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 FEV<sub>1</sub> 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 (IncRNA)-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 TGFβ 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