POSTERS

- 1. Identification of Lung Disease-associated Novel Transcripts and Alternative Splicing by RNA-sequencing John Brothers II, Bioinformatics Program, Boston University, Boston, MA
- 2. *Tracking Antiviral Responses Following Infection With Lassa Fever Virus* Ignacio Sanchez Caballero, Gracia Bonilla, Jae Yoon Chung, Bioinformatics Program, Boston University, Boston, MA
- 3. *Kinase-specific phosphorylation sites predicted with linear scoring functions* Özgür Demir, Freie Universität Berlin, Germany
- Gene expression profiles in nasal epithelium as a minimally invasive biomarker for the early detection of lung cancer
 Joseph P. Gerrein, Bioinformatics Program, Boston University, Boston, MA
- 5. Decoding ChIPseq with multiple binding events provides site detection with high-resolution and allows estimation of binding cooperativity Antonio Gomes, Bioinformatics Program, Boston University, Boston, MA
- 6. *Genomic Signatures of Carcinogenicity* Daniel Gusenleitner, Harold Gomez, and Tisha Melia, Bioinformatics Program, Boston University, Boston, MA
- Identifying Neighborhoods of Coordinated Gene Expression and Metabolite Profiles Timothy Hancock, Bioinformatics Center, Kyoto University, Japan
- 8. Finding Extensions of Pharmacogenomic Pathways based on Structural Variations by Data Assimilation Takanori Hasegawa, Bioinformatics Center, Kyoto University, Japan
- 9. Protein Complex Prediction Via Improved Verification Methods Using Constrained Domain-domain Matching Morihiro Hayashida, Bioinformatics Center, Kyoto University, Japan
- Comparative analysis of antigenic variant gene families of Plasmodium species
 Kazushi Hiranuka, Bioinformatics Center, Kyoto University, Japan
- 11. *Glycolysis in hepatocytes and hepatomas* Alexandra Iovkova, Max-Delbrück-Center for Molecular Medicine Berlin, Germany

- 12. Prediction of Protein Residue-Residue Contacts Using Conditional Random Field Based on Residue Coevolution Mayumi Kamada, Bioinformatics Center, Kyoto University, Japan
- 13. Supporting scientific workflows a lightweight approach Maciej M. Kańduła, Boku University Vienna, Austria
- 14. Label Propagation through Graph based Feature Reconstruction Masayuki Karasuyama, Bioinformatics Center, Kyoto University, Japan
- 15. Detecting Modulating Factors Causing Gene Network Alterations by Structural Equation Models Yuto Kataoka, University of Tokyo, Japan
- 16. *CySBML: a Cytoscape plugin for SBML* Matthias König, University Medicine Charité Berlin, Germany
- 17. A tool for improving RNA-Seq precision David P. Kreil, Chair of Bioinformatics, Boku University Vienna, Austria
- 18. *Phylogenetic analysis of eicosanoid biosynthesis enzymes* Sayaka Mizutani, Bioinformatics Center, Kyoto University, Japan
- 19. A Clique-Based Method Using Dynamic Programming for Unordered Tree Edit Distance Problem Tomoya Mori, Bioinformatics Center, Kyoto University, Japan
- 20. *FTMAP: Extended Protein Mapping with User-Selected Probe Molecules* Scott E. Mottarella, Bioinformatics Program, Boston University, Boston, MA
- 21. *Extraction of Reaction Sequence Motifs from Metabolic Pathways* Ai Muto, Bioinformatics Center, Kyoto University, Japan
- Comparative and functional analysis of intragenic miRNAs in metazoan genomes
 Yosuke Nishimura, Bioinformatics Center, Kyoto University, Japan
- 23. Challenges in benchmarking joint miRNA gene expression analysis Smriti Shridhar, Boku University Vienna, Austria
- 24. DNase-Seq analysis reveals dynamic effects of growth hormone pulses activating STAT5 on local chromatin structure in male mouse liver George Steinhardt and Andy Rampersaud, Bioinformatics Program, Boston University, Boston, MA
- 25. *Comparative Study on Frequent Itemset Mining-based Biclustering Methods* Kei-ichiro Takahashi, Bioinformatics Center, Kyoto University, Japan

- 26. *Stability and restoration in Canadian lynx and snowshoe hare population cycle* Lisa Uechi, Bioinformatics Center, Kyoto University, Japan
- 27. Finding Mutations in Cancer by Bayesian EM with Haplotype Sequences Naoto Usuyama, University of Tokyo, Japan
- 28. *Mathematical modeling of lipid droplets dynamic in hepatocytes* Christin Wallstab, University Medicine Charité Berlin, Germany
- 29. *Transcriptomic Changes in the Oral Mucosal Epithelium Reflect the Host Response to Indoor Coal Smoke Exposure* Teresa Wang, Bioinformatics Program, Boston University, Boston, MA