

POSTERS

1. *A comprehensive comparison of Gene Set Projection (GSP) methods*
Ali Amin-Mansour, Rui Hong, Boston University
2. *A fluctuation theorem for time series of signal-response models with the backward transfer entropy*
Andrea Auconi, Humboldt University Berlin
3. *Derivation of a bronchial airway gene expression signature associated with FEV₁ decline*
Elizabeth Becker, Boston University
4. *Principles of cooperative transcription factor binding revealed by nextPBM*
David Bray, Boston University
5. *Predicting microbial ecology from shotgun metagenomic data*
Aaron Chevalier, Anthony Federico, Jamie Strampe, Boston University
6. *Identifying minimal predictive networks from random forests with BowSaw*
Demetrius DiMucci, Boston University
7. *STASNet; Reverse engineering signaling networks from perturbation data*
Mathurin Dorel, Charité – University Medicine & Humboldt University
8. *Model reduction of a small metabolic-genetic network*
Neveen Eshtewy, Humboldt University Berlin
9. *A proteome allocation model of phototrophic growth: metabolic strategies in a light-limited chemostat*
Marjan Faizi, Humboldt University Berlin
10. *3D centroid extraction of primary mesenchyme cells in confocal images*
Dakota Hawkins, Boston University
11. *Know thy cells: the classification of tumor models by tissue, disease and sex*
Heather Selby, Boston University
12. TBA
David Jenkins, Boston University
13. *Correlating microbial associations for the microbial interaction network database*
Dileep Kishore, Boston University
14. *Capturing the differences between humoral immunity in the normal and tumor environments from Repertoire-Seq of B-cell receptors using supervised machine learning*
Hiroki Konishi, University of Tokyo
15. *Development of viral genome classification method based on sequence similarity*
Megumi Kuronishi, Kyoto University

16. *Pan-cancer module network analysis for identifying dominating networks across human cancers*
Chun-Yu Lin, JSPS Postdoctoral Fellow, Kyoto University
17. *Long noncoding RNA (lncRNA)-Protein coding gene (PCG) regulatory networks responsive to diverse xenobiotics in rat liver*
Kritika Karri, Boston University
18. *Single-cell analysis uncovers a vast diversity in intracellular viral defective interfering RNA content affecting influenza A virus replication*
Lam-Ha Ly, Max Planck Institute for Molecular Genetics
19. *Developing a predictive model for host response to Ebola infection*
Jeffery Maurer, Boting Ning, Nicholas O'Neill, Boston University
20. *Mutation calling from multiple tumor sequence data sets*
Takuya Moriyama, University of Tokyo
21. *Elucidating the gene-regulatory network in X-chromosome inactivation*
Verena Mutzel, Max Planck Institute for Molecular Genetics
22. *SIMPLE: sparse interaction model over peaks of molecules for fast, interpretable metabolite identification from tandem mass spectrometry*
Dai-Hai Nguyen, Kyoto University
23. *Co-existing feedback loops generate tissue-specific circadian rhythms*
Patrick Pett, Humboldt University Berlin
24. *Global landscape of mouse and human cytokine transcriptional regulation*
Sebastian Carrasco Pro, Boston University
25. *From a snapshot to dynamics of the cell cycle*
Daniel Schwabe, Max Delbrück-Center for Molecular Medicine
26. *Computational analysis of the impact of MYCN on the energy metabolism in neuroblastoma*
Mareike Simon, Max Delbrück Center for Molecular Medicine
27. *Modeling the impact of double X-dosage on signaling pathways implicated in pluripotency*
Zeba Sultana, Max Planck Institute for Molecular Genetics
28. *Single cell analysis reveals All-or-None G1 arrest decisions upon TGF β stimulation*
Guoyu Wu, Max Planck Institute for Molecular Genetics
29. *Genomic characterization of Medusavirus, a new giant virus infecting Acanthamoeba*
Genki Yoshikawa, Kyoto University
30. *Aligning gene expression time series with invariance to uniform scaling with multiple scaling factors*
Coleman Yu, Kyoto University