greenspan, National Cancer Institute, Bethesda, MD, USA

B36 PhosphoGAN: Enhancing the prediction process of general and kinase-specific phosphorylation sites. Mark Lennox, Queen's University Belfast, Belfast, Antrim, United Kingdom

B37 Predictive indicators in blood cell dynamics after therapy for AML identified using machine-learning optimized Voronoi compartmentalization. Christopher Benton, The University of Texas, MD Anderson Cancer Center, Houston, TX, USA

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B38 Semi-supervised feature learning for tumor growth prediction. Stewart He, Lawrence Livermore National Laboratory, Livermore, CA, USA

B39 The predictive power of drug pair synergy machine learning models is largely driven by the propensities of individual drugs to enhance or suppress synergy. Jason Gans, Bioscience Division, Los Alamos National Laboratory, Los Alamos, NM, US

B40 Uncertainty Quantification Analysis for Data-Driven Models of Cancer Cell Line Response. Cristina Garcia-Cardona, Los Alamos National Laboratory, Los Alamos, NM, US

B41 Using machine learning and natural language processing of the medical literature to simplify the meta-analyses of cancer susceptibility genes. Danielle Braun, Dana-Farber Cancer Institute/Harvard T.H. Chan School of Public Health, Boston, MA, USA

B42 Global analysis of gene expression changes associated with hypermutated cancer. Raphael Ferreira, Chalmers University of Technology, Goteborg, Sweden

B43 A high-throughput simulation-based-study shows a connection between Tumor Treating Fields dose at the tumor and patient outcome. Ze'ev Bomzon, Novocure ltd., Haifa, Israel

B44 Analysis of lung adenocarcinoma based on nuclear features and WHO subtype classification using deep convolutional neural networks on histopathology images. Francisco Zaldana, Department of Pathology and Laboratory Medicine, Rutgers Robert Wood Johnson Medical School, New Brunswick, New Jersey, USA

B45 ATHEERA: An Artificial Intelligence Powered Toolkit for Healthcare Data Extraction, ApprEhension and Reuse Applications. Tiancheng He, Informatics Development Department, Houston Methodist Hospital, Houston, Texas, USA

B46 The development of a software tool to manage research variables at Institutional scale.. Francisco Alves, A. C. Camargo Cancer Center, São Paulo, São Paulo, Brazil

B47 Artificial intelligence driven discovery of biomarkers in the immunotherapy of cancer.. Carsten Krieg, Medical University of South Carolina (MUSC), Charleston, SC, USA

B48 Development of a molecular classifier for the prediction of clinically significant cervical lymph node metastases in papillary microcarcinoma. Dilmi Perera, Memorial Sloan Kettering Cancer Center, New York, NY, USA

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B49 External validation of Lantern Pharma's Response Algorithm for Drug positioning and Rescue (RADR) using Paclitaxel clinical data. Yuvanesh Vedaraju, Lantern Pharma Inc, Dallas, Texas, United States

B50 Moving beyond genetic mutations to predict response to targeted therapies. Molly Carroll, University of Wisconsin-Madison, Madison, WI, USA

B51 Novel method for predicting patient responses to drug therapies using Lantern Pharma's Response Algorithm for Drug positioning and Rescue (RADR). Aditya Kulkarni, Lantern Pharma Inc, Dallas, Texas, United States

B52 Pan-cancer predictions of drug sensitivity based on protein-coding and non-coding RNA biomarkers. John Lloyd, University of Michigan, Ann Arbor, MI, US

B53 Personalization of cancer treatments with a CLIA-certified high-complexity and high-throughput drug sensitivity test. Carla Grandori, SEngine Precision Medicine, Seattle, WA, USA

B55 Understanding the patient side: Leveraging Big Data to understand and treat older cancer patients with comorbidities and geriatric problems. Martine Extermann, Moffitt Cancer Center, Tampa, FL, USA

B56 A rare case of a myeloid mutation expressed in T-cell acute lymphoblastic leukemia. Lisa Giscombe, Roger Williams Medical Center, Cranston, RI, US

B57 Integrating proteomic networks with genetic coessentiality to analyze mammalian protein complexes. Josh Pan, Harvard Medical School, Boston, MA, USA

B58 Model-agnostic feature importance using genomics data. Alexander Partin, Argonne National Laboratory, Argonne, Illinois, USA

B59 Bio-informative analysis for predicting the responsible patient of CSF-1R inhibitor treatment. Yi-Ru Lee, Development Center for Biotechnology, Taipei, Taiwan

B60 Automated image-based profiling identifies compound induced phenotypes in patient-derived organoids. Niklas Rindtorff, German Cancer Research Center (DKFZ), Heidelberg, Germany