

IBSB 2018 AGENDA
BOSTON UNIVERSITY
EICHENBAUM COLLOQUIUM ROOM
CENTER FOR INTEGRATED LIFE SCIENCE AND ENGINEERING (CILSE)
610 COMMONWEALTH AVENUE, BOSTON, MA

Sunday, July 15

5 pm - 7 pm Reception, CILSE Patio

Monday, July 16

8:30 BREAKFAST (CILSE Lobby)

9:15 OPENING REMARKS
Professor Thomas D. Tullius
Director, Bioinformatics Graduate Program, Boston University

SESSION I

9:30 *Know thy cells: the classification of tumor models by tissue, disease and sex*
Heather Selby, Boston University

10:00 *A fluctuation theorem for time series of signal-response models with the backward transfer entropy*
Andrea Auconi, Humboldt University Berlin

10:30 *SIMPLE: sparse interaction model over peaks of molecules for fast, interpretable metabolite identification from tandem mass spectrometry*
Dai-Hai Nguyen, Kyoto University

11:00 BREAK

11:15 *A mathematical model of proteome allocation in cyanobacteria to study regulation of phototrophic growth*
Marjan Faizi, Humboldt University Berlin

11:45 *Derivation of a bronchial airway gene expression signature associated with FEV₁ Decline*
Elizabeth Becker, Boston University

12:15 *Leveraging phylogeny tree information for somatic mutation calling*
Takuya Moriyama, University of Tokyo

12:45 BREAK

3:30 – 5:30 Poster Session (EVEN numbers)
24 Cummington Mall, Life Science and Engineering Building (LSEB Lobby)

Tuesday, July 17

8:30 BREAKFAST (CILSE Lobby)

SESSION II

9:30 *Discriminative models between normal and tumor immunity against repertoire sequences using convolutional neural networks*
Hiroki Konishi, University of Tokyo

10:00 *Long noncoding RNA (lncRNA)-Protein coding gene (PCG) regulatory networks responsive to diverse xenobiotics in rat liver*
Kritika Karri, Boston University

10:30 *Reverse engineering of neuroblastoma signaling networks*
Mathurin Dorel, Charité University Medicine & Humboldt University

11:00 BREAK

11:15 *Correlating microbial associations for the microbial interaction network database*
Dileep Kishore, Boston University

11:45 *Development of viral genome classification method based on sequence similarity*
Megumi Kuronishi, Kyoto University

12:15 POSTER SESSION & LUNCH (ODD numbers)
24 Cummington Mall, Life Science and Engineering Building (LSEB Lobby)

SESSION III (Session Chair: G. Benson)

3:00 *Single cell analysis reveals All-or-None G1 arrest decisions upon TGF β stimulation*
Guoyu Wu, Max Planck Institute for Molecular Genetics, Berlin

3:30 *Identifying minimal predictive networks from random forests with BowSaw*
Demetrius DiMucci, Boston University

5:00 Clambake
Bus leaves 24 Cummington Mall for ferry to Spectacle Island

Wednesday, July 18

9:30 BREAKFAST

SESSION IV

10:00 *Elucidating the gene-regulatory network in X-chromosome inactivation*
Verena Mutzel, Max Planck Institute for Molecular Genetics, Berlin

10:30 *Pan-cancer module network analysis for identifying dominating networks across human cancers*
Chun-Yu Lin, JSPS Postdoctoral Fellow, Kyoto University

11:00 BREAK

11:15 *3D centroid extraction of primary mesenchyme cells in confocal images*
Dakota Hawkins, Boston University

11:45 *Co-existing feedback loops generate tissue-specific circadian rhythms*
Patrick Pett, Humboldt University Berlin

12:15 BREAK

SESSION V (Session Chair: G. Benson)

3:30 *Genomic characterization of Medusavirus, a new giant virus infecting Acanthamoeba*
Genki Yoshikawa, Kyoto University

4:00 *Single cell gene expression in the cell cycle*
Daniel Schwabe, Max Delbrück Center for Molecular Medicine

4:30 *Principles of cooperative transcription factor binding revealed by nextPBM*
David Bray, Boston University

5:00 Closing Remarks

5:30 Farewell Barbecue
School of Communication Lawn at 640 Commonwealth Avenue