

**CSH-ASIA / AACR JOINT MEETING:
BIG DATA, COMPUTATION AND SYSTEMS BIOLOGY IN CANCER**

Wednesday, December 2 – Saturday, December 5, 2015

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| Wednesday | 7:00 pm | 1 Keynote Session |
| Thursday | 9:00 am | 2 Systems Biology and Computational Biology |
| Thursday | 2:00 pm | 3 Poster Session |
| Thursday | 7:00 pm | 4 Cancer Genomics and Bioinformatics |
| Friday | 9:00 am | 5 Functional Screening and Drug Discovery |
| Friday | 2:00 pm | 6 Regulation and Signaling |
| Friday | 6:00 pm | <i>Cocktails and Banquet</i> |
| Saturday | 9:00 am | 7 Models and Networks |
| Saturday | 12:30 pm | <i>Departure / Optional Old Suzhou Tour</i> |

Oral presentation sessions are located in the Watson Auditorium
Poster session and Chinese Tea & Beer Tasting are in the Poster Hall.
Cocktail social hour is held in the Poster Hall.

Optional Old Suzhou visits depart from the hotel lobby
**optional tour requires additional fee.*

Meal locations and times are as follows:
Breakfast Octagon 7:00am - 9:00am
Lunch Octagon 12:00am - 1:30pm
Dinner Octagon 6:00pm - 7:30pm
Banquet Suz Garden 7:00pm

More information will be available at CSHA office.
(Map at the end of this abstract book)

PROGRAM

WEDNESDAY, December 2—7:00 PM

SESSION 1 KEYNOTE SESSION

Chairpersons: **Xuegong Zhang**, Tsinghua University, Beijing, China
William Hahn, Dana-Farber Cancer Institute,
Harvard Medical School, Boston, Massachusetts, USA

Andrew Futreal

University of Texas M.D. Anderson Cancer Center

THURSDAY, December 3—9:00 AM

SESSION 2 SYSTEMS BIOLOGY AND COMPUTATIONAL BIOLOGY

Chairperson: **Satoru Miyano**, University of Tokyo, Tokyo, Japan

Genomic and epigenomic studies provide insights into the pathogenesis of liver cancer

Ze-Guang Han [20'+10']

Presenter affiliation: Shanghai Jiao Tong University, Shanghai, China;
Chinese National Human Genome Center at Shanghai, Shanghai, China.

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Co-expression and network motif models of cancer expression profiles

Cheng Li [20'+10']

Presenter affiliation: Peking University, Beijing, China.

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| Boosting systems understanding of cancer in new dimension by supercomputers <u>Satoru Miyano</u> [20'+10'] Presenter affiliation: The University of Tokyo, Tokyo, Japan. | 3 |
| Patterns of somatic aberrations in cancer genomes <u>Benjamin Raphael</u> [20'+10'] Presenter affiliation: Brown University, Providence, Rhode Island. | 4 |
| Fast dimension reduction and integrative clustering of multi-omics data using low-rank approximation—Application to cancer molecular classification Dingming Wu, Dongfang Wang, Michael Q. Zhang, <u>Jin Gu</u> [10'+5'] Presenter affiliation: Tsinghua University, Beijing, China. | 5 |
| Computational modeling of high-grade serous ovarian carcinoma dynamics—Implications for therapy and screening <u>Shengqing Gu</u> , Stephanie Lheureux, Azin Sayad, Liat Hogen Ben-David, Iryna Vyarvelska, Dongsheng Tu, Wendy Parulekar, Paulina Cybulska, Marcus Bernardini, Barry Rosen, Amit Oza, Benjamin G. Neel [10'+5'] Presenter affiliation: University of Toronto, Toronto, Canada. | 6 |
| A big-data computational approach to integrate TCGA data for genetic interactions in cancer <u>Yuan Ji</u> [10'+5'] Presenter affiliation: NorthShore University HealthSystem, Evanston, Illinois; The University of Chicago, Chicago, Illinois. | 7 |
| Improved prediction of RNA secondary structure by integrating the free energy model with restraints derived from experimental probing data <u>Zhi J. Lu</u> [10'+5'] Presenter affiliation: Tsinghua University, Beijing, China. | 8 |

SESSION 3 POSTER SESSION

- An individualized prognostic signature to predict disease-free survival of early stage hepatocellular carcinoma patients with distinct multi-omics prognostic characteristics**
Lu Ao, Xuekun Song, Xiangyu Li, Mengsha Tong, Jing Li, Mengyao Li, Hao Cai, Qingzhou Guan, You Guo, Zheng Guo
Presenter affiliation: Fujian Medical University, Fuzhou, China; Harbin Medical University, Harbin, China. 9
- An isoform-level gene expression QTL (isoQTL) analysis of the human glioblastoma multiforme genome**
Yingtao Bi, Ramana V. Davuluri
Presenter affiliation: Northwestern University Feinberg School of Medicine, Chicago, Illinois. 10
- Epigenetic regulation of STK11 mutation in lung adenocarcinoma**
Shengzhi Chang, Sukjoon Yoon
Presenter affiliation: Sookmyung Women's University, Seoul, South Korea. 11
- Identification of active transcriptional regulatory elements at an unprecedented resolution using support vector regression sheds light on the mechanism for tamoxifen resistance in breast cancer**
Tinyi Chu, Ed Rice, Sachi Horibata, Scott Coonrod, Charles Danko
Presenter affiliation: Cornell University, Ithaca, New York. 12
- Microarray-based cancer prediction model via one-gene**
Rui Dong, Daoqing Dai
Presenter affiliation: Tsinghua University, Beijing, China. 13
- Screening and characterization of small molecule compounds targeting lung cancer stem cells**
Hongying Gao, Xinglin Yang, Yun Zhang, Yu Rao, Wei Guo
Presenter affiliation: Tsinghua University, Beijing, China. 14
- Systematic characterization of cis-regulation on RNA stability**
Qingsong Gao, Wei Sun, Wei Chen
Presenter affiliation: Berlin Institute for Medical Systems Biology, Berlin, Germany. 15

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| Individualized differential expression analysis based on widely stable within-sample relative expression orderings across different gene expression profiling platforms <u>Qingzhou Guan</u> , Rou Chen, Hao Cai, Mengyao Li, Xiangyu Li, Mengsha Tong, Hongdong Li, Guini Hong, Zheng Guo Presenter affiliation: Fujian Medical University, Fuzhou, China. | 16 |
| Advanced high-throughput siRNA screening for cancer target discovery <u>Euna Jeong</u> , Sukjoon Yoon Presenter affiliation: Center for Advanced Bioinformatics and Systems Medicine, Seoul, South Korea. | 17 |
| Building a better mouse trap—Iterative design of mouse cancer models in a cancer genomics world <u>Eugene Ke</u> , Quan Zhu, Yifeng Xia, Junko Ogawa, Chad Myskiw, Inder Verma Presenter affiliation: Salk Institute for Biological Studies, La Jolla, California. | 18 |
| dbSUPER—An extensive and interactive database of super-enhancers <u>Aziz Khan</u> , Xuegong Zhang Presenter affiliation: Tsinghua University, Beijing, China. | 19 |
| Genomics of male breast cancer <u>Yongsoo Kim</u> , Karianne Schuurmann, Tesa Severson, Lodewyk Wessels, Wilbert Zwart Presenter affiliation: Netherlands Cancer Institute, Amsterdam, the Netherlands. | 20 |
| Comprehensive analysis of tumor - stroma interactome <u>Daisuke Komura</u> , Takayuki Isagawa, Reiko Sato, Kazuki Kishi, Ryohei Suzuki, Shumpei Ishikawa Presenter affiliation: Medical Research Institute, Tokyo Medical and Dental University, Tokyo, Japan. | 21 |
| Tackle the irreproducibility problem of transcriptional biomarkers for tumor metastasis with recurrence information <u>Mengyao Li</u> , Xiaofang Lin, Zhongjie Tang, Jun Cheng, Hao Cai, Xiangyu Li, Qingzhou Guan, Mengsha Tong, Zheng Guo, Hongdong Li Presenter affiliation: Fujian Medical University, Fuzhou, China. | 22 |

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| Protein-protein interactions on cell membrane modulate KRAS function <u>Yao-Cheng Li</u> , Geoffrey M. Wahl Presenter affiliation: The Salk Institute, La Jolla, California. | 23 |
| Different classes of human genes have different relative evolutionary novelty <u>Andrei A. Makashov</u> , Andrei P. Kozlov Presenter affiliation: The Biomedical Center, Saint-Petersburg, Russia; Peter the Great St.Petersburg Polytechnic University, Saint-Petersburg, Russia. | 24 |
| traseR—Trait-associated SNP enrichment analysis in genomic intervals Chen Li, <u>Zhaohui S. Qin</u> Presenter affiliation: Emory University, Atlanta, Georgia. | 25 |
| Multi-omics characteristics of stage II-III colorectal cancer subtypes discriminated by a robust prognostic signature for 5-fluorouracil-based chemotherapy <u>Mengsha Tong</u> , Weicheng Zheng, Hongdong Li, Xiangyu Li, Lu Ao, Jing Li, Guini Hong, Hao Cai, Mengyao Li, Qingzhou Guan, Zheng Guo Presenter affiliation: Fujian Medical University, Fuzhou, China. | 26 |
| Protein secondary structure prediction—Statistical analysis of torsion angles for K-mer amino acid sequences <u>Xiaogeng Wan</u> , Xinqi Gong, Stephen Yau Presenter affiliation: Tsinghua University, Beijing, China. | 27 |
| Topic model based purification of LC/GC-MS data acquired from heterogeneous samples in proteomic and metabolomic studies <u>Minkun Wang</u> , Tsung-Heng Tsai, Cristina Di Poto, Alessia Ferrarini, Guoqiang Yu, Habtom W. Resson Presenter affiliation: Georgetown University, Washington DC; Virginia Tech, Arlington, Virginia. | 28 |
| miR-650: a potential prognostic biomarker and therapeutic target in non-metastasis colorectal carcinoma Chunxian Zhou, Fengyun Cui, Jiali Li, Hongguang Zhu, Jiping Wang, <u>Shuyang Wang</u> Presenter affiliation: Fudan University Shanghai Medical College, Shanghai, China. | 29 |

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| Identifying alterations of DNA methylation in individual cancer patients with application to mutually exclusive analysis of genomic and epigenomic alterations <u>Haidan Yan</u> , Jun He, Yunqing Lin, Hongdong Li, Huaping Liu, Xuekun Song, Yunyan Gu, Zheng Guo Presenter affiliation: Fujian Medical University, Fuzhou, China; Harbin Medical University, Harbin, China. | 30 |
| An integrative pan-cancer-wide analysis of epigenetic enzymes reveals universal patterns of epigenomic deregulation in cancer <u>Zhen Yang</u> , Allison Jones, Martin Widschwendter, Andrew Teschendorff Presenter affiliation: Key Laboratory of Computational Biology, Shanghai, China. | 31 |
| Gene co-expression network guided functional CNV discovery <u>Jie Zhang</u> , Zhi Han, Kun Huang Presenter affiliation: The Ohio State University, Columbus, Ohio. | 32 |
| Targeted ctDNA sequencing in resectable pancreatic cancer patients <u>Yiqian Zhang</u> , Bo Song, Yi Huang, Paul Tang, Xinming Zhang, Lingchen Guo, Hongyan Wang, Grace Zhao, Johnny Sun, Shengrong Lin, Gang Jin, Kang Ying Presenter affiliation: AccruaGen, Inc., Shanghai, China. | 33 |
| Exploring scientific data reuse of the Cancer Genome Atlas (TCGA)—A view from full-text biomedical literature <u>Si Zheng</u> , Hong Y. Kang, Yang Pan, Jiao Li Presenter affiliation: Institute of Medical Information, Chinese Academy of Medical Sciences & Peking Union Medical College, Beijing, China. | 34 |

THURSDAY, December 3—4:30 PM

Chinese Tea and Beer Tasting

SESSION 4 **CANCER GENOMICS AND BIOINFORMATICS**

Chairperson: **Michael Shen**, Columbia University Medical Center,
New York, New York, USA

**Computational models to detect DNA modification and its
heterogeneity from third-generation sequencing data**

Zhixing Feng, Xuegong Zhang [20'+10']

Presenter affiliation: Tsinghua University, Beijing, China.

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**Elucidating gene-gene and gene-drug interactions in cancer with
next-generation functional genomics**

Martin Kampmann [20'+10']

Presenter affiliation: University of California, San Francisco, San
Francisco, California.

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Michael Shen [20'+10']

Presenter affiliation: Columbia University Medical Center, New York,
New York.

**Unearthing new genomic markers of drug response by improved
measurement of discriminative power**

Cuong C. Dang, Antonio Peon, Pedro J. Ballester [10'+5']

Presenter affiliation: Cancer Research Centre of Marseille, Marseille,
France.

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**Manifold-based integrative genomics approach for cancer patient
stratification**

Hao Ding, Chao Wang, Raghu Machiraju, Kun Huang [10'+5']

Presenter affiliation: The Ohio State University, Columbus, Ohio.

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**Two-step linear mixed model approach to differential alternative
splicing analysis**

Huining Kang, Li Luo, Scott A. Ness, Christine A. Stidley [10'+5']

Presenter affiliation: University of New Mexico, Albuquerque, New
Mexico.

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A hybrid computational strategy to address large scale genomic analysis

Navin Rustagi, Zhuoyi Huang, Narayanan Veeraghavan, Andrew Caroll, Eric Boerwinkle, Richard A. Gibbs, Manjunath G. Venkata, Fuli Yu [10'+5']

Presenter affiliation: Baylor College of Medicine, Houston , Texas. 40

A deep learning framework for modeling structural features of RNA-binding protein targets

Sai Zhang, Jingtian Zhou, Hailin Hu, Haipeng Gong, Ligong Chen, Chao Cheng, Jianyang Zeng [10'+5']

Presenter affiliation: Institute for Interdisciplinary Information Sciences, Beijing, China. 41

FRIDAY, December 4—9:00 AM

SESSION 5 FUNCTIONAL SCREENING AND DRUG DISCOVERY

Chairperson: **Andrea Califano**, Columbia University, New York, New York, USA

Integrated systematic genomic approaches to define cancer networks

William C. Hahn [20'+10']

Presenter affiliation: Dana-Farber Cancer Institute, Boston, Massachusetts; Broad Institute of MIT and Harvard, Cambridge, Massachusetts. 42

Systematic elucidation of druggable dependencies in human malignancies—A new take on precision medicine

Andrea Califano [20'+10']

Presenter affiliation: Columbia University, New York, New York. 43

Gordon Mills [20'+10']

Presenter affiliation: University of Texas M.D. Anderson Cancer Center, Houston, Texas.

Cancer systems biology—An NCI perspective for the future

Daniel Gallahan [20'+10']

Presenter affiliation: National Cancer Institute, Bethesda, Maryland. 44

Copy number analysis of whole-genome data using BIC-seq2 and its application to detection of cancer susceptibility variants

Ruibin Xi, Seemin Lee, Tae-Min Kim, Peter Park [10'+5']

Presenter affiliation: Peking University, Beijing, China.

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Integrative transcriptome analysis on primary tumor and PVTT samples reveals recurrent lncRNAs regulating hepatocellular carcinoma development and metastasis

Yang Yang, Jiapei Yuan, Xinbao Sun, Hanshuo Zhang, Yang Liu, Xu Zhang, Qiaoran Xi, Jianzhong Xi, Jin Gu, Lei Chen, Michael Q. Zhang, Zhi J. Lu [10'+5']

Presenter affiliation: Tsinghua University, Beijing, China.

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Data-driven discovery of oncogene ALK driven metastasis in lung cancer: an unexpected role of splicing factors ESRP1/2

Liye Zhang, Claudia Voena, Lydia Varesio, Matteo Menotti, Teresa Poggio, Filomena D. Giacomo, Elena Panizza, Cristina Mastini, Mara Compagno, Stefano Monti, Roberto Chiarle [10'+5']

Presenter affiliation: Boston University, Boston, Massachusetts.

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FRIDAY, December 4—2:00 PM

SESSION 6 REGULATION AND SIGNALING

Chairperson: **Hongyang Wang**, Eastern Hepatobiliary Surgery Hospital, Shanghai, China

Heterogeneity and challenges of human hepatocellular carcinoma

Hongyang Wang [20'+10']

Presenter affiliation: Eastern Hepatobiliary Surgery Hospital, Shanghai, China.

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Circuitry and dynamics of DNA methylation-dependent transcription regulatory networks in cancers

Yu Liu, Yang Liu, Zhengtao Xiao, Xuerui Yang [20'+10']

Presenter affiliation: Tsinghua University, Beijing, China.

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SCT promoter methylation is a highly discriminative biomarker for lung and many other cancers

Adwait Sathe, Yu-An Zhang, Xiaotu Ma, Adi F. Gazdar, Michael Q. Zhang [20'+10']

Presenter affiliation: The University of Texas at Dallas, Richardson, Texas; Tsinghua University, Beijing, China.

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The Cancer Cell Map Initiative

Trey Ideker, Nevan Krogan, Alan Ashworth, David Agard, Scott Lippman [20'+10']

Presenter affiliation: University of California San Diego, San Diego, California.

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FRIDAY, December 4—6:00 PM

COCKTAILS and BANQUET

SATURDAY, December 5—9:00 AM

SESSION 7 MODELS AND NETWORKS

Chairperson: **Cory Abate-Shen**, Columbia University Medical School, New York, New York, USA

Pan-cancer analyses reveal lincRNAs relevant to tumor diagnosis, subtyping and prognosis

Travers Ching, Karolina Peplowska, Sijia Huang, Xun Zhu, Yi Shen, Janos Molnar, Herbert Yu, Maarit Tiirikainen, Ben Fogelgren, Rong Fan, Lana Garmire [10'+5']

Presenter affiliation: University of Hawaii Cancer Center, Honolulu, Hawaii.

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Elucidating mRNA isoform complexity in cancer transcriptomes using massive RNA-seq data

Yi Xing [10'+5']

Presenter affiliation: University of California, Los Angeles, Los Angeles, California.

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Quantitative characteristics of microRNA mediated posttranscriptional regulation

Xiaowo Wang [20'+10']

Presenter affiliation: Tsinghua University, Beijing, China.

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Extensive coupling of transcriptional and translational regulation via usage of alternative transcription start sites

Xi Wang, Jingyi Hou, Wei Chen [20'+10']

Presenter affiliation: Max-Delbrück-Center for Molecular Medicine, Berlin, Germany.

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From mouse to man—Using cross-species analysis of genome-wide regulatory networks to elucidate mechanisms of prostate cancer

Cory Abate-Shen [20'+10']

Presenter affiliation: Columbia University, New York, New York.

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Genomic variants at mRNAs and lncRNAs dysregulate cancer genes by modulating microRNA activity

Hua-Sheng Chiu, Maria R. Martínez, Xuerui Yang, Andrea Califano, Pavel Sumazin [20'+10']

Presenter affiliation: Baylor College of Medicine, Houston, Texas.

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FANTOM project—Surprises from studies of mammalian transcriptomes

Piero Carninci [20'+10']

Presenter affiliation: RIKEN Center for Life Science Technologies, Kanagawa, Japan.

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Integrative analysis of transcriptional networks driving prostate cancer progression

Ping Gao, Yuehong Yang, Hang-Mao Lee, Ilaria Svezia, Qilai Huang, Gong-Hong Wei [10'+5']

Presenter affiliation: University of Oulu, Oulu, Finland.

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