

| Day 1: Jan 15, 2018. | | |
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| 09:15 - 09:50 | Registration Open | |
| 09:50 - 10:00 | Opening Remarks (Main Hall) | |
| 10:00 - 11:00 | Keynote Speech (Main Hall) Modeling cancer evolution from genomic data Dr. Niko Beerenwinkel | |
| 11:00 - 11:15 | Coffee Break | |
| Parallel Session | Comparative Genomics (Main Hall) Session Chair: TBA | Chemoinformatics (Room 1) Session Chair: TBA |
| 11:15 - 11:40 | Matching Algorithms for Assigning Orthologs after Duplication Events Guillaume Fertin, Falk Hurffner, Christian Komusiewicz and Manuel Sorge | Resource Cut, a New Bounding Procedure to Algorithms for Enumerating Tree-like Chemical Graphs Yuhei Nishiyama, Aleksandar Shurbevski, Hiroshi Nagamochi and Tatsuya Akutsu |
| 11:40 - 12:05 | Phylogenetic signal from rearrangements in 18 Anopheles species by joint scaffolding extant and ancestral genomes Yoann Anselmetti, Wandrille Duchemin, Eric Tannier, Cedric Chauve and Severine Berard | Optimization of memory use of fragment extension-based protein-ligand docking with an original fast minimum cost flow algorithm Keisuke Yanagisawa, Shunta Komine, Rikuto Kubota, Masahito Ohue and Yutaka Akiyama |
| 12:05 - 12:30 | Resolution effects in reconstructing ancestral genomes Chunfang Zheng, Yuji Jeong, Madisyn Turcotte and David Sankoff | cmFSM: A Scalable CPU-MIC Coordinated Drug-Finding Tool by Frequent Subgraph Mining Shunyun Yang, Quan Zou, Shaoliang Peng and Runxin Guo |
| 12:30 - 14:00 | Lunch | |
| Parallel Session | Sequence Alignment Algorithms (Main Hall) Session Chair: TBA | Microbiome Analysis and Mass Spectrometry Analysis (Room 1) Session Chair: TBA |
| 14:00 - 14:25 | Parallel Computation of the Burrows-Wheeler Transform of Short Reads Using Prefix Parallelism Kouichi Kimura and Asako Koike | Adjacent Y-ion Ratio Distributions and Its Application in Peptide Sequencing Tiancong Wang and Bin Ma |
| 14:25 - 14:50 | Hardness of Covering Alignment: Phase Transition in Post-Sequence Genomics Romeo Rizzi, Massimo Cairo, Veli Ma'kinen, Alexandru I. Tomescu and Daniel Valenzuela | An Approach for N-linked Glycan Identification from MS/MS Spectra by Target-Decoy Strategy Weiping Sun, Yi Liu and Kaizhong Zhang |
| 14:50 - 15:15 | Genome Read In-Memory (GRIM) Filter: Fast Location Filtering in DNA Read Mapping using Emerging Memory Technologies Jeremie Kim, Damla Senol, Hongyi Xin, Donghyuk Lee, Saugata Ghose, Mohammed Alser, Hasan Hassan, Oguz Ergin, Can Alkan and Onur Mutlu | KDiamend: a package for detecting key drivers in a molecular ecological network of disease Mengxuan Lyu, Jiaying Chen, Yiqi Jiang and Shuaicheng Li |
| 15:15 - 15:40 | Hardware Acceleration of BWA-MEM Genomic Short Read Mapping with Longer Read Length Ernst Houtgast, Vlad-Mihai Sima, Koen Bertels and Zaid Al-Ars | Dynamics of the human gut phageome during the antibiotics treatment Anna Górska, Silke Peter, Matthias Willmann, Ingo Autenrieth, Robert Schlager and Daniel Huson |
| 15:40 - 16:00 | Coffee Break | |
| Parallel Session | Sequence Analysis (Main Hall) Session Chair: TBA | Protein Structure Analysis (Room 1) Session Chair: TBA |
| 16:00 - 16:25 | SpliceVec: distributed feature representations for splice junction prediction Aparajita Dutta, Tushar Dubey, Kusum Kumari Singh and Ashish Anand | RaptorX-Angle: real-value and confidence prediction of protein backbone dihedral angles through a hybrid method of clustering and deep learning Yujuan Gao, Sheng Wang, Minghua Deng and Jinbo Xu |
| 16:25 - 16:50 | Towards Pan-Genome Read Alignment to Improve Variation Calling Daniel Valenzuela, Tuukka Norri, Niko Va'lima'ki, Esa Pitka'nen and Veli Ma'kinen | MEGADOCK-Web: an integrated database of high-throughput structure-based protein- protein interaction predictions Takanori Hayashi, Yuri Matsuzaki, Keisuke Yanagisawa, Masahito Ohue and Yutaka Akiyama |
| 16:50 - 17:15 | Efficient Algorithms for Polyploid Haplotype Phasing Dan He, Subrata Saha, Richard Finkers and Laxmi Parid | Computational analysis of the receptor binding specificity of novel influenza A/H7N9 viruses Xinrui Zhou, Jie Zheng, Fransiskus Xaverius Ivan, Rui Yin, Shoba Ranganathan, Vincent T. K. Chow and Chee Keong Kwoh |
| 17:15 - 17:40 | NGS-based likelihood ratio for identifying contributors in two- and three-person DNA mixtures Joshua Mun Wei Chan, Zicheng Zhao, Shuai Cheng Li and Yen Kaow Ng | CNNH_PSS: Protein 8-class Secondary Structure Prediction by Convolutional Neural Network with Highway Jiyun Zhou, Hongpeng Wang, Zhishan Zhao, Ruifeng Xu and Qin Lu |
| 17:40 - 18:40 | Poster Session (Room 2 & 3) | |

| Day 2: Jan 16, 2018. | | |
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| 09:15 - 09:30 | Registration Open | |
| 09:30 - 10:30 | Keynote Speech (Main Hall) AI-supported clinical sequencing in blood cancers Dr. Arinobu Tojo | |
| 10:30 - 10:45 | Coffee Break | |
| Parallel Session | Gene Expression Analysis (1) (Main Hall) Session Chair: TBA | Molecular Interaction Analysis (Room 1) Session Chair: TBA |
| 10:45 - 11:10 | The Aquatic Animals' Transcriptome Resource for Comparative Functional Analysis Chih-Hung Chou, Sheng-Da Hsu, Chia-Yu Liu, Yu-Hung Chen, Yu-Chen Liu, Wei-Yun Huang, Chung-Der Hsiao and Hsien-Da Huang | Probing the functions of long non-coding RNAs by exploiting the topology of global association and interaction network Lei Deng, Hongjie Wu and Jinpu Zhang |
| 11:10 - 11:35 | Identification of Usual Interstitial Pneumonia Pattern Using RNA-Seq and Machine Learning: Challenges and Solutions Yoonha Choi, Tiffany Ting Liu, Daniel Pankratz, Thomas Colby, Neil Barth, David Lynch, Sean Walsh, Ganesh Raghu, Giulia Kennedy and Jing Huang | Annotating activation/inhibition relationships to protein-protein interactions using Gene Ontology relations Soorin Yim, Hasun Yu, Dongjin Jang and Doheon Lee |
| 11:35 - 12:00 | A Gene Profiling Deconvolution Approach to Estimating Immune Cell Composition from Complex Tissues Wen-Yu Kuo, Shu-Hwa Chen, Sheng-Yao Su, Wei-Chun Chung, Jen-Ming Ho, Henry Horng-Shing Lu and Chung-Yen Lin | Protein complex prediction by date hub removal Iana Pyrogova and Limsoon Wong |
| 12:00 - 13:30 | Lunch | |
| Parallel Session | Phylogenetics (Main Hall) Session Chair: TBA | microRNA analysis (Room 1) Session Chair: TBA |
| 13:30 - 13:55 | GATC: A Genetic Algorithm for gene Tree Construction under the Duplication-Transfer- Loss model of evolution Emmanuel Noutahi and Nadia El-Mabrouk | Hierarchical Structural Component Analysis of microRNA-mRNA Integration Analysis Yongkang Kim, Sungyoung Lee, Sungkyoung Choi and Taesung Park |
| 13:55 - 14:20 | Computing the Diameter of the Space of Maximum Parsimony Reconciliations in the Duplication-Transfer-Loss Model Jordan Haack, Eli Zupke, Andrew Ramirez, Yi-Chieh Wu and Ran Libeskind-Hadas | Genome-wide identification and comprehensive analysis of microRNAs and phased small interfering RNAs in watermelon Li Liu, Shuchao Ren, Junqiang Guo, Qingyi Wang, Xiaotuo Zhang, Peiran Liao, Shipeng Li, Ramanjulu Sunkar and Yun Zheng |
| 14:20 - 14:45 | An Integrated Reconciliation Framework for Domain, Gene, and Species Level Evolution Lei Li and Mukul S. Bansal | Ouroboros Resembling Competitive Endoge-nous Loop (ORCEL) in circular RNAs revealed through transcriptome sequencing dataset analysis Yu-Chen Liu, Hsiao-Chin Hong, Chi-Dung Yang, Wei-Hsiang Lee, Hsin-Tzu Huang and Hsien-Da Huang |
| 14:45 - 15:10 | An Exact Algorithm for Sorting by Weighted Preserving Genome Rearrangements Tom Hartmann, Matthias Bernt and Martin Middendorf | Integrated microRNA and mRNA expression profile analysis of Tumor-Associated Macrophages after Exposure to Single-Dose Irradiation Wei-Hsiang Kung, Chi-Lung Lee, Chi-Dung Yang, Ching-Fang Yu, Men-Yee Chiew, Fang-Hsin Chen and Hsien-Da Huang |
| 15:10 - 15:30 | Coffee Break | |
| 15:30 - 16:30 | Keynote Speech (Main Hall) Whole-body and whole-organ clearing and imaging with single-cell resolution toward organism-level systems biology in mammals Dr. Hiroki R. Ueda | |
| 16:30 - 16:45 | Coffee Break | |
| Parallel Session | Gene Expression Analysis (2) (Main Hall) Session Chair: TBA | Network Analysis (Room 1) Session Chair: TBA |
| 16:45 - 17:10 | Identification of Condition Specific Cis- and Trans-acting Elements in Plant promoters under Various Endo- and Exogenous Stimuli Chi-Nga Chow, Yi-Fan Chiang-Hsieh, Chia-Hung Chien, Han-Qin Zheng, Nai-Yun Wu, Kuan-Chieh Tseng, Ping-Fu Hou and Wen-Chi Chang | Taming Asynchrony for Attractor Detection in Large Boolean Networks Andrzej Mizera, Jun Pang, Hongyang Qu and Qixia Yuan |
| 17:10 - 17:35 | Comparisons of gene coexpression network modules in breast cancer and ovarian cancer Shuqin Zhang | Discovery of Boolean Metabolic Networks: Integer Linear Programming Based Approach Yushan Qiu, Hao Jiang, Xiaoqing Cheng and Wai-Ki Ching |
| 17:35 - 18:00 | Automated Transition Analysis of Activated Gene Regulation during Diauxic Nutrient Shift in Escherichia Coli and Adipocyte Differentiation in Mouse Cells Yoichi Takenaka, Kazuma Mikami, Shigeto Seno and Hideo Matsuda | Counting motifs in dynamic networks Kingshuk Mukherjee, Md Mahmudul Hasan, Christina Boucher and Tamer Kahveci |
| 18:00 - 19:00 | Poster Session (Room 2 & 3) | |
| 19:00 - 21:00 | Banquet (Event Hall) | |

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| Day 3: Jan 17, 2018. | | |
| 09:00 - 09:30 | Registration Open | |
| 09:30 - 10:30 | Keynote Speech (Main Hall) In vitro reconstitution of oogenesis in the mouse; how to establish the culture, system, mostly empirical Dr. Katsuhiko Hayashi | |
| 10:30 - 10:45 | Coffee Break | |
| Parallel Session | Novel Analytic Methods (Main Hall) Session Chair: TBA | Systems Biology (Room 1) Session Chair: TBA |
| 10:45 - 11:10 | Prediction of enhancer-promoter interactions via natural language processing Wanwen Zeng, Mengmeng Wu, Rui Jiang | Composite mathematical modeling of calcium signaling behind neuronal cell death in Alzheimer's disease Bobby Ranjan, Ket Hing Chong and Jie Zheng |
| 11:10 - 11:35 | Estimation of Diffusion Constants from Single Molecular Measurement without Explicit Tracking Shunsuke Teraguchi and Yutaro Kumagai | Regulation of dual specificity phosphatases in breast cancer during initial treatment with Herceptin: A Boolean model analysis Petronela Buiga, Ari Elson, Lydia Tabernero and Jean-Marc Schwartz |
| 11:35 - 12:00 | Predicting and Understanding Comprehensive Drug-Drug Interactions via Semi- Nonnegative Matrix Factorization Yu Hui, Kui-Tao Mao, Jian-Yu Shi, Hua Huang, Zhi Chen, Kai Dong and Siu-Ming Yiu | Pathway-based approach using hierarchical components of rare variants to analyze multiple phenotypes Sungyoung Lee, Yongkang Kim, Sungkyoung Choi, Heungsun Hwang and Taesung Park |
| 12:00 - 13:30 | Lunch | |
| Parallel Session | Gene Expression Analysis (3) (Main Hall) Session Chair: TBA | Disease Analysis (Room 1) Session Chair: TBA |
| 13:30 - 13:55 | ncRNA-disease association prediction based on sequence information and tripartite network Takuya Mori, Hayliang Ngouv, Morihiro Hayashida, Tatsuya Akutsu and Jose Nacher | A new method to measure the semantic similarity from query phenotypic abnormalities to diseases based on the Human Phenotype Ontology Xiaofeng Gong, Jianping Jiang, Zhongqu Duan and Hui Lu |
| 13:55 - 14:20 | Tensor decomposition/principal component analysis based unsupervised feature extraction applied to brain gene expression and methylation profiles of social insects with multiple castes Y-H. Taguchi | VARReporter: Variant reporter for cancer research of massive parallel sequencing Po-Jung Huang, Chi-Ching Lee, Ling-Ya Chiu, Kuo-Yang Huang, Yuan-Ming Yeh, Chia-Yu Yang, Cheng-Hsun Chiu and Petrus Tang |
| 14:20 - 14:45 | Comprehensive analysis of coding-lncRNA gene co-expression network uncovers conserved functional lncRNAs in zebrafish Wen Chen, Xuan Zhang, Jing Li, Shulan Huang, Shuanglin Xiang, Xiang Hu and Changning Liu | |
| 14:45 - 15:00 | Closing Remarks / Award Ceremony (Main Hall) | |