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 Genome Duplication Events** **Guillaume Fertin**, Falk Hüffner, 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 Gabrielle Turcotte and **David Sankoff**	**[O6] Predicting and Understanding Comprehensive Drug-Drug Interactions via Semi- Nonnegative Matrix Factorization** Hui Yu , 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 Mäkinen, 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 S. Kim**, Damla Senol Cali, 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, Wei Dong, Zhou Fang and Shuaicheng Li
15:15 - 15:40	**[O10] Hardware Acceleration of BWA-MEM Genomic Short Read Mapping for Longer Read Lengths** **Ernst Houtgast**, Vlad-Mihai Sima, Koen Bertels and Zaid Al-Ars	**[O14] Dynamics of the human gut phageome during the antibiotics treatment** **Anna Górska**, Silke Peter, Matthias Willmann, Ingo Autenrieth, Robert Schlaberg 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 Välimäki, Esa Pitkänen and Veli Mäkinen	**[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 Kwoh
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.		
09:00 - 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**, Hsi-Yuan Huang, Wei-Chih Huang, Sheng-Da Hsu, Chung-Der Hsiao, Chia-Yu Liu, Yu-Hung Chen, Yu-Chen Liu, Wei-Yun Huang, Meng-Lin Lee, Yi-Chang Chen, 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** **Shu-Hwa Chen**, Wen-Yu Kuo, Sheng-Yao Su, Wei-Chun Chung, 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 Modeling 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, Tzong-Yi Lee, 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 Ngouv, 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)	