



2014 IEEE International Workshop on Genomic Signal Processing and Statistics at **GlobalSIP**

Atlanta, Georgia, USA, December 3-5, 2014

Registration and welcome reception

Venue: Georgia Tech Hotel & Conference Center (800 Spring St. NW, Atlanta, GA 30308)
Location: Main Lobby of Conference Center (2nd floor of Georgia Tech Hotel)
Opening times: December 2, Tuesday, 14:30–17:30
December 3 & 4, Wednesday & Thursday, 08:00–17:30
Welcome reception: December 2, 18:00–19:30 first floor

Conference rooms

GlobalSIP Plenary Talks: Grand Ball Room
All GENSIPS sessions: Conference Room 6

December 3

- 8:00 – 9:00 **GlobalSIP Plenary Talk** – Vincent Poor, Princeton University
Privacy-Utility Tradeoffs for Information Sources
- 9:00 – 9:15 Break
- 9:15 – 10:15 **GENSIPS Keynote** – Daniel Brat, MD, PhD, Emory University (Session Chair: Lee Cooper)
Advancing Precision Medicine in Adult Gliomas Using Data from The Cancer Genome Atlas
- 10:15 – 11:15 **OS1: Genomic Sequence Analysis** (Session Chair: Mohammadmahdi Rezaei Yousefi)
- (1) Optimal Haplotype Assembly with Statistical Pruning
Shreepriya Das; Haris Vikalo
University of Texas, Austin
 - (2) Improved Time-domain Approaches for Locating Exons in DNA Using Zero-phase Filtering
Ismail M. El-Badawy; Ashraf M. Aziz; Safa Gasser; Mohamed Khedr
Arab Academy for Science
 - (3) Relating Digital Information, Thermodynamic Stability, and Classes of Functional Genes in E. coli
Dawit Andualem Nigatu; Werner Henkel; Patrick Sobetzko; Georgi Muskhelishvili
Jacobs University Bremen
 - (4) De novo Transcriptome Assemblies and Annotation for Pacific Whiteleg Shrimp
Noushin Ghaffari; Osama Arshad; Hyundoo Jeong; John Thiltges; Michael Criscitiello; Byung-Jun Yoon; Aniruddha Datta; Charles Johnson
Texas A&M University; Hamad bin Khalifa University, Qatar
- 11:15 – 11:30 Tea Break
- 11:30 – 12:30 **OS2: Regression and Prediction** (Session Chair: Ranadip Pal)
- (1) Predicting Age at Loss of Ambulation in Duchenne Muscular Dystrophy with Deep Phenotypic Measures
Yinxue Wang; Yue Wang; Guoqiang Yu; Luca Bello; Eric Hoffman
Virginia Tech; Children's National Medical Center
 - (2) Fast Proximal Gradient Optimization of the Empirical Bayesian Lasso for Multiple Quantitative Trait Locus Mapping
Indika Appuhamilage; Anhui Huang; Xiaodong Cai
University of Miami

(3) Analysis of Multivariate Drug Sensitivity Dependence Structure using Copulas

Saad Haider; Ranadip Pal

Texas Tech University

(4) Multi-objective Optimization of Ensemble of Regression Trees using Genetic Algorithms

Qian Wan; Ranadip Pal

Texas Tech University

12:30 – 13:30 Lunch on Your Own

13:30 – 14:30 **Invited Highlights HL1** (Session Chair: May D. Wang)

(1) Inference of Correlated Hidden Markov Models with Application to ChIP-Seq Compendium Data

Steve Qin

Emory University

(2) Crowdsourcing Confidence Intervals

Gari Clifford

Emory University

(3) Novel Genotype-phenotype Associations in Human Cancers Enabled by Advanced Molecular Platforms and Computational Analysis of Whole Slide Images

Lee Cooper

Emory University

14:30 – 15:45 **OS3: Sequencing Data Analysis** (Session Chair: Guoqiang Yu)

(1) Towards Block-based Compression of Genomic Data with Random Access Functionality

Tom Paridaens; Yves Van Stappen; Wesley De Neve; Peter Lambert; Rik Van de Walle

Ghent University

(2) A Feasible Roadmap to Identifying Significant Intercellular Genomic Heterogeneity in Deep Sequencing Data

Guoqiang Yu; Niya Wang; Roger Wang; Sean Wang; Yue Wang

Virginia Tech; University of Michigan; University of Maryland

(3) Detecting Differentially Methylated mRNA from MeRIP-Seq with Likelihood Ratio Test

Lin Zhang; Jia Meng; Hui Liu; Xiaodong Cui; Shao-Wu Zhang; Yidong Chen; Yufei Huang

China University of Mining and Technology; Xi'an Jiaotong-Liverpool University; Northwestern Polytechnical University; UT Health Science Center at San Antonio; UT San Antonio

(4) Differential Analysis of RNA Methylome with Improved Spatial Resolution

Yu-Chen Zhang; Shao-Wu Zhang; Lian Liu; Lin Zhang; Hui Liu; Xiaodong Cui; Yufei Huang; Jia Meng

Northwestern Polytechnical University; China University of Mining and Technology; Xi'an Jiaotong-Liverpool University; UT San Antonio

(5) The Impact of RNA-seq Alignment Pipeline on Detection of Differentially Expressed Genes

Cheng Yang; Po-Yen Wu; John Phan; May Dongmei Wang

Georgia Tech; Emory University

15:45 – 18:00 **Tutorial T1** (Session Chair: Gari Clifford)

(1) Scalable Big Data in Global Health

Gari Clifford

Emory University

(2) Analysis of Single-cell Flow Cytometry Data

Peng Qiu

Georgia Tech and Emory University

18:00–19:30 **Reception**, Grand Ball Room, second floor

December 4

- 8:00 – 9:00 **GlobalSIP Plenary Talk** – Xiaoming Huo, Georgia Tech
Yet another Talk on the (Statistical) Challenges of Big Data
- 9:00 – 9:15 Tea Break
- 9:15 – 10:15 **GENSIPS Keynote** – Jie Liang, University of Illinois Chicago (Session Chair: May D. Wang)
Multiscale Spatial and Temporal Signaling and Patterning of Cells and Tissues: Stochastic Control Networks, 4D Nucleosome, and Tissue Wound Healing
- 10:15 – 11:15 **OS4: Gene Regulatory Networks** (Session Chair: Nidhal Bouaynaya)
- (5) Computationally Efficient Experimental Design Strategy for Reducing Gene Network Uncertainty
Roozbeh Dehghannasiri; Byung-Jun Yoon; Edward Dougherty
Texas A&M University; Hamad bin Khalifa University, Qatar
 - (1) Optimal Bayesian Cancer Prognosis with Model-Constrained Robust Intervention
Lori Anne Dalton; Mohammadmahdi Rezaei Yousefi
Ohio State University
 - (2) Optimal Fault Detection in Stochastic Boolean Regulatory Networks
Arghavan Bahadorinejad; Ulisses Braga-Neto
Texas A&M University
 - (3) Kernel Reconstruction: an Exact Greedy Algorithm for Compressive Sensing
Belhassen Bayar; Nidhal Bouaynaya; Roman Shterenberg
Rowan University; University of Alabama at Birmingham
- 11:15 – 11:30 Tea Break
- 11:30 – 12:30 **Invited Highlights HL2** (Session Chair: Ulisses Braga-Neto)
- (1) Cross-validation under Separate Sampling: Strong Bias and How to Correct It
Ulisses Braga-Neto
Texas A&M University
 - (2) Impact of RNA-Seq Data Analysis Pipelines on Gene Expression Estimation in SEQC Project by FDA-Led MAQC-III
May D Wang
- 12:30 – 13:30 Lunch on Your Own
- 13:30 – 14:30 **OS5: High-Dimensional Data Analysis** (Session Chair: Lori Anne Dalton)
- (1) A Statistical Approach to Identifying Significant Transgenerational Methylation Changes
Ye Tian; Yi Fu; Guoqiang Yu; Bai Zhang; Yue Wang
Google Inc; Virginia Tech
 - (2) A Naive-Bayes Approach to Bolstered Error Estimation in High-Dimensional Spaces
Xingde Jiang; Ulisses Braga-Neto
Texas A&M University
 - (3) Optimal Bayesian Feature Selection on High Dimensional Gene Expression Data
Ali Foroughi pour; Lori Anne Dalton
Ohio State University
 - (4) Robust Detection of Periodic Patterns in Gene Expression Microarray Data using Topological Signal Analysis
Saba Emrani; Hamid Krim
North Carolina State University

- 14:30 – 15:30 **OS6: Networks and System Modeling** (Session Chair: Xiaoning Qian)
- (1) Stochastic Coordinate Descent Frank-Wolfe Algorithm for Large-Scale Biological Network Alignment
Yijie Wang; Xiaoning Qian
Texas A&M University
 - (2) A Network-based Analysis of Ischemic Stroke using Parallel microRNA-mRNA Expression Profiles
Yingying Wang; Yunpeng Cai
Shenzhen Institutes of Advanced Technology, Chinese Academy of Sciences
 - (3) Sensitivity Analysis For Drug Effect Study: an NF-kB Pathway Example
Xiangfang Li; Sunday Ogedengbe; Lijun Qian; Edward Dougherty
Prairie View A&M University; Texas A&M University
 - (4) Modeling Ribosome Dynamics to Optimize Heterologous Protein Production in Escherichia coli
Scott Vu; Adriano Bellotti; Christopher Gabriel; Hayden Brochu; Eric Miller; Donald Bitzer; Mladen A Vouk
North Carolina State University
- 15:30 – 15:45 Tea Break
- 15:45 – 18:00 **Tutorial T2** (Session Chair: Peng Qiu)
- (1) Drug Sensitivity Prediction
Ranadip Pal
Texas Tech University
 - (2) Imaging Informatics
Yue Hou
Emory University
- 18:00–19:30 **Reception**, first floor

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Floor Map

