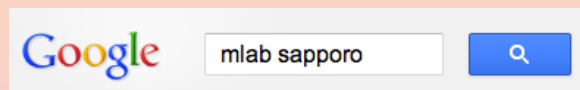


August 6 - 7, 2012

Creative Research Institution, Hokkaido University

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All researchers and students who are interested
in the talks below are welcome.



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— 20 inspiring talks —

Masashi Sugiyama (Tokyo Institute of Technology)

Recent Advances in Divergence Estimation: Theory, Algorithm, and Application

Shanfeng Zhu (Fudan University)

Efficient Semi-Supervised MEDLINE Document Clustering

Masayuki Karasuyama (Kyoto University)

Label Propagation through Graph-based Feature Reconstruction

Timothy Hancock (Kyoto University)

Imposing Network Structures on Feature Selection on Experimental Data

Jun Sese (Tokyo Institute of Technology)

Gene Expression Analysis in Polyploid Species using Next-Generation Sequencer

Yuichi Shiraishi (The University of Tokyo)

An Empirical Bayesian Framework for Mutation Detection from Cancer Genome Sequencing Data

Hirotoshi Saigo (Kyushu Institute of Technology)

Learning from Treatment History to Predict Response to Anti-HIV therapy

Yoshihiro Yamanishi (Kyushu University)

Machine Learning Methods to Analyze and Infer Drug-Target Interaction Networks

Hisashi Kashima (The University of Tokyo)

Link Prediction Methods for Bioinformatics

Canh Hao Nguyen (Kyoto University)

Latent Feature Kernels for Link Prediction

Motoki Shiga (Toyohashi University of Technology)

Efficient Semi-Supervised Learning on Multiple Graphs

Satoshi Morinaga (NEC)

Factorized Asymptotic Bayesian Inference for Learning Latent Variable Models

Marco Cuturi (Kyoto University)

Distances and Kernels on Discrete Structures

Hiroki Arimura (Hokkaido University)

Efficient Enumeration of Bounded-Size Subtrees in a Tree and Its Application to Tree Mining with Proximity Constraint

Jean-Philippe Vert (Mines ParisTech)

Structured Feature Selection for Genomic Data

Ichigaku Takigawa (Hokkaido University)

Learning Sparse Linear Models over Subgraph Indicators

Yasuo Tabei (JST ERATO)

Space-Efficient Multibit Tree for Large-Scale Chemical Fingerprint Searches

Koji Tsuda (AIST)

Fast Similarity Search with Succinct Trees

Kengo Sato (Keio University)

Simultaneous Aligning and Folding of RNA Sequences via Dual Decomposition

Atsuyoshi Nakamura (Hokkaido University)

Frequent Pattern Mining for Families of Dispersed Repeats in DNA Sequences