

Day 1: Jan 15, 2018.		
09:15 - 09:50	Registration Open	
09:50 - 10:00	Opening Remarks (Main Hall)	
10:00 - 11:00	<b>Keynote Speech (Main Hall)</b> <b>Modeling cancer evolution from genomic data</b> <b>Dr. Niko Beerenwinkel</b>	
11:00 - 11:15	Coffee Break	
Parallel Session	Comparative Genomics (Main Hall) Session Chair: TBA	Cheminformatics (Room 1) Session Chair: TBA
11:15 - 11:40	<b>[O1] Matching Algorithms for Assigning Orthologs after Duplication Events</b> Guillaume Fertin, Falk Hufnner, Christian Komusiewicz and Manuel Sorge	<b>[O4] Resource Cut, a New Bounding Procedure to Algorithms for Enumerating Tree-like Chemical Graphs</b> Yuhei Nishiyama, Aleksandar Shurbevski, Hiroshi Nagamochi and Tatsuya Akutsu
11:40 - 12:05	<b>[O2] Phylogenetic signal from rearrangements in 18 Anopheles species by joint scaffolding extant and ancestral genomes</b> Yoann Anselmetti, Wandrille Duchemin, Eric Tannier, Cedric Chauve and Severine Berard	<b>[O5] Optimization of memory use of fragment extension-based protein-ligand docking with an original fast minimum cost flow algorithm</b> Keisuke Yanagisawa, Shunta Komine, Rikuto Kubota, Masahito Ohue and Yutaka Akiyama
12:05 - 12:30	<b>[O3] Resolution effects in reconstructing ancestral genomes</b> Chunfang Zheng, Yuji Jeong, Madisyn Turcotte and David Sankoff	<b>[O6] Predicting and Understanding Comprehensive Drug-Drug Interactions via Semi-Nonnegative Matrix Factorization</b> 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: TBA	Microbiome Analysis and Mass Spectrometry Analysis (Room 1) Session Chair: TBA
14:00 - 14:25	<b>[O7] Parallel Computation of the Burrows-Wheeler Transform of Short Reads Using Prefix Parallelism</b> Kouichi Kimura and Asako Koike	<b>[O11] Adjacent Y-ion Ratio Distributions and Its Application in Peptide Sequencing</b> Tiancong Wang and Bin Ma
14:25 - 14:50	<b>[O8] Hardness of Covering Alignment: Phase Transition in Post-Sequence Genomics</b> Romeo Rizzi, Massimo Cairo, Veli Ma'kinen, Alexandru I. Tomescu and Daniel Valenzuela	<b>[O12] An Approach for N-linked Glycan Identification from MS/MS Spectra by Target-Decoy Strategy</b> Weiping Sun, Yi Liu and Kaizhong Zhang
14:50 - 15:15	<b>[O9] Genome Read In-Memory (GRIM) Filter: Fast Location Filtering in DNA Read Mapping using Emerging Memory Technologies</b> Jeremie Kim, Damla Senol, Hongyi Xin, Donghyuk Lee, Saugata Ghose, Mohammed Alser, Hasan Hassan, Oguz Ergin, Can Alkan and Onur Mutlu	<b>[O13] KDiamend: a package for detecting key drivers in a molecular ecological network of disease</b> Mengxuan Lyu, Jiaying Chen, Yiqi Jiang and Shuaicheng Li
15:15 - 15:40	<b>[O10] Hardware Acceleration of BWA-MEM Genomic Short Read Mapping with Longer Read Length</b> Ernst Houtgast, Vlad-Mihai Sima, Koen Bertels and Zaid Al-Ars	<b>[O14] Dynamics of the human gut phageome during the antibiotics treatment</b> 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	<b>[O15] SpliceVec: distributed feature representations for splice junction prediction</b> Aparajita Dutta, Tushar Dubey, Kusum Kumari Singh and Ashish Anand	<b>[O19] RaptorX-Angle: real-value and confidence prediction of protein backbone dihedral angles through a hybrid method of clustering and deep learning</b> Yujuan Gao, Sheng Wang, Minghua Deng and Jinbo Xu
16:25 - 16:50	<b>[O16] Towards Pan-Genome Read Alignment to Improve Variation Calling</b> Daniel Valenzuela, Tuukka Norri, Niko Va'lima'ki, Esa Pitka'nen and Veli Ma'kinen	<b>[O20] MEGADOCK-Web: an integrated database of high-throughput structure-based protein-protein interaction predictions</b> Takanori Hayashi, Yuri Matsuzaki, Keisuke Yanagisawa, Masahito Ohue and Yutaka Akiyama
16:50 - 17:15	<b>[O17] Efficient Algorithms for Polyploid Haplotype Phasing</b> Dan He, Subrata Saha, Richard Finkers and Laxmi Parid	<b>[O21] Computational analysis of the receptor binding specificity of novel influenza A/H7N9 viruses</b> Xinrui Zhou, Jie Zheng, Fransiskus Xaverius Ivan, Rui Yin, Shoba Ranganathan, Vincent T. K. Chow and Chee Keong Kwoh
17:15 - 17:40	<b>[O18] NGS-based likelihood ratio for identifying contributors in two- and three-person DNA mixtures</b> Joshua Mun Wei Chan, Zicheng Zhao, Shuai Cheng Li and Yen Kaow Ng	<b>[O22] CNNH_PSS: Protein 8-class Secondary Structure Prediction by Convolutional Neural Network with Highway</b> 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.		
09:00 - 09:30	Registration Open	
09:30 - 10:30	<b>Keynote Speech (Main Hall)</b> <b>AI-supported clinical sequencing in blood cancers</b> <b>Dr. Arinobu Tojo</b>	
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	<b>[O23] The Aquatic Animals' Transcriptome Resource for Comparative Functional Analysis</b> 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	<b>[O26] Probing the functions of long non-coding RNAs by exploiting the topology of global association and interaction network</b> Lei Deng, Hongjie Wu and Jinpu Zhang
11:10 - 11:35	<b>[O24] Identification of Usual Interstitial Pneumonia Pattern Using RNA-Seq and Machine Learning: Challenges and Solutions</b> Yoonha Choi, Tiffany Ting Liu, Daniel Pankratz, Thomas Colby, Neil Barth, David Lynch, Sean Walsh, Ganesh Raghu, Giulia Kennedy and Jing Huang	<b>[O27] Annotating activation/inhibition relationships to protein-protein interactions using Gene Ontology relations</b> Soorin Yim, Hasun Yu, Dongjin Jang and Doheon Lee
11:35 - 12:00	<b>[O25] A Gene Profiling Deconvolution Approach to Estimating Immune Cell Composition from Complex Tissues</b> Wen-Yu Kuo, Shu-Hwa Chen, Sheng-Yao Su, Wei-Chun Chung, Jen-Ming Ho, Henry Horng-Shing Lu and Chung-Yen Lin	<b>[O28] Protein complex prediction by date hub removal</b> 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	<b>[O29] GATC: A Genetic Algorithm for gene Tree Construction under the Duplication-Transfer- Loss model of evolution</b> Emmanuel Noutahi and Nadia El-Mabrouk	<b>[O33] Hierarchical Structural Component Analysis of microRNA-mRNA Integration Analysis</b> Yongkang Kim, Sungyoung Lee, Sungkyoung Choi and Taesung Park
13:55 - 14:20	<b>[O30] Computing the Diameter of the Space of Maximum Parsimony Reconciliations in the Duplication-Transfer-Loss Model</b> Jordan Haack, Eli Zupke, Andrew Ramirez, Yi-Chieh Wu and Ran Libeskind-Hadas	<b>[O34] Genome-wide identification and comprehensive analysis of microRNAs and phased small interfering RNAs in watermelon</b> Li Liu, Shuchao Ren, Junqiang Guo, Qingyi Wang, Xiaotuo Zhang, Peiran Liao, Shipeng Li, Ramanjulu Sunkar and Yun Zheng
14:20 - 14:45	<b>[O31] An Integrated Reconciliation Framework for Domain, Gene, and Species Level Evolution</b> Lei Li and Mukul S. Bansal	<b>[O35] Ouroboros Resembling Competitive Endogenous Loop (ORCEL) in circular RNAs revealed through transcriptome sequencing dataset analysis</b> Yu-Chen Liu, Hsiao-Chin Hong, Chi-Dung Yang, Wei-Hsiang Lee, Hsin-Tzu Huang and Hsien-Da Huang
14:45 - 15:10	<b>[O32] An Exact Algorithm for Sorting by Weighted Preserving Genome Rearrangements</b> Tom Hartmann, Matthias Bernt and Martin Middendorf	<b>[O36] Integrated microRNA and mRNA expression profile analysis of Tumor-Associated Macrophages after Exposure to Single-Dose Irradiation</b> 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	<b>Keynote Speech (Main Hall)</b> <b>Whole-body and whole-organ clearing and imaging with single-cell resolution toward organism-level systems biology in mammals</b> <b>Dr. Hiroki R. Ueda</b>	
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	<b>[O37] Identification of Condition Specific Cis- and Trans-acting Elements in Plant promoters under Various Endo- and Exogenous Stimuli</b> 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	<b>[O40] Taming Asynchrony for Attractor Detection in Large Boolean Networks</b> Andrzej Mizera, Jun Pang, Hongyang Qu and Qixia Yuan
17:10 - 17:35	<b>[O38] Comparisons of gene coexpression network modules in breast cancer and ovarian cancer</b> Shuqin Zhang	<b>[O41] Discovery of Boolean Metabolic Networks: Integer Linear Programming Based Approach</b> Yushan Qiu, Hao Jiang, Xiaoping Cheng and Wai-Ki Ching
17:35 - 18:00	<b>[O39] Automated Transition Analysis of Activated Gene Regulation during Diauxic Nutrient Shift in Escherichia Coli and Adipocyte Differentiation in Mouse Cells</b> Yoichi Takenaka, Kazuma Mikami, Shigeto Seno and Hideo Matsuda	<b>[O42] Counting motifs in dynamic networks</b> 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)	

Day 3: Jan 17, 2018.		
09:00 - 09:30	Registration Open	
09:30 - 10:30	<b>Keynote Speech (Main Hall)</b> <b>In vitro reconstitution of oogenesis in the mouse; how to establish the culture, system, mostly empirical</b> <b>Dr. Katsuhiko Hayashi</b>	
10:30 - 10:45	Coffee Break	
Parallel Session	<b>Systems Biology (Main Hall)</b> Session Chair: TBA	<b>Gene Expression Analysis (3) (Room 1)</b> Session Chair: TBA
10:45 - 11:10	<b>[O43] Composite mathematical modeling of calcium signaling behind neuronal cell death in Alzheimer's disease</b> Bobby Ranjan, Ket Hing Chong and Jie Zheng	<b>[O46] ncRNA-disease association prediction based on sequence information and tripartite network</b> Takuya Mori, Hayliang Ngouv, Morihiro Hayashida, Tatsuya Akutsu and Jose Nacher
11:10 - 11:35	<b>[O44] Regulation of dual specificity phosphatases in breast cancer during initial treatment with Herceptin: A Boolean model analysis</b> Petronela Buiga, Ari Elson, Lydia Tabernero and Jean-Marc Schwartz	<b>[O47] Tensor decomposition/principal component analysis based unsupervised feature extraction applied to brain gene expression and methylation profiles of social insects with multiple castes</b> Y-H. Taguchi
11:35 - 12:00	<b>[O45] Pathway-based approach using hierarchical components of rare variants to analyze multiple phenotypes</b> Sungyoung Lee, Yongkang Kim, Sungkyoung Choi, Heungsun Hwang and Taesung Park	<b>[O48] Comprehensive analysis of coding-lncRNA gene co-expression network uncovers conserved functional lncRNAs in zebrafish</b> Wen Chen, Xuan Zhang, Jing Li, Shulan Huang, Shuanglin Xiang, Xiang Hu and Changning Liu
12:00 - 13:30	Lunch	
Parallel Session	<b>Novel Analytic Methods (Main Hall)</b> Session Chair: TBA	<b>Disease Analysis (Room 1)</b> Session Chair: TBA
13:30 - 13:55	<b>[O49] Prediction of enhancer-promoter interactions via natural language processing</b> Wanwen Zeng, Mengmeng Wu, Rui Jiang	<b>[O51] A new method to measure the semantic similarity from query phenotypic abnormalities to diseases based on the Human Phenotype Ontology</b> Xiaofeng Gong, Jianping Jiang, Zhongqu Duan and Hui Lu
13:55 - 14:20	<b>[O50] Estimation of Diffusion Constants from Single Molecular Measurement without Explicit Tracking</b> Shunsuke Teraguchi and Yutaro Kumagai	<b>[O52] VAREporter: Variant reporter for cancer research of massive parallel sequencing</b> 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	<b>[O53] cmFSM: A Scalable CPU-MIC Coordinated Drug-Finding Tool by Frequent Subgraph Mining</b> Shunyun Yang, Quan Zou, Shaoliang Peng and Runxin Guo	
14:45 - 15:00	Closing Remarks / Award Ceremony (Main Hall)	