SOCIETY OF STATISTICS, COMPUTER AND APPLICATIONS

(https://ssca.org.in)

Web Workshop

DATE: 08-MAY-2021 (SATURDAY)

India: 0530 PM – 0845 PM
USA: 0800 AM – 1115 AM EST; 0700 AM – 1015 AM CST; 0500 AM– 0815 AM PST
UK: 0100 PM – 0415 PM BST

Topic: Statistical challenges in the analysis of high-dimensional biomedical data

Resource Person: Dr. Ramana V. Davuluri, Professor
Department of Biomedical Informatics, Stony Brook Cancer Center, Stony Brook, NY 11794, USA

Description:

The major objective of the workshop is to discuss opportunities and challenges for Statisticians in the analyses of massive high-dimensional datasets produced by recent Biotechnologies. High-throughput experimental methods, such as those that use massively parallel sequencing, are increasingly applied, generating multiple –omics (e.g., genomic, epigenomic, transcriptomic, etc.) data, for investigating problems ranging from basic biomedical research to clinical encounters. Indeed, application of these technologies by researchers around the world has been accumulating large volumes of -omics data on hundreds of bio-specimens. In addition, national collaborative efforts are building extensive databases, hosting clinical data on millions of patients, for example, individuals tested for COVID-19. However, statistical analysis and integration of data from different platforms (e.g., NGS, microarray, etc.) and various data-types (e.g., genomic, epigenomic, transcriptomic, clinical data from Electronic Health Records (EHR), etc.) remains a major challenge.

This workshop will begin with an overview of exciting developments in genomics over the past decade, followed by three presentations on statistical and computational methods for (a) early severity prediction of COVID-19, and (b) 3D genome data analyses, and (c) deep learning on high-dimensional biomedical datasets – a data integration strategy that combines clinical and omics data. Our goal is to enable future research and collaborative opportunities between statisticians and bioinformatics practitioners.

For Registration, click the link:

https://tinyurl.com/yxa6bkck

Click the links below for
Workshop Schedule
Registration Fee etc.
Speaker Bios

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Workshop Schedule (08-May-2021)

Time in India	Speaker	Topic
0530 PM - 0545 PM	Dr. Ramana V. Davuluri Stony Brook Cancer Center, Stony Brook, USA	Opening
Ramana.Davuluri@stonybrookmedicine.edu		
0545 PM - 0630 PM	Dr. Richard Moffitt Stony Brook University, Stony Brook, USA	Statistical challenges in analysis of EHR data; clinical characterization and early severity prediction of COVID-19
richard.moffitt@stonybrookmedicine.edu		
0630 PM - 0715 PM	Dr. Yanrong Ji Northwestern University, Chicago, IL, USA	Deep representation learning on high-dimensional biomedical datasets
yanrongji2021@u.northwestern.edu		
0715 PM - 0800 PM	Dr. Ferhat Ay Centre for Cancer Immunotherapy, LaJolla Institute for Immunology, LaJolla, CA, USA	Computational methods for studying the 3D organization of the human genome
ferhatay@lji.org		
0800 PM - 0830 PM	All Participants	Discussion
0830 PM - 0845 PM	SSCA	Closing

Registration Fee

All those participants, especially the research scholars, desirous of getting a participation certificate, may deposit online a sum of Rs. 100 (Rupees one hundred only) towards registration. The details of the bank account are given below: For all others, there is **NO** registration sum to be paid.

Account Details:
Payee's Account Name: Society of Statistics, Computer and Applications
Savings Bank Account Number: 430010100000648
IFSC Code: UTIB0000430
Bank Address: C.R. Park, New Delhi

Register at: **https://tinyurl.com/yxa6bkck**

Contact for queries A. Dhandapani, Vice President, SSCA (dhandapani.appavoo@gmail.com)

V.K. Gupta
President, SSCA

Speaker Bios:

Ramana Davuluri got his MSc and PhD from IASRI, under the mentorship of Dr. VK Gupta. His Ph.D. thesis in Design of Experiments fetched him Young Scientist Merit Certificate from the Indian Science Congress Association. He briefly worked as Asst Professor at Acharya NG Ranga Agricultural University before moving to USA as a Postdoctoral Fellow in Bioinformatics. He held faculty positions at The Ohio State University, Columbus, Ohio (2001-2007), The Wistar Institute, Philadelphia, PA (2007-2014), before joining Northwestern University Feinberg School of Medicine, Chicago as Full Professor with tenure and Director of Cancer Informatics in the Robert H Lurie Comprehensive Cancer Center. Ramana recently moved to Dept of Biomedical Informatics, Stony Brook University School of Medicine and Cancer Center as Full Professor. He is currently serving as a regular member of Biomedical Informatics, Library and Data Science (BILDS) Review Committee, National Library of Medicine, NIH. Continuously funded by National Institutes of Health, Ramana leads a group of PhD-level Statisticians and Computer Scientists, with primary focus on developing innovative data-science solutions for health and biomedical research.

Richard Moffitt received his B.S. and Ph.D. from the Dept. of Biomedical Engineering at Georgia Tech and Emory University, and completed his postdoctoral research in the Lineberger Cancer Center at the University of North Carolina. He joined the BMI department at Stony Brook University as an Assistant Professor in 2017. The Moffitt lab uses bioinformatics and engineering approaches to improve scientific understanding and patient care in cancer. Dr. Moffitt's current research projects include (A) Predictive models in pancreatic adenocarcinoma, with a focus on precision medicine and patient response to therapy; (B) Mixture modeling and next generation sequencing techniques to study tumor, stromal and immune contributions to tumor biology; (C) Translational bioinformatics and biostatistics methods development for tumor biology and medical data.

Yanrong Ji ("Jerry" as he is popularly known) received his B.S. in Biochemistry from University of Wisconsin-Madison. He is an Insight Health Data Science Fellow and PhD student at Northwestern University. His thesis project involves developing of computational tools for gene regulation and cancer precision therapy, including cancer subtyping, novel biomarker and drug discovery studies, via multi-omics data analysis and application of machine learning/deep learning algorithms and data science techniques. He has published 5 research papers, lead developer of DNABERT – pre-trained Bidirectional Encoder Representations from Transformers model for DNA-language in genome. He is expected to graduate soon and will join CVS Health as Data Science Advisor, Clinical Trial Services.

Ferhat Ay received his B.S. degrees in Computer Engineering and Mathematics both from Middle East Technical University (METU), Turkey in 2007 and his Ph.D. in Computer Science at the University of Florida in 2011. He subsequently joined the Department of Genome Sciences at the University of Washington as a Computing Innovation Fellow awarded by Computing Research Association and National Science Foundation (NSF). He was a Research Assistant Professor in the Department of Preventive Medicine-Health and Biomedical Informatics at Northwestern University in 2015 before establishing his lab at the La Jolla Institute for Allergy and Immunology (LJI) in 2016. He is currently the Institute Leadership Associate Professor of Computational Biology at LJI, an adjunct faculty at the UC San Diego School of Medicine, and an affiliate faculty of the UCSD Bioinformatics Ph.D. Program. His primary research areas are bioinformatics, computational biology, epigenomics, and regulatory genomics. His lab works on understanding the relationship between three-dimensional genome architecture and gene regulation in the context of different diseases including cancer, malaria, and immune-mediated diseases. He is a recipient of an R35 MIRA grant from NIH and serves as an Associate Editor of PLoS Computational Biology.