## POSTERS

- Systematic Integration of Ligand Chemistry and Protein Resemblance for Novel Drug Repurposing Opportunities Against Ebola Viral Disease Priyanka Banerjee, Charité – University Medicine Berlin and Humboldt University
- Logical Analysis of Perturbation Data
  Katinka Becker, Institute for Mathematics, Free University Berlin
- Chromatin State Patterns at Sex-Biased Transcription Factor Binding Sites Provide Clues to the Mechanisms of Sex-Biased Hepatic Transcriptional Regulation Gracia M. Bonilla, Bioinformatics Graduate Program, Boston University
- Bacterial Strain Tracking Across the Human Skin Landscape
  Allyson L. Byrd, Translational and Function Genomics Branch, National Human Genome Research Institute, NIH and Bioinformatics Graduate Program, Boston University
- Identifying Allele-Specific Expression in Brain Tissue from Parkinson's Disease Patients
   Demetrius DiMucci, Rachael Ivison, David Jenkins, Bioinformatics
   Graduate Program, Boston University
- Stabilization of Rafts in Hepatocyte Canalicular Membrane through Proteins
   Johannes Eckstein, Institute of Biochemistry, Charité – University Medicine Berlin

- Bayesian Method for HLA Genotyping from Whole Genome Sequencing Data
   Shuto Hayashi, Human Genome Center, The Institute of Medical
   Science, The University of Tokyo
- Cataloging VNTRs in the Human Genome
  Yozen Hernandez, Bioinformatics Graduate Program, Boston University
- Role of the DPAGT1/β-catenin/YAP Signaling Network in Oral Squamous Cell Carcinoma Vinay Kartha, Bioinformatics Graduate Program, Boston University
- 10. Characterization of Chromatin-Associated Protein-RNA Complexes Marcin Kolinski, Max-Delbrück-Center for Molecular Medicine and Computational Systems Biology Research Training Group, Humboldt University
- 11. Dynamical Modelling of DNA Damage-Dependent NF-κB Activation Fabian Konrath, Max-Delbrück-Center for Molecular Medicine
- Protein Secondary Structure Prediction: Raising the Bar Gerrit Korff and Ernst Walter Knapp, Macromolecular Modeling Group, Free University Berlin
- Diversity of Marine Giant DNA Viruses
  Tomoko Mihara, Bioinformatics Center, Institute for Chemical Research, Kyoto University
- Khoesan Bushmen Display Distinctive DNA Methylation Landscapes
  Brenna A. LaBarre, Bioinformatics Graduate Program, Boston
  University and Genome Functional Analysis Section, Translational and

Functional Genomics Branch, National Human Genome Research Institute, NIH

- 15. Hepatic lincRNAs: High Promoter Conservation and Dynamic, Sex-Dependent Transcriptional Regulation by Growth Hormone (GH) Tisha Melia, Bioinformatics Graduate Program, Boston University
- Advances in Cancer Systems Biology with Supercomputer
  Satoru Miyano, Human Genome Center, The Institute of Medical
  Science, The University of Tokyo
- Accurate Detection of Small Proportion of Cancer through Deep Sequencing Data Takuya Moriyama, Human Genome Center, The Institute of Medical Science, The University of Tokyo
- Chromatin Accessibility Alterations Due to Plasma Growth Hormone Pulses in Male Mouse Liver Andy Rampersaud, Bioinformatics Graduate Program, Boston University
- GTEx Assignment of Cancer Cell Lines by Tissue of Origin Heather Selby, Bioinformatics Graduate Program, Boston University and Dana-Farber Cancer Institute
- Gene Networks from Time Series with Spike-and-Slab Feature Selection
   Edgar Steiger, Max Planck Institute for Molecular Genetics and Computational Molecular Biology Group, Berlin, Germany
- 21. Analysis of Transcription Factors HNF6 and CUX2 Reveal a Possible Molecular Mechanism for Sex-specific Gene Expression in Mouse Liver

George F. Steinhardt IV, Bioinformatics Graduate Program, Boston University

- DemFeature: Upgraded from DemPred
  Hao Wang, Institute of Chemistry and Biochemistry, Free University of Berlin
- 23. An Improving SVM-Based Prediction for Dicer Cleavage Site Using Loop/Bulge Length
   Yu Bao, Bioinformatics Center, Institute for Chemical Research, Kyoto University
- Compiling a Minicircle Genome for Trypanosoma Brucei
  Tyler Faits and Tian Yu, Bioinformatics Graduate Program, Boston
  University
- Balanced Benchmarks Show Simple Approaches Succeed with Growing Numbers
   Maciej M. Kańduła and David P. Kreil, Boku University Vienna
- 26. *Peturbation Experiments Reveal Internal Interactions* Torsten Gross, Institute for Theoretical Biology, Humboldt University
- 27. Implementation of the Sodium-Calcium Exchanger in a Model of the Rabbit Ventricular Cardiomyocyte with Spatially Resolved Calcium Cycling
   Janine Vierheller, Stephen Gilbert, Wilhelm Neubert, Chamakuri
   Nagaiah and Martin Falcke
   Max-Delbrück Centre for Molecular Medicine

- 28. A Computational Method that Identifies Repositioned Drug Candidates by Finding Inversely Correlated Cellular Functions Under Disease and Drug Perturbations Hsiao-Rong Chen, Zhenjun Hu, and Charles DeLisi, Bioinformatics Graduate Program, Boston University and Graduate Program in Translational Molecular Medicine, Boston University School of Medicine
- 29. Breadth-first Search Based Approach to Enumerating Chemical Compounds Containing Outerplanar Fused Benzen Ring Substructures Jira Jindalertudomdee, Bioinformatics Center, Institute for Chemical Research, Kyoto University
- 30. *PathoAssem: Genome Assembly from Metagenomic Samples* Demarcus Briers, Sean Corbett, Junmin Wang, William Evan Johnson, and Gary Benson, Bioinformatics Graduate Program, Boston University and Department of Medicine, Boston University School of Medicine
- 31. Effects of Structural Variation on Fetal Hemoglobin Expression Levels in Different Populations Katherine Norwood, Elmutaz M. Shaikho Elhaj Mohammed, and Anastasia Gurinovich, Bioinformatics Graduate Program, Boston University