

Day 1: Jan 15, 2018.		
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 Session Chair: Dr. Yasubumi Sakakibara	
11:00 - 11:15	Coffee Break	
Parallel Session	Comparative Genomics (Main Hall) Session Chair: Dr. Laxmi Parida	Chemoinformatics (Room 1) Session Chair: Dr. Shuqin Zhang
11:15 - 11:40	[O1] Matching Algorithms for Assigning Orthologs after Duplication Events Guillaume Fertin, Falk Hußner, Christian Komusiewicz and Manuel Sorge	[O4] 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	[O2] 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	[O5] 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	[O3] Resolution effects in reconstructing ancestral genomes Chunfang Zheng, Yuji Jeong, Madisyn Turcotte and David Sankoff	[O6] 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
12:30 - 14:00	Lunch	
Parallel Session	Sequence Alignment Algorithms (Main Hall) Session Chair: Dr. Guillaume Fertin	Microbiome Analysis and Mass Spectrometry Analysis (Room 1) Session Chair: Dr. Naoaki Ono
14:00 - 14:25	[O7] Parallel Computation of the Burrows-Wheeler Transform of Short Reads Using Prefix Parallelism Kouichi Kimura and Asako Koike	[O11] Adjacent Y-ion Ratio Distributions and Its Application in Peptide Sequencing Tiancong Wang and Bin Ma
14:25 - 14:50	[O8] Hardness of Covering Alignment: Phase Transition in Post-Sequence Genomics Romeo Rizzi, Massimo Cairo, Veli Ma'kinen, Alexandru I. Tomescu and Daniel Valenzuela	[O12] 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	[O9] GRIM-Filter: Fast seed location filtering in DNA read mapping using processing-in-memory technologies Jeremie Kim, Damla Senol, Hongyi Xin, Donghyuk Lee, Saugata Ghose, Mohammed Alser, Hasan Hassan, Oguz Ergin, Can Alkan and Onur Mutlu	[O13] KDiamend: a package for detecting key drivers in a molecular ecological network of disease Mengxuan Lyu, Jiaxing Chen, Yiqi Jiang and Shuaicheng Li
15:15 - 15:40	[O10] Hardware Acceleration of BWA-MEM Genomic Short Read Mapping with Longer Read Length Ernst Houtgast, Vlad-Mihai Sima, Koen Bertels and Zaid Al-Ars	[O14] Dynamics of the human gut phageome during the antibiotics treatment Anna Górka, 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: Dr. Y.-H. Taguchi	Protein Structure Analysis (Room 1) Session Chair: Dr. Mukul Bansal
16:00 - 16:25	[O15] SpliceVec: distributed feature representations for splice junction prediction Aparajita Dutta, Tushar Dubey, Kusum Kumari Singh and Ashish Anand	[O19] 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	[O16] Towards Pan-Genome Read Alignment to Improve Variation Calling Daniel Valenzuela, Tuukka Norri, Niko Va'lima'ki, Esa Pitka'nen and Veli Ma'kinen	[O20] 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	[O17] Efficient Algorithms for Polyploid Haplotype Phasing Dan He, Subrata Saha, Richard Finkers and Laxmi Parida	[O21] 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 Kwok
17:15 - 17:40	[O18] 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	[O22] 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 for odd numbers (Room 2 & 3)	

Day 2: Jan 16, 2018.		
09:15 - 09:30	Registration Open	
09:30 - 10:30	Keynote Speech (Main Hall) AI-supported clinical sequencing in blood cancers Dr. Arinobu Tojo Session Chair: Dr. Yasubumi Sakakibara	
10:30 - 10:45	Coffee Break	
Parallel Session	Gene Expression Analysis (1) (Main Hall) Session Chair: Dr. Yutaro Kumagai	Molecular Interaction Analysis (Room 1) Session Chair: Dr. Jose Nacher
10:45 - 11:10	[O23] 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	[O26] 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	[O24] 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	[O27] 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	[O25] A Gene Profiling Deconvolution Approach to Estimating Immune Cell Composition from Complex Tissues Wen-Yu Kuo, Shu-Hwa Chen, Sheng-Yao Su, Wei-ChunChung, Jen-Ming Ho, Henry Horng-Shing Lu and Chung-Yen Lin	[O28] Protein complex prediction by date hub removal Iana Pyrogova and Limsoon Wong
12:00 - 13:30	Lunch	
Parallel Session	Phylogenetics (Main Hall) Session Chair: Dr. Daniel Valenzuela	microRNA analysis (Room 1) Session Chair: Dr. Minghua Deng
13:30 - 13:55	[O29] GATC: A Genetic Algorithm for gene Tree Construction under the Duplication-Transfer- Loss model of evolution Emmanuel Noutahi and Nadia El-Mabrouk	[O33] Hierarchical Structural Component Analysis of microRNA-mRNA Integration Analysis Yongkang Kim, Sungyoung Lee, Sungkyoung Choi and Taesung Park
13:55 - 14:20	[O30] 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	[O34] 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	[O31] An Integrated Reconciliation Framework for Domain, Gene, and Species Level Evolution Lei Li and Mukul S. Bansal	[O35] Ouroboros Resembling Competitive Endogenous 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	[O32] An Exact Algorithm for Sorting by Weighted Preserving Genome Rearrangements Tom Hartmann, Matthias Bernt and Martin Middendorf	[O36] 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 Session Chair: Dr. Yoshihiro Yamanishi	
16:30 - 16:45	Coffee Break	
Parallel Session	Gene Expression Analysis (2) (Main Hall) Session Chair: Dr. Alexis Vandenbon	Network Analysis (Room 1) Session Chair: Dr. Jean-Marc Schwartz
16:45 - 17:10	[O37] 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	[O40] Taming Asynchrony for Attractor Detection in Large Boolean Networks Andrzej Mizera, Jun Pang, Hongyang Qu and Qixia Yuan
17:10 - 17:35	[O38] Comparisons of gene coexpression network modules in breast cancer and ovarian cancer Shuqin Zhang	[O41] Discovery of Boolean Metabolic Networks: Integer Linear Programming Based Approach Yushan Qiu, Hao Jiang, Xiaoqing Cheng and Wai-Ki Ching
17:35 - 18:00	[O39] 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	[O42] Counting motifs in dynamic networks Kingshuk Mukherjee, Md Mahmudul Hasan, Christina Boucher and Tamer Kahveci
18:00 - 19:00	Poster Session for even numbers (Room 2 & 3)	
19:00 - 21:00	Banquet (Event Hall)	

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 Session Chair: Dr. Yoshihiro Yamanishi	
10:30 - 10:45	Coffee Break	
Parallel Session	Systems Biology (Main Hall) Session Chair: Dr. Emmanuel Barillot	Gene Expression Analysis (3) (Room 1) Session Chair: Dr. Limsoon Wong
10:45 - 11:10	[O43] Composite mathematical modeling of calcium signaling behind neuronal cell death in Alzheimer's disease Bobby Ranjan, Ket Hing Chong and Jie Zheng	[O46] ncRNA-disease association prediction based on sequence information and tripartite network Takuya Mori, Hayliang Ngouy, Morihiro Hayashida, Tatsuya Akutsu and Jose Nacher
11:10 - 11:35	[O44] 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	[O47] 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
11:35 - 12:00	[O45] Pathway-based approach using hierarchical components of rare variants to analyze multiple phenotypes Sungyoung Lee, Yongkang Kim, Sungkyoung Choi, Heungsun Hwang and Taesung Park	[O48] 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
12:00 - 13:30	Lunch	
Parallel Session	Novel Analytic Methods (Main Hall) Session Chair: Dr. Jun Pang	Disease Analysis (Room 1) Session Chair: Dr. Mitsunori Kayano
13:30 - 13:55	[O49] Prediction of enhancer-promoter interactions via natural language processing Wanwen Zeng, Mengmeng Wu, Rui Jiang	[O51] 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	[O50] Estimation of Diffusion Constants from Single Molecular Measurement without Explicit Tracking Shunsuke Teraguchi and Yutaro Kumagai	[O52] VAREporter: 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	[O53] cmFSM: A Scalable CPU-MIC Coordinated Drug-Finding Tool by Frequent Subgraph Mining Shunyun Yang, Quan Zou, Shaoliang Peng and Runxin Guo	
14:45 - 15:00	Closing Remarks / Award Ceremony (Main Hall)	