



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 B

Tuesday, October 16, 2018

5:15-7:15 p.m.

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



30th Anniversary AACR Special Conference

Convergence: Artificial Intelligence, Big Data and Prediction in Cancer

October 14-17, 2018 | Newport, RI



Poster Session B

Tuesday, October 16, 2018

5:15-7:15 p.m.

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



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 B

Tuesday, October 16, 2018

5:15-7:15 p.m.

- 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



30th Anniversary AACR Special Conference

Convergence: Artificial Intelligence, Big Data and Prediction in Cancer

October 14-17, 2018 | Newport, RI



Poster Session B

Tuesday, October 16, 2018

5:15-7:15 p.m.

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



30th Anniversary AACR Special Conference

Convergence: Artificial Intelligence, Big Data and Prediction in Cancer

October 14-17, 2018 | Newport, RI



Poster Session B

Tuesday, October 16, 2018

5:15-7:15 p.m.

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