

Day 1 Monday, December 15

| 8:15 - 19:00 | Registration desk open | | |
|---------------|--|---|---|
| | 3F Auditorium | 3F Media hall | 4F Meeting room1 |
| 8:45 - 9:00 | Opening remarks | | |
| 9:00 - 10:00 | Keynote speech 1 Introduction: Hiroyuki Toh, Computational Biology Research Center, AIST Masami Yokata HIRAI Understanding of plant metabolism via metabolomics-based mathematical modeling | | |
| 10:15 - 11:15 | Session 1.1A Session Chair: Huai-Kuang Tsai, Institute of Information Science, Academia Sinica | Session 1.1B Session Chair: Jun Sese, Computational Biology Research Center, AIST | Session 1.1C Session Chair: Kenta Nakai, Institute of Medical Science, The University of Tokyo |
| 10:15 - 10:45 | P31 U–system approach for predicting metabolic behaviors and responses based on an alleged metabolic reaction network. <u>Kansuporn Srivudthsak</u> , Yuji Sawada, Yukako Chiba, Yui Yamashita, Shigehiko Kanaya, Hitoshi Onouchi, Toru Fujiwara, Satoshi Naito, Ebernard O. Voit, Fumihide Shiraishi and Masami Yokota Hirai. | P87 PRIGSA: Protein Repeat Identification by Graph Spectral Analysis. <u>Broto Chakrabarty</u> and Nita Parekh. | P92 A regulatory similarity measure using the location information of transcription factor binding sites in <i>Saccharomyces cerevisiae</i> . <u>Wei-Sheng Wu</u> , Ming-Liang Wei, Chia-Ming Yeh and <u>Tien-Hao Chang</u> . |
| 10:45 - 11:15 | P06 Analytical study of robustness of a negative feedback oscillator by multiparameter sensitivity. <u>Kazuhiro Maeda</u> and Hiroyuki Kurata. | P19 Randomized Subspace Learning for Proline Cis-Trans Isomerization Prediction. Kamal Taha, <u>Paul Yoo</u> and Sami Muhaidat. | P15 Identifying cooperative transcription factors in yeast using multiple data sources. <u>Wei-Sheng Wu</u> , Mei-Huei Jhu and Fu-Jou Lai. |
| 11:15 - 13:00 | Lunch at various restaurants in walk distance of venue | | |
| 13:00 - 14:00 | Keynote speech 2 Introduction: Paul Horton, Computational Biology Research Center, AIST. Thomas LENGAUER Custom-tailoring combination drug therapies with bioinformatics | | |
| 14:15 - 16:15 | Session 1.2A Session Chair: Toutai Mituyama, Computational Biology Research Center, AIST | Session 1.2B Session Chair: Susumu Goto, Kyoto University Bioinformatics Center | Session 1.2C Session Chair: Yasubumi Sakakibara, Dept. Biosciences and Informatics, Keio University |
| 14:15 - 14:45 | P05 RASA: Robust Alternative Splicing Analysis for Human Transcriptome Arrays. <u>Junhee Seok</u> , Weihong Xu, Ronald Davis and Wenzhong Xiao. | P90 Curatable Named-entity Recognition using Semantic Relations. <u>Yi-Yu Hsu</u> and Hung-Yu Kao. | P69 Efficient calculation of exact probability distributions of integer features on RNA secondary structures. <u>Ryota Mori</u> , Michiaki Hamada and Kiyoshi Asai. |
| 14:45 - 15:15 | P30 TIGAR2: sensitive and accurate estimation of transcript isoform expression with longer RNA-Seq reads. <u>Naoki Nariai</u> , Kaname Kojima, Takahiro Mimori, Yukuto Sato, Yosuke Kawai, Yumi Yamaguchi-Kabata and Masao Nagasaki. | P88 An Integrative Approach for Measuring Semantic Similarities using Gene Ontology. <u>Jiajie Peng</u> , Hongxiang Li, Qinghua Jiang, Yadong Wang and Jin Chen. | P12 Improving miRNA-mRNA Interaction Predictions. Daniel Tabas-Madrid, Ander Muniategui, Ignacio Sánchez-Caballero, Dannys Martínez-Herrera, Carlos Oscar S. Sorzano, Angel Rubio and <u>Alberto Pascual-Montano</u> . |
| 15:15 - 15:45 | HL116 Comparison of CAGE and RNA-seq transcriptome profiling using clonally amplified and single-molecule next-generation sequencing. <u>Hideya Kawaji</u> , Marina Lizio, Masayoshi Itoh, Mutsumi Kanamori-Katayama, Ai Kaiho, Hiromi Nishiyori-Sueki, Jay W. Shin, Miki Kojima-Ishiyama, Mitsuoki Kawano, Mitsuyoshi Murata, Noriko Ninomiya-Fukuda, Sachi Ishikawa-Kato, Sayaka Nagao-Sato, Shohei Noma, Yoshihide Hayashizaki, Alistair R.R. Forrest and Piero Carninci. | P22 PIERO ontology for analysis of biochemical transformations: Effective implementation of reaction information in the IUBMB Enzyme List. <u>Masaaki Kotera</u> , Yosuke Nishimura, Zen-Ichi Nakagawa, Ai Muto, Yuki Moriya, Shinobu Okamoto, Shuichi Kawashima, Toshiaki Katayama, Toshiaki Tokimatsu, Minoru Kanehisa and Susumu Goto. | T6 Data-driven Science: SGI for Genomics Analysis <u>SGI - James Reaney</u> . |
| 15:45 - 16:15 | | P81 Discovering novel protein-protein interactions by measuring the protein semantic similarity from biomedical literature. Jung-Hsien Chiang and <u>Jiun-Huang Ju</u> . | |
| 16:15 - 16:40 | Coffee Break | | |
| 16:40 - 17:40 | Poster session 1 | | |
| 17:40 - 18:40 | ISCB open business meeting | | |
| 19:00 | Venue closed | | |

Day 2 Tuesday, December 16

| | | | |
|---------------|---|---|---|
| 8:10 - 18:00 | Registration desk open | | |
| | 3F Auditorium | 3F Media hall | 4F Meeting room1 |
| 8:30 - 9:30 | <p>Keynote speech 3 Introduction: Mark Ragan, Institute for Molecular Bioscience, the University of Queensland</p> <p>Limsoon WONG Delivering a quantum leap in the reproducibility, precision, and sensitivity of gene-expression-profile analysis even when sample size is extremely small</p> | | |
| 9:45 - 11:15 | <p>Session 2.1A Session Chair: Wataru Iwasaki, Graduate School of Science, The University of Tokyo</p> | <p>Session 2.1B Session Chair: Yana Bromberg, Rutgers University</p> | <p>Session 2.1C Session Chair: Paul Horton, Computational Biology Research Center, AIST</p> |
| 9:45 - 10:15 | <p>P82 Systematic Approach to Escherichia coli Cell Population Control using a Genetic Lysis Circuit. <u>Chih-Yuan Hsu</u>, Tsu-Chun Yu, Ling-Jiun Lin, Rei-Hsing Hu and Bor-Sen Chen.</p> | <p>P76 IPED2X: A Robust Pedigree Reconstruction Algorithm for Complicated Pedigrees. <u>Dan He</u> and Eleazar Esquin.</p> | <p>S1 Getting involved! Activities of Asia-Pacific Bioinformatics Network (APBioNet) . <u>Asif M. Khan</u>, Tin Wee Tan, Christian Schönbach, Shoba Ranganathan.</p> |
| 10:15 - 10:45 | <p>HL108 On the limits of computational functional genomics for bacterial lifestyle prediction. <u>Eudes Barbosa</u>, Richard Rottger, Anne-Christin Hauschild, Vasco Azevedo and Jan Baumbach.</p> | <p>P09 AucPR: An AUC-based approach using penalized regression for disease prediction with high-dimensional omics data. <u>Wenbao Yu</u> and Taesung Park.</p> | <p>S2 Bioinformatics opportunities in Central Asia. <u>Christian Schönbach</u>, Asif M. Khan, Tin Wee Tan and Shoba Ranganathan.</p> |
| 10:45 - 11:15 | <p>P94 GWAMAR: Genome-wide assessment of mutations associated with drug resistance in bacteria. <u>Michal Wozniak</u>, Jerzy Tiuryn and Limsoon Wong.</p> | <p>P86 CaMoDi: A new method for fast Cancer Module Discovery. <u>Alexandros Manolakos</u>, Idoia Ochoa, Kartik Venkat, Andrea Goldsmith and Olivier Gevaert.</p> | <p>T5 An ABC (Accelerated Bio Computation), using the FPGA based massively parallel architecture RIVYERA. <u>SciEngines, GmbH</u>.</p> |
| 11:15 - 13:00 | Lunch at various restaurants in walk distance of venue | | |
| 13:00 - 14:00 | <p>Keynote speech 4 Introduction: Burkhard Rost, Technical University Munich</p> <p>Janet KELSO What we have learned from sequencing archaic human genomes</p> | | |
| 14:15 - 16:15 | <p>Session 2.2A Session Chair: Koji Tsuda, Graduate School of Frontier Sciences, University of Tokyo</p> | <p>Session 2.2B Session Chair: Kentaro Tomii, Computational Biology Research Center, AIST</p> | <p>Session 2.2C Session Chair: Chung-Yen Lin, Institute of Information Science, Academia Sinica</p> |
| 14:15 - 14:45 | <p>HL106 Detecting Evolutionary Strata on the Human X Chromosome in the Absence of Gametologous Y-Linked Sequences. <u>Rajeev Azad</u>, Ravi Shanker Pandey and Melissa Wilson Sayres.</p> | <p>P56 Implementing a modeling software for animated protein-complex interactions using a physics simulation library. <u>Yutaka Ueno</u>, Shuntaro Ito and Akihiko Konagaya.</p> | <p>P51 LFCseq: a nonparametric approach for differential expression analysis of RNA-seq data. Bingqing Lin, Li-Feng Zhang and Xin Chen.</p> |
| 14:45 - 15:15 | <p>P18 Identification of conserved and polymorphic STRs for personal genomes. <u>Chien-Ming Chen</u>, Chi-Pong Sio, Yu-Lun Lu, Hao-Teng Chang, Chin-Hwa Hu and Tun-Wen Pai.</p> | <p>P67 ReSAPP: Predicting overlapping protein complexes by merging multiple sampled partitions of proteins. <u>So Kobiki</u> and Osamu Maruyama.</p> | <p>P39 Modeling DNA affinity landscape through two-round support vector regression with weighted degree kernels. Xiaolei Wang, <u>Hirovuki Kuwahara</u> and Xin Gao.</p> |
| 15:15 - 15:45 | <p>P66 SoloDel: A probabilistic model for detecting low-frequent somatic deletions from unmatched sequencing data. <u>Junho Kim</u>, Sanghyeon Kim, Hojung Nam, Sangwoo Kim and Doheon Lee.</p> | <p>P29 Discovery of Small Protein Complexes from PPI Networks. <u>Chern Han Yong</u>, Osamu Maruyama and Limsoon Wong.</p> | <p>P71 Supervised learning method for predicting chromatin boundary associated insulator elements. Pawel Badnarz and <u>Bartek Wilczynski</u>.</p> |
| 15:45 - 16:15 | <p>P21 Trans-species learning of cellular signaling systems with bimodal deep belief networks. Lujia Chen, Chunhui Cai, Vicky Chen and <u>Xinghua Lu</u>.</p> | <p>T3 Biological databases and modern computer science: Toxygates and EzCatDB. LEVEL FIVE - <u>Nozomi Nagano</u>, Johan Nyström-Persson, Kazuyoshi Ikeda, Yoshinobu Igarashi, Kenji Mizuguchi, Kentaro Tomii and Shinichi Honiden.</p> | |
| 16:15 - 16:40 | Coffee break | | |
| 16:40 - 17:40 | Poster session 2 | | |
| 18:00 | Venue closed | | |
| 18:30 - 20:00 | Conference dinner at GRAND PACIFIC LE DAIBA | | |

Day 3 Wednesday, December 17

| 8:15 - 18:00 | Registration desk open | | |
|---------------|---|--|------------------|
| | 3F Auditorium | 3F Media hall | 4F Meeting room1 |
| 9:00 - 10:00 | <p>Keynote speech 5 Introduction: Hideo Matsuda, Graduate School of Information Science and Technology, Osaka University</p> <p>Shinya KURODA Temporal coding of insulin action</p> | | |
| 10:15 - 12:15 | <p>Session 3.1A Session Chair: Sachiyo Aburatani, Computational Biology Research Center, AIST</p> | <p>Session 3.1B Session Chair: Martin C. Frith, Computational Biology Research Center, AIST</p> | |
| 10:15 - 10:45 | <p>P58 Robustness analysis on interspecies interaction network for iron and glucose competition between <i>Candida albicans</i> and zebrafish during infection. <u>Che Lin</u>, Chin-Nan Lin, Yu-Chao Wang, Fang-Yu Liu, Yu-Wen Chien, Yung-Jun Chuang, Chung-Yu Lan, Wen-Ping Hsieh and Bor-Sen Chen.</p> | <p>HL111 A Set of Structural Features Defines the Cis-Regulatory Modules of Antenna- Expressed Genes in <i>Drosophila melanogaster</i>. <u>Yosvany López</u>, Alexis Vandenbon and Kenta Nakai.</p> | |
| 10:45 - 11:15 | <p>P23 Dynamics of enhancers in myeloid antigen presenting cells upon LPS stimulation. <u>Alexis Vandenbon</u>, Shunsuke Teraguchi, Osamu Takeuchi, Yutaka Suzuki and Daron Standley.</p> | <p>P70 AKSmooth: Human colon methylome profiling using low-coverage bisulfite sequencing data. <u>Junfang Chen</u>, Pavlo Lutsik, Ruslan Akulenko, Jörn Walter and Volkhard Helms.</p> | |
| 11:15 - 11:45 | <p>HL109 Optimal Implementations for Reliable Circadian Clocks. <u>Yoshihiko Hasegawa</u> and Masanori Arita.</p> | <p>HL115 Bisulfighter: accurate detection of methylated cytosines and differentially methylated regions. <u>Yutaka Saito</u>, Junko Tsuji and Toutai Mituyama.</p> | |
| 11:45 - 12:15 | <p>HL105 Identifying active gene sub-networks from time-course gene expression profiles using TimeXNet. <u>Ashwini Patil</u> and Kenta Nakai.</p> | <p>T4 Ion Reporter™ - Local & Cloud based NGS Data Analysis Solution for Ion Torrent™. <u>Life Technologies Japan Ltd.</u></p> | |
| 12:15 - 13:30 | Lunch at venue | | |
| 13:30 - 15:30 | <p>Session 3.2A Session Chair: Paul Horton, Computational Biology Research Center, AIST</p> | <p>Session 3.2B Session Chair: Tetsuo Shibuya, Institute of Medical Science, The University of Tokyo</p> | |
| 13:30 - 14:00 | <p>T7 Data-driven Science: SGI for Genomics Analysis <u>SGI - James Reaney.</u></p> | <p>P55 An $O(m \log m)$-time algorithm for detecting superbubbles. Wing-Kin Sung, <u>Kunihiko Sadakane</u>, Tetsuo Shibuya, Abha Belorkar and Iana Pyrogova.</p> | |
| 14:00 - 14:30 | <p>HL107 The last straw did not break the camel's back: searching for causative variants of polygenic disease disregards individual predisposing genomic differences. <u>Yana Bromberg</u>, Peter Kahn and Burkhard Rost.</p> | <p>P77 An Efficient Search Algorithm for Finding Genomic-range Overlaps Based on the Maximum Range Length. Ho-Sik Seok, Taemin Song, Sek Won Kong and <u>Kyu-Baek Hwang</u>.</p> | |
| 14:30 - 15:00 | <p>T2 Odaiba as a hub for bringing genome informatics innovation to society and industry. <u>AIST - Jun Sese.</u></p> | <p>P91 HyDA-Vista: Towards Optimal Guided Selection of k-mer Size for Sequence Assembly. Seyed Basir Shariat Razavi, Narjes Sadat Movahedi Tabrizi, Hamidreza Chitsaz and <u>Christina Boucher</u>.</p> | |
| 15:00 - 15:30 | | <p>P34 Aligned Genomic Data Compression via Improved Modeling. <u>Idoia Ochoa</u>, Mikel Hernaez and Tsachy Weissman.</p> | |
| 15:30 - 16:00 | Coffee Break | | |
| 16:00 - 17:00 | <p>Keynote speech 6 Introduction: Kiyoshi Asai, Graduate School of Frontier Sciences, The University of Tokyo</p> <p>Alfonso VALENCIA Cancer Genomics and Computational Biology</p> | | |
| 17:00 - 17:30 | Award ceremony and closing remarks | | |
| 18:00 | Venue closed | | |