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MIDSOUTH COMPUTATIONAL BIOLOGY & BIOINFORMATICS SOCIETY

UAB INFORMATICS INSTITUTE
The University of Alabama at Birmingham

16th Annual Conference of the Midsouth Computational Biology & Bioinformatics Society

MCBIOS 2019

Informatics for Precision Medicine

March 28-30, 2019
Hilton Birmingham at UAB
Birmingham, AL

Table of Content

Welcome Letter

Welcome to the 16th annual conference of the Midsouth Computational Biology and Bioinformatics Society (MCBIOS) on the campus of the University of Alabama at Birmingham! MCBIOS’19 is a premier, annual gathering for bioinformaticians, computational biologists and biological data scientists throughout the Midwest and Southeast regions of the United States. On behalf of MCBIOS and the MCBIOS ’19 organizing committee, I hope you will have a pleasant time in and around Birmingham.

This year, we will meet to focus the conference theme, “Informatics for Precision Medicine,” to showcase research breakthroughs, tool development and biomedical applications in this rapidly emerging topic of national interest. Aiming to improve patient response, biomedical researchers in precision medicine increasingly resort to analyzing individual-level data, including those collected from multiple omics platforms, clinical visits or mobile devices. This trend brings forth new informatics challenges in biomedical data representation, data standardization, data integration, data processing, data modeling, data sharing, knowledge discovery, and translational applications. I am excited that many of you, experts in various informatics subjects above, will report at the conference biomedical data science research advancements in clinical genomic knowledge-base, healthcare artificial intelligence (AI) decision making software, disease therapeutic simulation algorithms, mobile health apps and many more subjects. Our work today will profoundly impact how we and our children interact with healthcare systems of the future.

While in Birmingham, we hope you enjoy the beautiful spring weather, fine dining, national historical sites, state parks and Southern hospitality.

We thank our various sponsors, including UAB School of Medicine, UAB Informatics Institute, O’Neal Comprehensive Cancer Center at UAB, UAB Center for Clinical and Translational Science, UAB Hugh Kaul Precision Medicine Institute, and BBVA Compass Bank, and particularly, MCBIOS for their generous support of our conference.

Again, a warm welcome and my very best wishes to an enjoyable stay in Birmingham!

Sincerely yours,

Jake Y. Chen, Ph.D.
MCBIOS '19 General Chair
Birmingham, AL

About MCBIOS

Mission

The mission of MCBIOS is to foster networking and collaboration promote the professional development of members and supporting our student members.

Objectives

- Advance the understanding of bioinformatics and computational biology
- Bring together scientists of various backgrounds and disciplines
- Facilitate the collaboration of researchers with similar or complementary backgrounds to solve biological, health and/or medical problems
- Promote education in bioinformatics and computational biology
- Inform the general public on the results and implications of current research in bioinformatics and computational biology
- Promote other activities that will contribute to the development of bioinformatics and computational biology MCBIOS Bylaws Current version (Amended Feb 20, 2010)

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Ujwani Nukala, Student Member, Ph.D. Candidate, UALR/UAMS joint bioinformatics program.

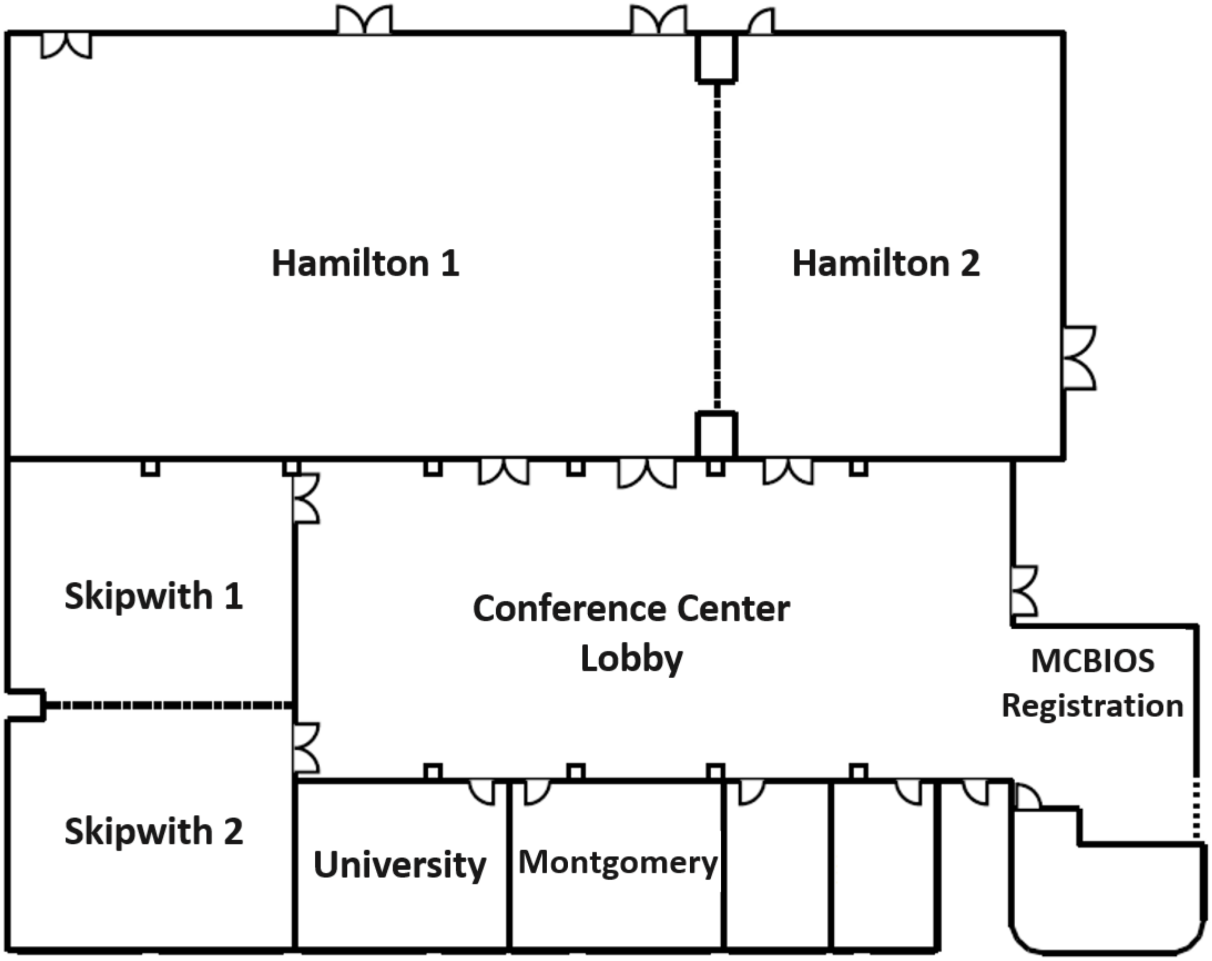
About MCBIOS 2019

March 28-30, 2019

Hilton Birmingham at UAB

Birmingham, AL

Informatics for Precision Medicine



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MCBIOS 2019 Program-at-a-Glance

Day 1: Thursday, March 28, 2019

9:00 a.m. – 4:00 p.m. Registration and Poster Setup

9: 00 a.m. – 1:00 p.m.	**Pre-conference Program:** UAB ATTIS at MCBIOS 2019		
MCBIOS 2019 Meeting Begins **Registration in the Conference Lobby**			
1:00 – 4:00 p.m.	**Tutorial 1** Single-Cell Genomic Data Analysis **Hamilton 2**	**Tutorial 2** Metabolomics Data Analysis **Skipwith 2**	**Student Session:** Career Development **Skipwith 2**
4:00 – 5:00 p.m.	**Poster Session / Coffee Break** **Conference Lobby, Hamilton 1**		
5:00 – 6:00 p.m.	**Keynote Talk** **Semi-Supervised Learning to the Rescue: Towards Deep Understanding of Coding Variant Effects** **Presenter: Predrag Radivojac, Ph.D., Northeastern University** **Hamilton 1**		
6:00 – 6:30 p.m.	**Poster Session / Coffee Break** **Conference Lobby, Hamilton 1**		
6:30 – 8:00 p.m.	**Dinner (Opening Reception)** **Hamilton 1**		

Day 2: Friday, March 29, 2019

8:00 a.m. – 4:00 p.m. Registration

	Track 1: Clinical Genomics **Hamilton 2**	**Track 2:** Drug Discovery and Informatics **Skipwith 2**	**Young Scientist Excellence Award** **Skipwith 1**
8:00 – 9:20 a.m.	**Breakout Session 1** Integration of Omics Data with Clinical Information Session Chair: Chindo Hicks, LSU	**Breakout Session 3** In Silico Drug Discovery in the Era of Precision Medicine Session Chair: Zhichao Liu, NCTR/FDA	**Postdoc Award Presentation**

9:25 - 10:45 a.m.	**Breakout Session 2** Omics Data in Real-world Settings Session Chair: Dong Wang, NCTR/FDA	**Breakout Session 4** Computer-Aided Drug Discovery and Development Session Chair: Daisuke Kihara, Purdue U	**Student Award Presentation**
10:45 – 11:00 a.m.	**Coffee Break** **Conference Lobby**		
11:00 a.m. - 12:00 p.m.	**Keynote Talk** **Brain Genomics** **Presenter: Mark Gerstein, Ph.D., Yale University** **Hamilton 1**		
12:00 – 1:20 p.m.	**Lunch and Sponsor Presentations** **Hamilton 1**		
	Track 3: Translational Bioinformatics **Hamilton 2**	**Track 4:** Genome Biology **Skipwith 2**	**Track 5:** Biomedical Informatics **Skipwith 1**
1:30 – 2:50 p.m.	**Breakout Session 5** Protein Structural Bioinformatics Session Chair: Debswapna Bhattacharya, Auburn U	**Breakout Session 7** Microbial Genomic Analysis for Public Health Session Chair: Steven Foley, NCTR/FDA	**Breakout Session 9** Biomedical Informatics Session Chair: Wen Zou, NCTR/FDA
2:55 – 4:15 p.m.	**Breakout Session 6** New Informatics Methods for Precision Medicine Session Chair: Zhaohui "Steve" Qin, Emory U	**Breakout Session 8** Challenges and Solutions for Analysis of Gene Expression Data Session Chair: Wei (Vivian) Zhuang, NCTR/FDA	**Breakout Session 10** Heterogeneous Biomedical Information Visualization Session Chair: Huanmei Wu, IUPUI
4:15 – 5:00 p.m.	**Poster Session / Coffee Break** **Conference Lobby, Hamilton 1**		
5:00 - 6:00 p.m.	**Keynote Talk** **Genomic Medicine for Understudied Populations: Lessons from Colombia** **Presenter: King Jordan, Ph.D., Georgia Institute of Technology** **Hamilton 1**		
6:00 – 6:30 p.m.	**Poster Session / Coffee Break** **Conference Lobby, Hamilton 1**		
6:30 – 8:00 p.m.	**Dinner** **Hamilton 1**		

Day 3: Saturday, March 30, 2019

7:00-8:00 a.m.	**Student Session:** Student Mentoring Meeting **Hamilton 2**	
	Track 6: Computational Biology and Machine Learning **Hamilton 2**	**Track 7:** Emerging Technologies **Skipwith 2**
8:00 – 9:20 a.m.	**Breakout Session 11** Machine Learning in Biomedicine Session Chair: Thanh Minh Nguyen, UAB	**Closed Session:** MCBIOS’19 Board Meeting **Magic City Boardroom**
9:25 – 10:45 a.m.	**Breakout Session 12** Computational Biology Session Chair: Steve Barnes, UAB	**Breakout Session 13** Emerging Computational Approaches for Drug Discovery and Development Session Chair: Minjun Chen, NCTR/FDA
10:45 – 11:00 a.m.	**Coffee Break** **Conference Lobby**	
11:00 a.m. - 12:00 p.m	**Keynote Talk** **Clinical Applications of Genomic Medicine: The State of the Art** **Presenter: Josh F. Peterson, M.D., MPH, FACMI, Vanderbilt University Medical Center** **Hamilton 1**	
12:00 – 1:15 p.m.	**Lunch and Award Announcement** **Hamilton 1**	
1:15-2:00 p.m.	**Roundtable Discussion**	**Expert Panels** Bioinformatics Education: What's the right curriculum for future translational biomedical data scientists?
	Hamilton 1	**Hamilton 2**
	MCBIOS 2019 Ends	

Keynote Speakers and Presentation Abstracts

Keynote Talk 1, Thursday, March 28, 2019 - 5:00 p.m.

Semi-Supervised Learning to the Rescue: Towards Deep Understanding of Coding Variant Effects

Predrag Radivojac, Ph.D.
Professor of Computer Sciences
Khoury College of Computer Sciences
Northeastern University

Abstract: A major goal in computational biology is the development of algorithms, analysis techniques, and tools towards deep mechanistic understanding of life at a molecular level. In the process, computational biology must take advantage of the new developments in artificial intelligence and machine learning, and then extend beyond pattern analysis to provide testable hypotheses for experimental science. This talk will focus on our recent contributions to understanding molecular mechanisms of disease and relevant related work. We will first discuss the development of semi-supervised machine learning techniques for partially observable domains such as molecular biology; that is, methods for accurate estimation of frequency of occurrence of hard-to-measure and rare events. We will then show how these methods play key roles in inferring protein cellular roles and phenotypic effects of genomic mutations, with an emphasis on understanding the molecular mechanisms of human genetic disease. We assessed the value of these methods in the wet lab where we tested the molecular mechanisms behind selected de novo mutations in a cohort of individuals with neurodevelopmental disorders. We will conclude by discussing implications of this work on future research in machine learning, genome interpretation, and precision health.

Bio: Predrag Radivojac is a Professor of Computer Science at Northeastern University, where he recently moved from Indiana University. Prof. Radivojac received his Bachelor's and Master's degrees in Electrical Engineering from the University of Novi Sad and University of Belgrade, Serbia. His Ph.D. degree is in Computer Science from Temple University (2003) under the direction of Prof. Zoran Obradovic and co-direction of Prof. Keith Dunker. In 2004 he held a post-doctoral position in Keith Dunker's lab at Indiana University School of Medicine, after which he joined Indiana University Bloomington. Prof. Radivojac's research is in the areas of computational biology and machine learning with specific interests in protein function, MS/MS proteomics, genome interpretation, and precision health. He received the National Science Foundation (NSF) CAREER Award in 2007 and is an August-Wilhelm Scheer Visiting Professor at Technical University of Munich (TUM) as well as an honorary member of the Institute for Advanced Study at TUM. At Indiana University, he was Associate Chair of the Department of Computer Science and a co-Director of all of Informatics and Data Science for the multi-campus Precision Health Initiative. Prof. Radivojac's projects have been regularly supported by NSF and National Institutes of Health (NIH). He is currently an Editorial Board member for the journal Bioinformatics, Associate Editor for PLoS Computational Biology, and serves his third term (elected) on the Board of Directors of the International Society for Computational Biology (ISCB).

Keynote Talk 2, Friday, March 29, 2019 – 11:00 a.m.

Brain Genomics

Mark Gerstein, Ph.D.
Albert L Williams Professor of Biomedical Informatics
Professor of Molecular Biophysics & Biochemistry and of Computer Science
Co-Director of the Yale Program in Computational Biology & Bioinformatics
Yale University

Abstract: Despite progress in defining genetic risk for psychiatric disorders, their molecular mechanisms remain elusive. Addressing this, the PsychENCODE Consortium has generated a comprehensive online resource for the adult brain across 1866 individuals. The PsychENCODE resource contains ~79,000 brain-active enhancers, sets of Hi-C linkages, and topologically associating domains; single-cell expression profiles for many cell types; expression quantitative-trait loci (QTLs); and further QTLs associated with chromatin, splicing, and cell-type proportions. Integration shows that varying cell-type proportions largely account for the cross-population variation in expression (with >88% reconstruction accuracy). It also allows the building of a gene regulatory network, linking genome-wide association study variants to genes (e.g., 321 for schizophrenia). We embed this network into an interpretable deep-learning model, which improves disease prediction by ~6-fold versus polygenic risk scores and identifies key genes and pathways in psychiatric disorders.

Bio: After graduating from Harvard with a A.B. in physics in 1989, Prof. Mark Gerstein earned a doctorate in theoretical chemistry and biophysics from Cambridge University in 1993. He did postdoctoral research in bioinformatics at Stanford University from 1993 to 1996. He came to Yale in 1997 as an assistant professor in the Department of Molecular Biophysics and Biochemistry, and since 1999, in the Computer Science Department. He was named an associate professor in 2001, and the following year became co-director of the Yale Computational Biology and Bioinformatics Program. Gerstein has published appreciably in the scientific literature, with >400 publications in total, including a number of them in prominent venues, such as Science, Nature, and Scientific American. His research is focused on bioinformatics, and he is particularly interested in data science & data mining, macromolecular geometry & simulation, human genome annotation & disease genomics, and genomic privacy.

Keynote Talk 3, Friday, March 29, 2019 – 5:00 p.m.

Genomic medicine for understudied populations: lessons from Colombia

King Jordan, Ph.D.
Director of Bioinformatics Graduate Program
Associate Professor of Biology
School of Biology
Georgia Institute of Technology

Abstract: Genomic medicine promises to revolutionize healthcare. However, genomics research remains heavily biased towards European-ancestry cohorts, while understudied populations bear a disproportionate disease burden. This genomics research gap has the potential to exacerbate existing health disparities. Closing the gap will require: (i) more genomics research on diverse populations, (ii) better methods so that insights from current studies can be applied across populations, and (iii) development of local capacity so that genomic approaches to healthcare can be implemented worldwide. Our group is working on these three areas together with collaborators from the country of Colombia in South America. Our research and development efforts are focused on neighboring populations in Colombia with distinct ancestry profiles: Antioquia (European) and Chocó (African). We are investigating the role that genetic ancestry plays in the epidemiology of type 2 diabetes (T2D) and patient drug response (pharmacogenomics) in these two populations. Chocó has significantly higher predicted genetic risk for T2D compared to Antioquia, and the elevated genetic risk for T2D in Chocó is correlated with higher African ancestry. Despite its higher genetic risk, the population of Chocó has a three-times lower observed T2D prevalence than Antioquia, indicating that environmental factors better explain differences in T2D outcomes for Colombia. Our exploration of dietary and lifestyle factors in Chocó illustrates how low socioeconomic status can divergently manifest as a T2D protective factor in developing countries. A number of pharmacologically relevant genetic variants show anomalous allele frequencies within and between the two Colombian populations, and these differences are also associated with their distinct genetic ancestry profiles. For example, one particular variant in the SLCO1B1 gene (rs4149056), which is associated with an increased risk of toxicity to a commonly prescribed statin, is found at relatively high frequency in Antioquia and associated with European ancestry. We have developed and validated an inexpensive allele-specific PCR assay to test for the presence of such population-enriched pharmacogenomic variants in resource-limited settings like Colombia. We hope that our population-centered approach can serve as a model for the application of genomic methods to healthcare in understudied populations worldwide.

Bio: Dr. King Jordan is an Associate Professor in the School of Biological Sciences and Director of the Bioinformatics Graduate Program at the Georgia Institute of Technology. He received a BS in Biology from the University of Colorado (1992) and a PhD in Genetics from the University of Georgia (1998). Before coming to Georgia Tech in 2006, Dr. Jordan worked at the National Center for Biotechnology Information (NCBI), the bioinformatics division of the US National Institutes of Health (NIH). Members of Dr. Jordan's laboratory at Georgia Tech (http://jordan.biology.gatech.edu) conduct bioinformatics research with an emphasis on the analysis of 'big data' for understanding the molecular genetic determinants of human health. His group's research efforts involve both the development and application of computational tools specifically tailored for genomic sequence analysis as well as various 'omics' functional analyses. Dr. Jordan is also actively engaged in the development of bioinformatics and genomics capacity in Latin America. He was named a Fulbright fellow to Colombia in 2012 and 2016, and he is the Co-Founder and Director of the PanAmerican Bioinformatics Institute (http://panambioinfo.org). In addition to his academic research, Dr. Jordan consults with industry partners to provide custom solutions to their bioinformatics challenges via his company Genomic Informatics Consulting (http://www.genomeinforma.com/), and he leads the Applied Bioinformatics Laboratory (ABiL http://abil.ihrc.com), a private-public partnership between IHRC Inc. and the Georgia Tech Bioinformatics Program. ABiL scientists work collaboratively with clients from the government, academic and industry sectors to provide data analysis services along with workforce development and training in bioinformatics.

Keynote Talk 4, Saturday, March 30, 2019 – 11:00 a.m.

Clinical Applications of Genomic Medicine: The State of the Art

Josh F. Peterson, M.D., MPH, FACMI
Program Director, Masters of Applied Clinical Informatics
Associate Professor of Biomedical Informatics
Associate Professor of Medicine
Vanderbilt University Medical Center

Abstract: The field of genomic medicine has been transformed by dramatic reductions in the cost and ease of obtaining clinical-grade genotyping or sequencing data. Interest in implementing pharmacogenomics to tailor medical therapies, sequencing to screen for Mendelian traits, and application of polygenic risk scores to predict incident chronic diseases has surged. What has lagged the advances in the laboratory is the technical ability to broadly and repeatedly access stored genomic data for patient care, and to deliver evidence based and patient context sensitive recommendations for treatment or further screening once genetic risks are identified. This talk will review the progress that is being made in translating newer applications in germline genomic medicine to routine patient care. We will discuss the landscape of NIH-funded projects pioneering large scale genetic population screening and implementation, and review the remaining challenges to making these technologies accessible to all.

Bio: Josh Peterson, M.D., MPH is Associate Professor with appointments in the Departments of Biomedical Informatics and Medicine at Vanderbilt University Medical Center (VUMC), and an internist with an active primary care practice. Dr. Peterson's research interests are in precision medicine with a focus on translating genomic technologies to routine clinical care. Over his 20-year career in clinical informatics, he has led the design and implementation of clinical decision support systems to improve drug safety. Currently, he leads implementation of one of the largest pharmacogenomics implementations in the US – PREDICT. He serves as a principle investigator for an NIH funded project to simulate the clinical impact and cost-effectiveness of sequencing large populations over their lifetime. He also leads two NIH-sponsored genomic medicine consortia: eMERGE (Electronic Medical Records and Genomics) where he is principle investigator of the Coordinating Center and co-Chair of the Outcomes Workgroup and IGNITE 2 where he serves as principle investigator for the VUMC site.

Podium Presentations

Day 2: Friday, March 29, 2019	
YOUNG SCIENTIST EXCELLENCE AWARDS	
8:00 – 9:20 a.m.	**Young Scientist in Excellence Awards for Postdoctoral Fellows (Skipwith 1)** **Session Chair – Inimary Toby**, Ph.D., *Assistant Professor, University of Dallas, Irving, TX*
8:00 – 8:20 a.m.	AOP Network as a Framework to Study Adverse Effect: A Case with DILI **Kapil Khadka**, Ph.D., *FDA, National Center for Toxicological Research, Jefferson, AR*
8:20 – 8:35 a.m.	Interpreting System-level Cancer Mechanisms Through Rule Learning **Haoran Chen**, Ph.D., *Department of Electrical and Computer Engineering, Texas A&M University, College Station, TX*
8:35 – 8:50 a.m.	Assessment of Technical Repeatability for Germline Variants Detected from Whole Genome Sequencing (WGS) Data **Bohu Pan**, Ph.D., *FDA, National Center for Toxicological Research, Jefferson, AR*
8:50 - 9:05 a.m.	Improved Imaging May Help Achieve Better Species Level Accuracy in Identifying Food Contaminating Beetles **Tanmay Bera,** Ph.D., *FDA, Division of Bioinformatics and Biostatistics, National Center for Toxicological Research, Jefferson, AR*
9:05 – 9:20 a.m.	Development of Software for Facilitating Quality Control of POPs Detection in Food and Animal Feeds **Wenjing Guo**, Ph.D., *FDA, National Center for Toxicological Research, Jefferson, AR*

YOUNG SCIENTIST EXCELLENCE AWARDS	
9:25 – 10:45 a.m.	**Young Scientist Excellence Award for Students (Skipwith 1)** **Session Chair – Inimary Toby**, Ph.D., *Assistant Professor, University of Dallas, Irving, TX*
9:25 – 9:45 a.m.	The Biology Behind the Epigenetic Clock **Hunter Porter**, *Oklahoma Medical Research Foundation, Oklahoma City, OK*
9:45 – 10:00 a.m.	GS-Rank: Disease Gene Prioritization Based on Network and Gene Sets, and an Alzheimer's Disease Study **Zongliang Yue**, *Informatics Institute, School of Medicine, University of Alabama at Birmingham, Birmingham, AL*
10:00 – 10:15 a.m.	Identifying Novel Drugs for Treatment of Neurodegenerative Diseases Using a Quantitative Structure-Activity Relationships Approach **Samuel Kakraba**, *Department of Biochemistry and Molecular Biology, University of Arkansas for Medical Sciences, Little Rock, AR*
10:15 - 10:30 a.m.	Does Inclusion of Residue-Residue Contact Information Boost Protein Threading? **Sutanu Bhattacharya**, *Department of Computer Science and Software Engineering, Auburn University, Auburn, AL*
10:30 – 10:45 a.m.	Use of Chemoinformatics and Molecular Docking in the Design of Peripherally-Restricted CB1 Antagonists **Ayooluwa Aderibigbe**, *University of Mississippi, Oxford, MS*

Day 2: Friday, March 29, 2019	
TRACK 1: CLINICAL GENOMICS	
8:00 – 9:20 a.m.	**Breakout Session 1: Integration of Omics Data with Clinical Information (Hamilton 2)** **Session Chair** – **Chindo Hicks,** Ph.D., *Professor of Genetics and Bioinformatics, LSU School of Medicine, New Orleans, LA* **Session Overview** The session aims at providing a framework and platform for presenting and discussing bioinformatics enabled multidisciplinary biomedical research for the establishment of a new 21st century biomedicine that both (a) fully exploits the fruit of the genomic revolution for clinical practice and (b) allows clinical care to be leveraged to advance population and basic biological research to improve human health.
8:00 – 8:20 a.m.	**Session Featured Speaker** **TITLE** **Matthew Might,** Ph.D., *UAB School of Medicine, Director, Hugh Kaul Precision Medicine Institute at UAB*
8:20 – 8:35 a.m.	Exome Sequencing Identifies Glycosylation Defects as a Probable Cause of Immune-Mediated Thrombotic Thrombocytopenic Purpura **Malay Kumar Basu**, Ph.D., *Department of Pathology, University of Alabama at Birmingham, Birmingham, AL*
8:35 – 8:50 a.m.	Network Analysis Reveals Differential Proteomic and Transcriptomic Signatures Associated with TGF-B1 Treatment of IMR-90 Cells **Ava Wilson,** *Graduate Student, University of Alabama at Birmingham, Birmingham, AL*
8:50 - 9:05 a.m.	Characterizing Mutually Exclusive Mutations in Pan-Cancer **Yifan Zhang,** *Graduate Student, University of Arkansas at Little Rock*
9:05 – 9:20 a.m.	Classification Methods for Accurate Gene Family Identification in Complex Genomes **George Popescu,** Ph.D., *Mississippi State University, Starkville, MS*

TRACK 1: CLINICAL GENOMICS	
9:25 – 10:45 a.m.	**Breakout Session 2: Omics Data in Real-World Settings (Hamilton 2)** **Session Chair** – **Dong Wang,** Ph.D., *Senior Statistician, FDA National Center for Toxicological Research, Jefferson, AR* **Session Overview** With the dramatic advance of modern molecular biology techniques like next generation sequencing, it is now feasible to collect a huge amount of data on each patient (or model organism) with reasonable cost. This provides an excellent opportunity to discover new biological mechanisms and develop new therapeutic strategies. However, the real world is always messy. Data collected from general populations are subject to various sources of variation, confounding factors, missingness, and errors. High throughput data, due to the increased dimensionality, can further aggravate these problems. Thus special modeling techniques need to be applied to avoid erroneous conclusions. In this session, several experts in this area will discuss their experience in dealing with omics data sets in real world settings and explain commonly used methodologies in analyzing complex real world data.
9:25 – 9:45 a.m.	**Session Featured Speaker** Hierarchical Models for Analyzing Large-Scale Clinical and Molecular Data **Nengjun Yi,** Ph.D., *Sir David Cox Endowed Professor in Biostatistics, University of Alabama Birmingham, AL*
9:45 – 10:00 a.m.	Predicting Gene Expression Using DNA Methylation in Three Human Populations **Xiangqin Cui**, Ph.D., *Associate Professor and Director of VA Analytics Core, Emory University, Atlanta, GA*
10:00 – 10:15 a.m.	Statistical Challenges and Opportunities for Biomarkers Based on Deep Sequencing and Other New Technologies **Dong Wang,** Ph.D., *Senior Statistician, FDA National Center for Toxicological Research, Jefferson, AR*
10:15 - 10:30 a.m.	Link Genomics and Clinical Outcomes, An Integrated Approach **Xueyuan Cao,** Ph.D., *Assistant Professor, University of Tennessee Health Science Center (UTHSC), Memphis, TN*
10:30 – 10:45 a.m.	PAST: The Future of GWAS Studies **Adam Thrash,** Ph. D., *Research Associate, Institute for Genomics, Biocomputing & Biotechnology, Mississippi State University, Starkville, MS*

TRACK 2: DRUG DISCOVERY AND INFORMATICS	
8:00 – 9:20 a.m.	<u>**Breakout Session 3:**</u> **In Silico Drug Discovery in the Era of Precision Medicine (Skipwith 2)** **Session Chair** – **Zhichao Liu**, Ph.D., *FDA National Center for Toxicological Research, Jefferson, AR* **Co-moderator** – **Ting Li,** *University of Arkansas for Medical Sciences (UAMS)* **Session Overview** The aim of this session is to cover the many facets of computational drug discovery to promote precision medicine. Topics included in this session include: how to apply data mining in pharmacovigilance and pharmacogenomics; integrating NGS technologies into computational drug discovery and development; and how the Artificial Intelligence revolution is affecting computational drug discovery and development.
8:00 – 8:20 a.m.	<u>**Session Featured Speaker**</u> FDALabel Database on Amazon Cloud with Rich Drug Labeling Information to Advance the Application of Precision Medicine **Hong Fang, Ph.D.,** *FDA National Center for Toxicological Research, Jefferson, AR*
8:20 – 8:35 a.m.	Integration of Real-Word Information to Capture Drug-Induced Liver Injury Evidence **Shraddha Thakkar, Ph.D.,** *FDA National Center for Toxicological Research, Jefferson, AR*
8:35 – 8:50 a.m.	Tracing Drug Induced Liver Injury (DILI) Signatures by Harnessing Cancer Cell Lines **Ting Li**, *University of Arkansas for Medical Sciences (UAMS)*
8:50 – 9:05 a.m.	Drug Labeling Identification Based on Scene Text Detection and Recognition **Xiangwen Liu**, *University of Arkansas at Little Rock*
9:05 – 9:20 a.m.	Toward a High Reproducible Targeted Sequencing Diagnosis for Precision Oncology – Efforts from SEQCII Consortium **Dan Li, Ph.D.,** *FDA National Center for Toxicological Research, Jefferson, AR*

TRACK 2: DRUG DISCOVERY AND INFORMATICS	
9:25 – 10:45 a.m.	<u>**Breakout Session 4:**</u> **Computer-Aided Drug Discovery and Development (Skipwith 2)** **Session Chair – Daisuke Kihara**, *Purdue University, West Lafayette, IN* **Session Overview** In the recent drug discovery, computational methods are widely accepted and routinely used in many steps of the drug development process. Computational methods are not only effective in reducing the time and the cost of the drug discovery but also helped building new strategies and concepts, which include drug repurposing, fragment-based drug design, and finding cryptic drug binding sites. This session overviews new computational techniques and cases where computational methods played a key role in successful drug development.
9:25 – 9:45 a.m.	<u>**Session Featured Speaker**</u> Classification of Ligand-Binding Pockets in Proteins with Deep Learning **Michal Brylinski,** Ph.D., *Louisiana State University*
9:45 – 10:00 a.m.	GS-Rank: disease gene prioritization based on network and gene sets, and an Alzheimer’s disease study **Zhongliang Yue**, Ph.D., *Indiana University/Purdue University, Indianapolis, IN*
10:00 – 10:15 a.m.	Antagonist Induced Androgen Receptor Structure Changes Elucidated by Docking and Dynamics Simulation **Suguna Devi Sakkiah**, Ph.D., *FDA National Center for Toxicological Research, Jefferson, AR*
10:15 - 10:30 a.m.	CGPE: A User-Friendly Gene and Pathway Explore Webserver for Public Cancer Transcriptional Data **Jiannan Liu**, *Indiana University/Purdue University, Indianapolis, IN*
10:30 – 10:45 a.m.	Characterization of Mitochondria Morphology by Deep Learning Neural Network Model **Zhenhua Shang**, *University of South Carolina*

TRACK 3: TRANSLATIONAL BIOINFORMATICS	
1:30 – 2:50 p.m.	**Breakout Session 5: Protein Structural Bioinformatics (Hamilton 2)** **Session Chair** – **Debswapna Bhattacharya**, Ph.D., *Department of Computer Science and Software Engineering, Auburn University, Auburn, AL* **Session Overview** Protein structural bioinformatics is a major topic of research in computational biology and bioinformatics. With continued development in high-throughput sequencing technologies and with the new revolutionary advances in cryo-electron microscopy (cryo-EM), protein structural data are rapidly accumulating at various resolutions. Alongside, latest developments in computational side including the deep learning revolution have shown promising progress to model and mine patterns in multi-resolution protein structural data. This session is designed to bring together scientists in computational and biological sciences to explore the current state-of-the-art research in all aspects of protein structural bioinformatics including structure, function, dynamics, and interaction, thereby providing insights to the molecular basis of various diseases and facilitating the development of novel therapeutic strategies.
1:30 – 1:50 p.m.	**Session Featured Speaker** Computational Protein Structure Modeling for Medium to Low Resolution Cryo-Electron Microscopy Density Maps **Daisuke Kihara,** Ph.D., *Department of Biological Sciences and Computer Science, Purdue University, West Lafayette, IN*
1:50 – 2:05 p.m.	Improving Structure-Based Prediction of Transcription Factor Binding Sites **Jun-tao Guo,** Ph.D., *Department of Bioinformatics and Genomics, University of North Carolina at Charlotte, Charlotte, NC*
2:05 – 2:20 p.m.	Internal Symmetry in Proteins: Detection, Characterization and Outlook **Dukka KC,** Ph.D., *Computational Science and Engineering Department, North Carolina A&T State University, Greensboro, NC*
2:20 – 2:35 p.m.	Global Quality Assessment of Individual Protein Models by Random Forest and Novel Statistical Potentials **Zheng Wang,** Ph.D., *Department of Computer Science, University of Miami, Coral Gables, FL*
2:35 – 2:50 p.m.	Weisfeiler-Lehman Graph Neural Network for Drug-Target Interaction Prediction **Hafez Eslami Manoochehri**, University of Texas at Dallas

TRACK 3: TRANSLATIONAL BIOINFORMATICS	
2:55 – 4:15 p.m.	**Breakout Session 6: New Informatics Methods in Precision Medicine (Hamilton 2)** **Session Chair** – **Steve Qin,** Ph.D., *Department of Biostatistics and Bioinformatics, Emory University* **Session Overview** Precision Medicine advocates for the practice of customized disease treatment and prevention such that all clinical decisions are made based on the characteristics of individual patients. The precision medicine framework has been enthusiastically endorsed by the health care community and is set to have a profound impact on the health care practice. However, adopting the precision medicine ideology in the clinics requires solving a series technical challenges, particularly in informatics and data analytics. To serve this newly emerge area of research, this session will showcase the latest research developments in the informatics area in the advancement of precision medicine.
2:55 – 3:15 p.m.	**Session Featured Speaker** UALCAN: An Integrated Data Mining Tool for Molecular Sub-Type Based Expression Analysis **Sooryanarayana Varambally**, Ph.D., *Department of Pathology, University of Alabama at Birmingham*
3:15 – 3:30 p.m.	Integrating DNA and RNA for Actionable Alterations Discovery in Human Cancer **Rendong Yang**, Ph.D., The Hormel Institute
3:30 – 3:45 p.m.	Dissecting Differential Signals in High-Throughput Data from Complex Tissues **Ziyi Li**, Ph.D., *Department of Biostatistics and Bioinformatics, Emory University*
3:45 – 4:00 p.m.	An Integrated System Biology Approach Yields Drug Repositioning Candidates for the Treatment of Heart Failure **Guodong Yang**, Ph.D., *Emory University School of Medicine*
4:00 – 4:15 p.m.	Network-Based Association Study of Protein Sets and Applications in Gene Ontology Enrichment Analysis **Hao-Bo Guo**, Ph.D. *College of Engineering and Computer Science, University of Tennessee at Chattanooga.*

TRACK 4: GENOME BIOLOGY	
1:30 – 2:50 p.m.	**Breakout Session 7: Microbial Genome Analyses for Public Health (Skipwith 2)** **Session Chair – Steven Foley,** Ph.D., *Deputy Director, Division of Microbiology, NCTR/FDA, Jefferson, AR* **Session Overview** With the increasing availability of high-throughput DNA sequencing technologies, the ability to analyze microbial genomic data in efficient manners to dissect biological questions is vitally important. This session will have a focus on microbial safety and public health and explore the analyses of DNA sequencing and protein interactions. Speakers will focus on the application of microbiome sequencing in food processing environments to help understand how food pathogens may persist in these environments; on efforts to develop bioinformatics tools utilizing proteomics and genomic sequencing data to predict potential pathogenicity of bacterial pathogens and the development of improved tools to understand genetic diversity. Taken together this session should provide an excellent overview of the approaches for using high-throughput sequencing, proteomics and bioinformatics tools to inform public health decisions on bacterial pathogens.
1:30 – 1:50 p.m.	**Session Featured Speaker** Application of Microbiome Sequencing in Food Processing Environments **Steven Ricke,** Ph.D., *Center for Food Safety, University of Arkansas, Fayetteville, AR*
1:50 – 2:05 p.m.	CYPminer: An Automatable Cytochrome P450 Identification, Classification, and Data Analysis Tool for Genome Data Sets from All Kingdoms. **Ohgew Kweon,** Ph.D., *Research Microbiologist, Division of Microbiology, , National Center for Toxicological Research, FDA, Jefferson, AR*
2:05 – 2:20 p.m.	Computational Prediction of Host-Pathogen Protein Interactions in Melioidosis Pathogen *Burkholderia pseudomallei* and Human Reveals Novel Virulence Factors and Infectivity Mechanisms **Chathumadavi Ediriweera,** *Graduate Student*, *Utah State University, Logan, UT*
2:20 – 2:35 p.m.	Development of a *Salmonella Enterica* Virulence Database and Associated Analysis Tools **Jing Han,** Ph.D., *Research Microbiologist, Division of Microbiology, , National Center for Toxicological Research, FDA, Jefferson, AR*
2:35 – 2:50 p.m.	Diversity, Distribution and Transmission Potential of Antimicrobial Resistance and Virulence Factors among Incompatibility Group A/C, FIB and I1 Plasmids from Members of the Enterobacteriaceae **Steven Foley,** Ph.D., *Deputy Director, Division of Microbiology, , National Center for Toxicological Research, FDA, Jefferson, AR*

TRACK 4: GENOME BIOLOGY	
2:55 – 4:15 p.m.	**Breakout Session 8: Challenges and Solutions for Analysis of Gene Expression Data (Skipwith 2)** **Session Chair** – ***Wei Vivian Zhuang*****,** Ph.D., *Division of Bioinformatics and Biostatistics, National Center for Toxicological Research, FDA* **Session Overview** – This session is organized to reflect the MCBIOS 2019 theme (Information for Precision Medicine) as gene expression data have many applications in precision medicine research and precision medicine needs reproducible gene expression data and analysis to succeed. Specifically, the presentation topics will cover new statistical framework and methods to mitigate the irreproducibility caused by common analytical corrections for incomplete gene expression quantification, as well as a summary of challenges in gene expression data collection and analysis.
2:55 – 3:15 p.m.	**Session Featured Speaker** Impact of Pre-Analytical and Analytical Variables in the Quantification of Transcript Levels **Luísa Camacho**, Ph.D., *Division of Biochemical Toxicology, National Center for Toxicological Research, FDA, Jefferson, AR*
3:15 – 3:30 p.m.	A Nonparametric Statistical Method to Analyze Incomplete Gene Expression Data **Wei Vivian Zhuang**, Ph.D., *Division of Bioinformatics and Biostatistics, National Center for Toxicological Research, FDA, Jefferson, AR*
3:30 – 3:45 p.m.	GMDR: A Machine Learning Method for Identifying Multifactor Interactions **Xiang-Yang Lou**, Ph.D., *Department of Pediatrics, University of Arkansas for Medical Sciences, Little Rock, AR*
3:45 – 4:00 p.m.	A Machine Learning Approach to Genome Quality Assessment **Adam Thrash**, Ph.D. Candidate, *Institute for Genomics, Biocomputing & Biotechnology; Department of Computer Science and Engineering, Mississippi State University, Starkville, MS*
4:00 – 4:15 p.m.	Orion: Hunting Stable Genes **Winston Miller**, *Department of Molecular Bioinformatics, University of Tennessee Health Science Center, Memphis, TN*

TRACK 5: BIOMEDICAL INFORMATICS	
1:30 – 2:50 p.m.	**<u>Breakout Session 9:</u> Biomedical Informatics (Skipwith 1)** **Session Chair** – **Wen Zou,** Ph.D., *National Center for Toxicological Research, US Food and Drug Administration* **Session Overview** Biomedical informatics, as the interdisciplinary section of biological science, health care, information science, and computer science, is playing more and more important roles in improving human health. Biomedical informatics has been an emerging field for decades and it covers a wide area including clinical informatics, bioinformatics, imaging informatics, consumer health informatics, etc. In the big data generation, the increasing adoption of electronic health records (EHRs) and fast growing of outcome research and genomics has brought the new expectations to the data-driven decision making on disease intervention and prevention. This session includes researches which apply principles and algorithms of computer and information science to the advancement of life science research, patient care and public health.
1:30 – 1:50 p.m.	**Session Featured Speaker** Biomedical Informatics: Using Data to Improve Human Health **Ahmad Baghal,** MD, MS, *University of Arkansas for Medical Sciences, Little Rock, AR.*
1:50 – 2:05 p.m.	Deep Learning for *In Silico* Predictive Toxicology **Chaoyang Zhang,** Ph.D., *University of Southern Mississippi, Hattiesburg, MS.*
2:05 – 2:20 p.m.	Approaches Towards Verification and Validation of Model Systems **Erich A. Peterson**, Ph.D., *University of Arkansas for Medical Sciences, Little Rock, AR.*
2:20 – 2:35 p.m.	PubQC, The Automated Publication Quality Control System **Aleksandra Perz,** Student, *Oklahoma Medical Research Foundation*
2:35 – 2:50 p.m.	Data Mining on Prescription Opioid Use and Associated Medical Disorder Studies **Junxiu Zhou,** Ph.D. Candidate, *National Center for Toxicological Research, US Food and Drug Administration*

TRACK 5: BIOMEDICAL INFORMATICS	
2:55 – 4:15 p.m.	**<u>Breakout Session 10:</u> Heterogeneous Biomedical Information Visualization (Skipwith 1)** **Session Chair** – **Huanmei Wu**, *Indiana University Purdue University Indianapolis* **Session Co-Chair** – **Zongliang Yue**, *University of Alabama – Birmingham* **Session Overview** This session will introduce the audience the knowledge, skills, tool development, and existing packages biomedical data visualization to facility interdisciplinary collaborations. Speakers will review the ongoing research community effort in visualization practices in biomedical research to promote data integration, data analysis, and result interpretation. There is a national need to develop the next generation biomedical workforce and attract more workers into research and the application of big biomedical data. The audience from this session will apply the information from the session to successfully utilize, explore and visualize the massive biomedical and clinical data. They can use the tools and research outcomes introduced from the meeting in their research.
2:55 – 3:15 p.m.	**<u>Session Featured Speaker</u>** Heterogeneous Biomedical Information Visualization **Huanmei Wu**, Ph.D., *Indiana University/Purdue University, Indianapolis, IN*
3:15 – 3:30 p.m.	Explore, Analyze, and Publish RNA-Seq, DNA-Seq, and Gene Function Data with Integrated Genome Browser **Ann Loraine**, Ph.D., *University of North Carolina at Charlotte*
3:30 – 3:45 p.m.	Segmentation of Smartphone-Based Retina Images for Diabetic Retinopathy Detection **Mahmut Karakaya**, Ph.D., *University of Central Arkansas*
3:45 – 4:00 p.m.	An Easily Adaptable Targeted Sequencing Panel Viewer for Research and Clinical Use **Cody Ashby**, Ph.D., *Arkansas State University*
4:00 – 4:15 p.m.	Combining the Power of Your Local Computer with Cloud-Based Bioinformatics Resources for Visualizing Genomic Data **Nowlan Freese**, Ph.D., *University of North Carolina at Charlotte*

Day 3: Saturday, March 30, 2019	
TRACK 6: COMPUTATIONAL BIOLOGY AND MACHINE LEARNING	
8:00 – 9:20 a.m.	**Breakout Session 11: Machine Learning in Biomedicine (Hamilton 2)** **Session Chair –Thanh Nguyen,** *Informatics Institute, University of Alabama at Birmingham* **Session Overview** Machine Learning, whose theories are to answer the question of choosing the most likely successful hypothesis, is a critical component in the future Precision Medicine. The section will introduce the most recent development of machine learning techniques to the bioinformaticians and provide guidance on selecting which technique to solve which specific problem. With decades of development, the capacity of machine learning in solving Precision Medicine problems has been proven in many case-studies. Through cumulative experience in machine learning, it is recognized that it is necessary to highlight the important assumptions, to test whether the data meet these assumptions, to explain the key logical concepts different techniques such that the bioinformatician can use machine learning in the scenario-decision style.
8:00 – 8:20 a.m.	**Session Featured Speaker** Interpreting System-Level Cancer Mechanisms Through Rule Learning **Suping Deng,** Ph.D.**,** *Department of Electrical and Computer Engineering, Texas A&M University, College Station, TX*
8:20 – 8:35 a.m.	SVM-GlutarySite: A Support Vector Machine-Based Prediction of Glutarylation Sites from Protein Sequences **Hussam Al-barakati,** Ph.D.**,** *Computational Science and Engineering Department at North Carolina A&T State University, Greensboro, NC*
8:35 – 8:50 a.m.	Feature Importance in Protein Inter-Residue Contact Prediction **Anthony Ackah-Nyanzu,** *University of Missouri - St. Louis*
8:50 - 9:05 a.m.	Improved Contact Prediction Using Novel Deep Convolutional Neural Network Architectures **Sri Harsha Akurathi,** *University of Missouri - St. Louis*
9:05 – 9:20 a.m.	Reading the Book of Life: The Language of Genomes **Malay Kumar Basu**, Ph.D., *University of Alabama, Birmingham*

TRACK 6: COMPUTATIONAL BIOLOGY AND MACHINE LEARNING	
9:25 – 10:45 a.m.	**Breakout Session 12: Computational Biology (Hamilton 2)** **Session Chair** – **Stephen Barnes**, Ph.D., *University of Alabama, Birmingham* **Session Overview** The goal of this session is to highlight novel, groundbreaking developments in metabolomics as applied to Bioinformatics and Computational Biology. Omics-based approaches have typically been domain-constrained; for example, in the analysis of transcriptomics data, but not parallel proteomics data, or in analysis of proteomics data, but not metabolomics data, etc. This session will draw together diverse speakers to explore important topics in computational biology.
9:25 – 9:45 a.m.	**Session Featured Speaker** New-Generation Single-Cell Mass Spectrometry Tools Enable Trace-level Analysis of Metabolites in the Live Embryo **Erika Portero,** Ph.D., *University of Maryland, College Park, MD*
9:45 – 10:00 a.m.	Single-Cell RNA-Seq Analysis of Retinal Ganglion Cells **Siamak Yousefi**, Ph.D., *University of Tennessee Health Science Center*
10:00 – 10:15 a.m.	Validation Study Data Analysis for Minimally Invasive Surgery Simulators **Jake Farmer,** Student, *University of Central Arkansas, Conway, AR*
10:15 - 10:30 a.m.	Fluid Flow in Virtual Arthroscopic Tear Diagnosis and Evaluation Platform (VATDEP) **Aditya Dendukuri,** Student, *University of Central Arkansas, Conway, AR*
10:30 – 10:45 a.m.	Repurposing Immortalized Cell Line-based Transcriptomic Profiling Assays for Drug-induced Liver Injury with a PRank Method **Liyuan Zhu,** Ph.D., *National Center for Toxicological Research, US Food and Drug Administration, Jefferson, AR*

TRACK 7: EMERGING TECHNOLOGIES	
9:25 – 10:45 a.m.	**Breakout Session 13: Emerging Computational Approaches for Drug Discovery and Development (Skipwith 2)** **Session Chair** – **Annie Lumen,** Ph.D., *National Center for Toxicological Research, US FDA, NCTR* **Student Co-Moderator** – **Kristin McEuen Ashby,** *Graduate Student, University of Arkansas at Little Rock, Little Rock, AR* **Session Overview** It is generally recognized that drug discovery and development are very time and resources consuming processes. There is an increasing effort within the community to apply advanced computational power to improve the productivity for streamline drug discovery, design, development and safety evaluation. In this session, we will have a panel of speakers to introduce a variety of computational techniques applied in their cutting-edge researches, such as pharmacokinetic and biologically based mathematical models, machine learning techniques, and data mining. These computational techniques will be used to deal with the challenging issues encountered by drug developers and regulators, including biological modeling for predicting drug's pharmacokinetics, drug metabolism prediction, reactive metabolites identification, and drug safety evaluation such as drug-induced liver injury.
9:25 – 9:45 a.m.	**Session Featured Speaker** Lamisil (Terbinafine) Bioactivation Pathways Revealed Through Modeling and Experimental Approaches **Grover P. Miller,** Ph.D., *University of Arkansas for Medical Sciences, Little Rock, AR*
9:45 – 10:00 a.m.	Computational Tools for Predicting Drug Dosimetry in Pregnant Women **Annie Lumen,** Ph.D., *National Center for Toxicological Research, US FDA, NCTR*
10:00 – 10:15 a.m.	Genetic and Clinical Factors Associated with the Development of Chronic Drug Induced Liver Injury **Kristin McEuen Ashby,** *Graduate Student*, *University of Arkansas at Little Rock, Little Rock, AR*
10:15 - 10:30 a.m.	Antioxidant Tocols as Potent Radiation Countermeasures **Ujwani Nukala,** *Graduate Student, University of Arkansas for Medical Science, Little Rock, AR*
10:30 – 10:45 a.m.	The Development of a Hepatotoxicity Database for Herbal and Dietary Supplement **Jieqiang Zhu** Ph.D., *National Center for Toxicological Research, US FDA, NCTR*

ORAL PRESENTERS

Authors	Organization	Presentation Title	Time	Date	Room
Anthony Ackah-Nyanzu and Badri Adhikari	University of Missouri - St. Louis	Feature importance in protein inter-residue contact prediction	8:35 – 8:50am	Saturday, 3/30/19	Hamilton 2
Sri Harsha Akurathi and Badri Adhikari	University of Missouri - St. Louis	Improved contact prediction using novel deep convolutional neural network architectures	8:50 - 9:05am	Saturday, 3/30/19	Hamilton 2
Hussam Albarakati, Hiroto Saigo, Robert Newman and Dukka KC	North Carolina A&T State University	SVM-GlutarySite: A support vector machine-based prediction of Glutarylation sites from protein sequences	8:20 – 8:35am	Saturday, 3/30/19	Hamilton 2
Cody Ashby, Eileen Boyle, Michael Rutherford, Yan Wang, Michael Bauer, Christopher Wardell and Brian Walker	University of Arkansas for Medical Sciences	An Easily Adaptable Targeted Sequencing Panel Viewer for Research and Clinical Use	3:45 – 4:00pm	Friday, 3/29/19	Skipwith 1
Kristin Ashby, Ayako Suzuki, Fang Hong, Huixiao Hong, Mary Yang, Elizabeth Pierce and Minjun Chen	UALR/UAMS/NCTR	Genetic and clinical factors associated with the development of chronic drug induced liver injury	10:00 – 10:15am	Saturday, 3/30/19	Skipwith 2
Ayooluwa Aderibigbe, Pankaj Pandey and Robert Doerksen	University of Mississippi	Use of chemoinformatics and molecular docking in the design of peripherally-restricted CB1 antagonists	10:25 – 10:40am	Friday, 3/29/19	Skipwith 1
Ahmad Baghal	University of Arkansas for Medical Sciences	Biomedical Informatics: Using Data to Improve Human Health	1:30 – 1:50pm	Friday, 3/29/19	Skipwith 1
Eric Bell, Zi Liu, **Yongsheng Bai** and Yang Zhang	University of Michigan	Identification of protein-protein interactions for genes with miRNA target relationship	8:00 – 8:20am	Friday, 3/29/19	Hamilton 2
Lijia Yu, Deepak Kumar Tanwar, Emanuel Diego S. Penha, Yuri I. Wolf, Eugene V. Koonin and **Malay Kumar Basu**	University of Alabama at Birmingham	Reading the book of life: the language of genomes	9:05 – 9:20am	Saturday, 3/30/19	Hamilton 2
Malay Kumar Basu, Elizabeth Staley, Konstantine Halkidis, Nicole Kocher, Bryan Guillory, Lawrence Williams, Marisa Marques, Wenjing Cao and X. Long Zheng	University of Alabama, Birmingham	Exome sequencing identifies glycosylation defects as a probable cause of immune-mediated thrombotic thrombocytopenic purpura	8:20 – 8:35am	Friday, 3/29/19	Hamilton 2
Tanmay Bera, Hongjian Ding, Howard Semey, Leihong Wu, Zhichao Liu, Barnes Barnes, Darryl Langley, Monica Pava-Ripoll, Himansu Vyas, Weida Tong and Joshua Xu	National Center for Toxicological Research	Improved imaging may help achieve better species level accuracy in identifying food contaminating beetles	8:45 - 9:00am	Friday, 3/29/19	Skipwith 1
Sutanu Bhattacharya and Debswapna Bhattacharya	Auburn University	Does Inclusion of Residue-Residue Contact Information Boost Protein Threading?	10:10 - 10:25am	Friday, 3/29/19	Skipwith 1
Michal Brylinski	Louisiana State University	Classification of ligand-binding pockets in proteins with deep learning	9:25 – 09:45am	Friday, 3/29/19	Skipwith 2

Luisa Camacho	National Center for Toxicological Research	Impact of pre-analytical and analytical variables in the quantitation of transcript levels	2:55 – 3:15pm	Friday, 3/29/19	Skipwith 2
Xueyuan Cao	University of Tennessee Health Science Center	Link genomics and clinical outcomes, an integrated approach	10:15 - 10:30am	Friday, 3/29/19	Hamilton 2
Haoran Chen, Suping Deng and Yang Shen	Texas A&M University	Interpreting System-level Cancer Mechanisms through Rule Learning	8:15 – 8:30am	Friday, 3/29/19	Skipwith 1
Minjun Chen. Presenter: **Jieqiang Zhu**	National Center for Toxicological Research	The development of a hepatotoxicity database for herbal and dietary supplement	10:30 – 10:45am	Saturday, 3/30/19	Skipwith 2
Xiangqin Cui	Emory University	Predicting Gene Expression Using DNA methylation in Three Human Populations	9:45 – 10:00am	Friday, 3/29/19	Hamilton 2
Tansel Halic, **Aditya Dendukuri,** Mustafa Tunc, Shahryar Ahmadi, Sinan Kocakara and Sreekanth Venkata	University of Central Arkansas	Fluid Flow in Virtual Arthroscopic Tear Diagnosis and Evaluation Platform (VATDEP)	10:15 - 10:30am	Saturday, 3/30/19	Hamilton 2
Haoran Chen, **Suping Deng** and Yang Shen	Texas A&M University	Interpreting System-level Cancer Mechanisms through Rule Learning	8:00 – 8:20am	Saturday, 3/30/19	Hamilton 2
Chathumadavi Ediriweera and Rakesh Kaundal	Utah State University	Computational Prediction of Host-Pathogen Protein Interactions in Melioidosis pathogen Burkholderia pseudomallei and Human reveals novel Virulence Factors and Infectivity Mechanisms	2:05 – 2:20pm	Friday, 3/29/19	Skipwith 2
Hong Fang	National Center for Toxicological Research	FDALabel Database on Amazon Cloud with Rich Drug Labeling Information to Advance the Application of Precision Medicine	8:00 – 8:20am	Friday, 3/29/19	Skipwith 2
Tansel Halic, **Jake Farmer**, Doga Demirel, Mustafa Tunc, Shahryar Ahmadi, Kevin Sexton and Sreekanth Venkata	University of Central Arkansas	Validation Study Data Analysis for Minimally Invasive Surgery Simulators	10:00 – 10:15am	Saturday, 3/30/19	Hamilton 2
Steven Foley, Jing Han, Bijay Khajanchi and Suad Algarni	National Center for Toxicological Research	Diversity, Distribution and Transmission Potential of Antimicrobial Resistance and Virulence Factors among Incompatibility Group A/C, FIB and I1 Plasmids from Members of the Enterobacteriaceae	2:35 – 2:50pm	Friday, 3/29/19	Skipwith 2
Nowlan Freese, Ann Loraine, Jill Jenkins, Karthik Raveendran, Kiran Korey, Mason Meyer, Pawan Bole, Pranav Tambvekar, Riddhi Patil, Sai Charan Reddy Vallapureddy, Srishtee Marotkar and Srishti Tiwari	Univeristy of North Carolina, Charlotte	Combining the power of your local computer with cloud-based bioinformatics resources for visualizing genomic data	4:00 – 4:15pm	Friday, 3/29/19	Skipwith 1

Hao-Bo Guo	University of Tennessee at Chattanooga.	Network-based association study of protein sets and applications in gene ontology enrichment analysis	4:00 – 4:15pm	Friday, 3/29/19	Hamilton 2
Jun-tao Guo	University of North Carolina at Charlotte, Charlotte, NC	Improving Structure-based Prediction of Transcription Factor Binding Sites	1:50 – 2:05pm	Friday, 3/29/19	Hamilton 2
Wenjing Guo, Jeffrey Archer, Morgan Moore, Jeffrey Bruce, Michelle McLain, Sina Shojaee, Wen Zou, Russell Fairchild and Huixiao Hong	National Center for Toxicological Research	Development of Software for Facilitating Quality Control of POPs Detection in Food and Animal Feeds	9:00 – 9:15am	Friday, 3/29/19	Skipwith 1
Jing Han, Hailin Tang and Steven Foley	National Center for Toxiciological Research	Development of a Salmonella enterica Virulence Database and Associated Analysis Tools	2:20 – 2:35pm	Friday, 3/29/19	Skipwith 2
Samuel Kakraba, Srinivas Ayyadevara, Robert J. Shmookler Reis, Narsimha R. Penthala, Peter A Crooks and Cesar M. Compadre	University of Arkansas for Medical Sciences/ University of Arkansas at Little Rock	Identifying novel drugs for treatment of neurodegenerative diseases using a quantitative structure-activity relationships approach	9:55 – 10:10am	Friday, 3/29/19	Skipwith 1
Mahmut Karakaya and Recep Hacisoftaoglu	University of Central Arkansas	Segmentation of Smartphone-based Retina Images for Diabetic Retinopathy Detection	3:30 – 3:45pm	Friday, 3/29/19	Skipwith 1
Dukka KC	North Carolina A&T State University, Greensboro, NC	Internal symmetry in proteins: detection, characterization and outlook	2:05 – 2:20pm	Friday, 3/29/19	Hamilton 2
Kapil Khadka	National Center for Toxicological Research	AOP Network as a framework to study adverse effect: a case with DILI	8:00 – 8:15am	Friday, 3/29/19	Skipwith 1
Daisuke Kihara	Purdue University	Computational protein structure modeling for medium to low resolution cryo-electron microscopy density maps	1:30 – 1:50pm	Friday, 3/29/19	Hamilton 2
Ohgew Kweon, Seong-Jae Kim, Seongwon Nho, Dongryeoul Bae, Jungwhan Chon, Mark Hart, Jae Hyun Kim, Dong-Heon Baek, Young-Chang Kim, Wenjun Wang Wang, Sung-Kwan Kim, John Sutherland and Carl Cerniglia	National Center for Toxicological Research	CYPminer: An Automatable Cytochrome P450 Identification, Classification, and Data Analysis Tool for Genome Data Sets from All Kingdoms.	1:50 – 2:05pm	Friday, 3/29/19	Skipwith 2
Dan Li, Binsheng Gong and Joshua Xu	National Center for Toxiciological Research	Toward a highly reproducible targeted sequencing diagnosis for precision oncology	9:05 – 9:20am	Friday, 3/29/19	Skipwith 2
Ting Li, Shraddha Thakkar and Weida Tong	NCTR/UALR/UAMS	Tracing Drug Induced Liver Injury (DILI) signatures by harnessing cancer cell lines	8:35 – 8:50am	Friday, 3/29/19	Skipwith 2

Ziyi Li	Emory University	Dissecting differential signals in high-throughput data from complex tissues	3:30 – 3:45pm	Friday, 3/29/19	Hamilton 2
Jiannan Liu, Chuanpeng Dong, Yunlong Liu and Huanmei Wu	Indiana University Purdue University Indianapolis	CGPE: A user-friendly gene and pathway explore webserver for public cancer transcriptional data	10:15 - 10:30am	Friday, 3/29/19	Skipwith 2
Xiangwen Liu, Xiaowei Xu, Joseph Meehan, John Ho, Sandra Abbott, Lisa Creason, Weida Tong, Leihong Wu and Joshua Xu	FDA, National Center for Toxicological Research (NCTR) / University of Arkansas at Little Rock	Drug Labeling Identification based on Scene Text Detection and Recognition	8:50 - 9:05am	Friday, 3/29/19	Skipwith 2
Ann Loraine, Nowlan Freese, Charan Vallapureddy, Jill Jenkins, Kiran Korey, Karthik Raveendran, Mason Meyer, Pawan Bole, Pranav Tambvekar, Srishtee Marotkar, Riddhi Patil and Srishti Tiwari	Univeristy of North Carolina, Charlotte	Explore, analyze, and publish RNA-Seq, DNA-Seq, and gene function data with Integrated Genome Browser	3:15 – 3:30pm	Friday, 3/29/19	Skipwith 1
Xiang-Yang Lou	University of Arkansas for Medical Sciences	GMDR: A machine learning method for identifying multifactor interactions	3:30 – 3:45pm	Friday, 3/29/19	Skipwith 2
Annie Lumen	National Center for Toxicological Research	Computational tools for predicting drug dosimetry in pregnant women	9:45 – 10:00am	Saturday, 3/30/19	Skipwith 2
Hafez Eslami Manoochehri, Susmitha Sri Kadiyala and Mehrdad Nourani	University of Texas at Dallas	Weisfeiler-Lehman Graph Neural Network for Drug-Target Interaction Prediction	2:35 – 2:50pm	Friday, 3/29/19	Hamilton 2
Grover Miller	University of Arkansas for Medical Sciences	Lamisil (terbinafine) bioactivation pathways revealed through modeling and experimental approaches	9:25 – 09:45am	Saturday, 3/30/19	Skipwith 2
Winston Miller and Daniel Johnson	University of Tennessee Health Science Center	Orion: Hunting Stable Genes	4:00 – 4:15pm	Friday, 3/29/19	Skipwith 2
Ujwani Nukala, Awantika Singh, Shraddha Thakkar, Mahmoud Kiaei, Rupak Pathak, Nukhet Aykin-Burns, Philip Breen and Cesar Compadre	Joint Bioinformatics Graduate Program, University of Arkansas at Little Rock	Antioxidant Tocols as Potent Radiation Countermeasures	10:15 - 10:30am	Saturday, 3/30/19	Skipwith 2
Bohu Pan and Huixiao Hong	National Center for Toxicological Research	Assessment of technical repeatability for germline variants detected from whole genome sequencing (WGS) data	8:30 – 8:45am	Friday, 3/29/19	Skipwith 1
Aleksandra Perz, Cory Giles, Jonathan Wren, Zane Dennis and Constantin Georgescu	Oklahoma Medical Research Foundation	PubQC, the automated publication quality control system	2:20 – 2:35pm	Friday, 3/29/19	Skipwith 1

Erich A. Peterson	University of Arkansas for Medical Sciences	Approaches Towards Verification and Validation of Model Systems	2:05 – 2:20pm	Friday, 3/29/19	Skipwith 1
George Popescu	Mississippi State University	Classification methods for accurate gene family identification in complex genomes	9:05 – 9:20am	Friday, 3/29/19	Hamilton 2
Hunter Porter, Xiavan Roopnarinesingh, Cory Giles, Willard Freeman and Jonathan Wren	University of Oklahoma Health Sciences Center	The Biology Behind the Epigenetic Clock	9:25 – 9:40am	Friday, 3/29/19	Skipwith 1
Erika P. Portero, Zhichao Liu, Rosemary M. Onjiko, Chen Zeng, and Peter Nemes	University of Maryland, College Park	New-generation Single-Cell Mass Spectrometry Tools Enable Trace-level Analysis of Metabolites in the Live Embryo	9:25 – 09:45am		
Steven Ricke	University of Arkansas, Fayetteville	Application of Microbiome Sequencing in Food Processing Environments	1:30 – 1:50pm	Friday, 3/29/19	Skipwith 2
Suguna Devi Sakkiah and Huixiao Hong	National Center for Toxiciological Research	Antagonist Induced Androgen Receptor Structure Changes Elucidated by Docking and Dynamics Simulation	10:00 – 10:15am	Friday, 3/29/19	Skipwith 2
Zhenhua Shang and Shannon Davis	University of South Carolina	Characterization of mitochondria morphology by deep learning neural network model	10:30 – 10:45am	Friday, 3/29/19	Skipwith 2
Shraddha Thakkar	National Center for Toxicological Research	Integration of real-word information to capture Drug-induced liver injury evidence	8:20 – 8:35am	Friday, 3/29/19	Skipwith 2
Adam Thrash, Federico Hoffmann and Andy Perkins	Mississippi State University	A Machine Learning Approach to Genome Quality Assessment	3:45 – 4:00pm	Friday, 3/29/19	Skipwith 2
Adam Thrash, Juliet D. Tang, Mason DeOrnellis and Marilyn L. Warburton	Mississippi State University	PAST: the future of GWAS studies	10:30 – 10:45am	Friday, 3/29/19	Hamilton 2
Sooryanarayana Varambally	University of Alabama Birmingham	UALCAN: An integrated data mining tool for molecular sub-type based expression analyses	2:55 – 3:15pm	Friday, 3/29/19	Hamilton 2
Dong Wang	National Center for Toxiciological Research	Statistical Challenges and Opportunities for Biomarkers Based on Deep Sequencing and Other New Technologies	10:00 – 10:15am	Friday, 3/29/19	Hamilton 2
Zheng Wang	University of Miami	Global quality assessment of individual protein models by random forest and novel statistical potentials	2:20 – 2:35pm	Friday, 3/29/19	Hamilton 2
Ava Wilson, Victor Thannickal, James Mobley and Merry-Lynn McDonald	University of Alabama at Birmingham	Network Analysis Reveals Differential Proteomic and Transcriptomic Signatures Associated with TGF-B1 Treatment of IMR-90 Cells	8:35 – 8:50am	Friday, 3/29/19	Hamilton 2
Huanmei Wu	Indiana University Purdue University Indianapolis	Heterogeneous Biomedical Information Visualization	2:55 – 3:15pm	Friday, 3/29/19	Skipwith 1

Guodong Yang, Zhaohui Qin and Aiqun Ma	Emory University	An integrated system biology approach yields drug repositioning candidates for the treatment of heart failure	3:45 – 4:00pm	Friday, 3/29/19	Hamilton 2
Rendong Yang	The Hormel Institute	Integrating DNA and RNA for actionable alterations discovery in human cancer	3:15 – 3:30pm	Friday, 3/29/19	Hamilton 2
Nengjun Yi	University of Alabama Birmingham	Hierarchical Models for Analyzing Large-Scale Clinical and Molecular Data	9:25 – 09:45am	Friday, 3/29/19	Hamilton 2
Siamak Yousefi, Hao Chen, Jesse Ingels and Robert Williams	University of Tennessee Health Science Center	Single-cell RNA-seq analysis of retinal ganglion cells	9:45 – 10:00am	Saturday, 3/30/19	Hamilton 2
Zhongliang Yue	Indiana University Purdue University Indianapolis	GS-rank: disease gene prioritization based on network and gene sets, and an Alzheimer's disease study	9:45 – 10:00am	Friday, 3/29/19	Skipwith 2
Zongliang Yue and Jake Chen	University of Alabama at Birmingham	GS-rank: disease gene prioritization based on network and gene sets, and an Alzheimer's disease study	9:40 – 9:55am	Friday, 3/29/19	Skipwith 1
Chaoyang Zhang, Gabriel Idakwo, Sundar Thangapandian, Joseph Luttrell, Zhaoxian Zhou, Huixiao Hong and Ping Gong	University of Southern Mississippi	Deep Learning for In Silico Predictive Toxicology	1:50 – 2:05pm	Friday, 3/29/19	Skipwith 1
Yifan Zhang and Mary Yang	University of Arkansas at Little Rock	Characterizing mutually exclusive mutations in pan-cancer	8:50 - 9:05am	Friday, 3/29/19	Hamilton 2
Junxiu Zhou	National Center for Toxicological Research	Data Mining on Prescription Opioid Use and Associated Medical Disorder	2:35 – 2:50pm	Friday, 3/29/19	Skipwith 1
Liyuan Zhu, Shraddha Thakkar, Ruth Roberts, Weida Tong and Zhichao Liu	National Center for Toxicological Research	Repurposing Immortalized Cell Line-based Transcriptomic Profiling Assays for Drug-induced Liver Injury with a PRank Method	10:30 – 10:45am	Saturday, 3/30/19	Hamilton 2
Wei Zhuang, Luísa Camacho, Camila Silva and Huixiao Hong	National Center for Toxicological Research	A Nonparametric Statistical Method to Analyze Incomplete Gene Expression Data	3:15 – 3:30pm	Friday, 3/29/19	Skipwith 2

Poster Presentations

POSTER PRESENTATIONS			
Poster#	**Authors**	**Poster Title**	**Type**
2	Himangi Srivastava and George Popescu	Methods for inference and analysis of signaling networks from time series data	Student
5	Liangqun Lu and Bernie Daigle	Prognostic Analysis of Histopathological Images Using Pre-Trained Convolutional Networks	Student
9	James Courtney	Statistical Testing for PTSD Biomarkers	Student
13	Mazen Istanbouli and Bernie J. Daigle Jr.	Multi-Omics Biomarker Discovery for Post-Traumatic Stress Disorder	Student
15	Xiavan Roopnarinesingh, Cory Giles, Hunter Porter, Chase Brown, Aleksandra Perz, Constantin Georgescu and Jonathan Wren	Classification of biological features using collapsed gene methylation	Student
16	Zhuo He, Haipeng Tang, Daniel McGonigle, Chaoyang Zhang, Zhixin Jiang and Weihua Zhou	A Deep-Learning-Based Segmentation Method for Left Ventricle on Gated SPECT Myocardial Perfusion Images	Student
20	Chase Brown, Jonathan Wren and Rheal Towner	Bioinformatic detection of synergy for synergistic drug repurposing	Student
21	Ted Ling Hu	Singular Value Decomposition: Data-Driven Feature Selection for Transcriptomics Data Sets	Student
23	Daniel McGonigle, Chen Zhao, Haipeng Tang, Chaoyang Zhang, Zhuo He, Robert Bober and Weihua Zhou	Deep Learning to Extract Coronary Arteries from Fluoroscopy Angiography	Student
27	Megan Breitbach, Ryne Ramaker, Kevin Roberts, Robert Kimberly and Devin Absher	Epigenetic Defects in the B-cell lineage of SLE Patients Display Population-Specific Patterns	Student
59	Ohgew Kweon, Seong-Jae Kim, Seongwon Nho, Dongryeoul Bae, Jungwhan Chon, Mark Hart, Jae Hyun Kim, Dong-Heon Baek, Young-Chang Kim, Wenjun Wang Wang, Sung-Kwan Kim, John Sutherland and Carl Cerniglia	CYPminer: An Automatable Cytochrome P450 Identification, Classification, and Data Analysis Tool for Genome Data Sets from All Kingdoms.	Professional
60	Gokhan Yavas, Huixiao Hong and Wenming Xiao	A Novel Metric for Assessing the Quality of de novo Assemblies	Professional
66	Mehmet Alpaydin, Sinan Kockara, Tansel Halic, Deepak Chittajallu and Henry Wong	A Virtual Training and Mole Mapping Platform for Total Body Photography	Student
67	Emre Ermisoglu, Sinan Kockara, Deepak Chittajallu, Tansel Halic and Henry Wong	Content Based Dermoscopic Image Retrieval for Diagnostic Decision Support	Student
68	Sutanu Bhattacharya and Debswapna Bhattacharya	Does inclusion of residue-residue contact information boost protein threading?	Student
70	Tansel Halic, Aditya Dendukuri, Mustafa Tunc, Shahryar Ahmadi, Sinan Kockara and Sreekanth Venkata	Fluid Flow for Virtual Arthroscopic Skill Trainer	Student
71	Doga Demirel, Berk Cetinsaya, Tansel Halic, Sinan Kockara, Dirk Reiners and Shahryar Ahmadi	An Iterative Approach for Partition-based Optimization Model for Generative Anatomy Modeling Language	Postdoctoral Fellow
73	Minjun Chen, Jieqiang Zhu, Jieun Seo, Sanglong Wang, Kristin Ashby, Ballard Rodney, Dianke Yu, Baitang Ning, Rajiv Agarwal, Jürgen Borlak and Weida Tong	THE DEVELOPMENT OF A HEPATOTOXICITY DATABASE FOR HERBAL AND DIETARY SUPPLEMENT	Professional
74	Peng Xu and Zechen Chong	Meiotic recombination in human genomes: a landscape of crossovers and non-crossover gene conversions	Postdoctoral Fellow

75	Nathaniel Hill, Taylor Ingle, Zhichao Liu, Leihong Wu, Junshuang Yang, Guangxu Zhou, Mary Yang, Weida Tong and Hong Fang	Utilizing FDALabel to Identify Adverse Drug Reaction Patterns in Antidepressants	Student
76	Eric Zhang, Thi Nguyen, Son Do Hai Dang, Thanh Nguyen, Wuqiang Zhu and Jay Zhang	Identification and pharmaceutical targeting of putative gene networks critical for closure of the cardiomyocyte proliferative window in large mammals: a blueprint	Student
77	Jiande Wu, Tarun Karthik Kumar Mamidi and Chindo Hicks	Breast Cancer Type Classification Using Machine Learning	Professional
78	Chindo Hicks, Tarun Karthik Kumar Mamidi and Jiande Wu	Bioinformatics for Integrating Germline and Somatic mutations in Cancer	Professional
79	Tarun Karthik Kumar Mamidi, Jiande Wu and Chindo Hicks	Mapping the Genomic and Epigenomic Mutation Interaction Landscape in Indolent and Aggressive Prostate Cancer	Professional
80	Mehran Ghafari, Hao-Bo Guo, Weiwei Dang and Hong Qin	Automatic Evaluation of Cellular Lifespan from Time-lapsed Microscopic Images	Student
81	Cord Carter, Cesar Compadre, Weida Tong and Shraddha Thakkar	USING STRUCTURE-BASED AND BIOLOGICAL DESCRIPTORS ANALYSIS TO ENHANCE THE PREDICTION OF DRUG-INDUCED LIVER INJURY	Student
82	Qi Li and Mary Yang	Biomarker Detection for Alzheimer's Disease based on MRI data analysis	Student
84	Thi Tran-Nguyen, Tongbin Zhang, Son Dang and Steven Duncan	Determining bronchial gene expression signature of Chronic Obstructive Pulmonary Diseases (COPD) by Machine Learning (ML) Techniques	Student
85	Vikram Pillai, Catherine Zander, Leland Mayne, Walter Englander and Long Zheng	Hydrogen exchange mass spectrometry reveals allosteric interactions between the distal and the proximal domains of human ADAMTS13	Postdoctoral Fellow
86	Inimary Toby	Characterizing the immune repertoire using data mining approaches	Professional
88	Michael Behring, Upender Manne, Akinyemi Ojesina, Howard Wiener, Yuanfan Ye, Sadeep Shrestha and Ana Vazquez	Signature-based tumor immunophenotype varies by molecular subtype but not by lymph node metastatic status in invasive ductal breast cancer	Postdoctoral Fellow
89	George Clement Dobbins, Donquan Chen, Jake Chen and Shannon Ross	Variant and Principal Component Analysis Applied to Next Generation Sequencing of Cytomegalovirus (CMV) Genomes from Congenitally Infected Infants with Symptomatic Infection and CMV-Related Hearing Loss	Professional
90	Ali Alalawi, Kaylee Henry, Md Abul Hayat, Hanna K. Jensen, Melvin S. Dassinger, Jeffrey M. Burford, Patrick C. Bonasso, Kevin W. Sexton, Jingxian Wu and Morten O. Jensen	Propofol affects peripheral venous tone in anesthetized patients	Student
91	Ayoola B Moses, Mary F Nakamya, Leslie A Shack, Justin A Thornton, Juhyeon Lim, Hyungjin Eoh, Edwin Swiatlo and Bindu Nanduri	CADAVERINE AND CAPSULE BIOSYNTHESIS IN STREPTOCOCCUS PNEUMONIAE	Professional
92	Anderson Butler, Dan Johnston, Simranjit Kaur and Farah Lubin	Context fear memory formation is regulated by hippocampal lncRNA-mediated histone methylation changes	Student
93	Karen Galarneau, Cathy Gresham, Carolina Stenfeldt, James J Zhu, Jonathan Arzt and Bindu Nanduri	Pathway analyses of host transcriptomic data for understanding host responses to foot-and-mouth disease virus	Postdoctoral Fellow
94	Roshan Darji, Jennifer Fisher and Brittany Lasseigne	Chromosomal instability metrics across human cancers	Professional
95	Jarrod Harman, Jessie Guidry and Jeff Gidday	Sexual Disparities in Retinal Function: Using MS and Bioinformatics to Quantify Differences in the Underlying Proteome	Student

96	Vishal Oza and Laura Reed	Constructing a graphical (network) model of the Drosophila melanogaster metabolome	Student
97	Dongying Li, Leihong Wu, Dianke Yu, Bridgett Knox, Si Chen, Lei Guo, Weida Tong and Baitang Ning	Characterization of Non-coding RNA and mRNA Interaction for Gene Regulation in Drug Metabolism and Hepatotoxicity	Postdoctoral Fellow
98	Robert Doerksen, Pankaj Pandey, Shamba Chatterjee, Christina Stallings and Sudeshna Roy	HYBRID VIRTUAL SCREENING APPROACH FOR THE IDENTIFICATION OF NOVEL MRAY INHIBITORS FOR TUBERCULOSIS CHEMOTHERAPY	Professional
99	Fang Chen, Venkata Melapu and Shuang Z. Tu	HEMODYNAMIC SIMULATION USING A HYBRID FINITE VOLUME/FINITE ELEMENT INCOMPRESSIBLE FLOW	Student
100	Robin Ghosh, Md Mohiuddin Hasan, Anirudh Reddy Cingreddy and Venkata Melapu	APPLICATIONS OF MACHINE LEARNING AND ARTIFICIAL INTELLIGENCE IN CLASSIFYING CANCER BY GENE EXPRESSION MONITORING	Student
101	Anirudh Reddy Cingireddy, Robin Gosh, Venkata Kiran Melapu, Cheronika Manyfield-Donald and Md Mohiuddin Hasan	EVALUATION AND COMPARISON OF VARIOUS FACTORS EFFECTING VASCULAR DEMENTIA AND ALZHEIMER’S DISEASE THROUGH MACHINE LEARNING AND ARTIFICIAL INTELLIGENCE	Student
103	David Mery, Amanda J. Compadre Compadre, Ordóñez Paola E, Philip J. Breen, Cesar M Compadre and Monica L Guzman	Uncovering Antileukemic Compounds from Nature through Analysis of Plant-Plant Interactions	

Tutorials

Day 1: Thursday, March 28, 2019	
TUTORIALS AND STUDENT CAREER DEVELOPMENT	
1:00 - 4:00 p.m.	**Tutorial 1: Single-Cell Genomic Data Analysis (Hamilton 2)** **Principle Instructor** – **Min Gao,** Ph.D., Informatics Institute, UAB **Tutorial Overview** – The single-cell analyses will allow researchers to uncover new and potentially unexpected biological discoveries relative to traditional profiling methods that assess bulk populations. This tutorial is to provide an overview of the laboratory and computational method involved in generating and analyzing single cell data. Participants will be introduced to the workflow of single cell analysis, the principles of single cell platforms, including Fluidigm C1/ Biomark, 10xGenomics, BD Rhapsody, and iCell8, and will focus on different solutions of 10xGenomics. The tutorial will introduce the main computational algorithms and tools for single cell data analysis, including demultiplexing sequence alignment, quality control, identifying clusters of cells and performing analyses to assign cell identity and function. We will also give an introduction of single-cell RNA sequencing in immunology and use Loupe browser to show how to work with single cell V(D)J seq data. There will be a hands-on case study on single cell RNAseq data analysis. Analyses will be performed by using Seurat in R interfaces.
1:00 - 1:10 p.m.	Introduction and Overview **Min Gao, Ph.D.,** *Informatics Institute, UAB*
1:10 - 1:40 p.m.	Introduction of Single-Cell Analysis **Shanrun Liu, Ph.D.,** *CFCC single cell core, UAB*
1:40 - 2:25 p.m.	Computational Techniques for Single-Cell Data Analysis **Jake Chen, Ph.D.,** *Informatics Institute, UAB*
2:45 - 3:15 p.m.	Single-Cell RNA Sequencing in Immunology **Christopher Fucile,** MS, *Informatics Institute, UAB*
3:15 - 4:00 p.m.	Single-Cell RNAseq Data Analysis – Case Study (hands-on) **Min Gao**, Ph.D., *Informatics Institute, UAB*

TUTORIALS AND STUDENT CAREER DEVELOPMENT	
1:00 - 4:00 p.m.	**Tutorial 2: Metabolomics Data Analysis (Skipwith 2)** **Principle Instructor** – **Stephen Barnes**, Ph.D., Professor Pharmacology & Toxicology, UAB
1:00 - 1:10 p.m.	Introduction to the Tutorial Session **Stephen Barnes**, Ph.D., *Professor Pharmacology & Toxicology, UAB* **Xiuxia Du**, Ph.D. *UNC-Charlotte*
1:10 - 1:40 p.m.	Analyzing Metabolomics Data Using MZmine **Xiuxia Du,** Ph.D. *UNC-Charlotte*
1:40 - 2:25 p.m.	The Principal Features of XCMS **Stephen Barnes**, Ph.D., *Professor Pharmacology & Toxicology, UAB* **Xiuxia Du**, Ph.D. *UNC-Charlotte*
2:45 - 3:15 p.m.	Statistical Analysis of Metabolomics Data Using Metaboanalyst 4.0 **Stephen Barnes**, Ph.D., *Professor Pharmacology & Toxicology, UAB*
3:15 - 4:00 p.m.	Identifying Metabolic Pathways Imbedded in Metabolomics Data Using Mummichog **Stephen Barnes**, Ph.D., *Professor Pharmacology & Toxicology, UAB* **Xiuxia Du**, Ph.D. *UNC-Charlotte*

Student Sessions

Career Development – Day 1: Thursday, March 28, 2019 – 1:00 to 4:00 p.m.

The mission of the MidSouth Computational Biology and Bioinformatics Society is to foster collaborative research in bioinformatics and computational biology by providing a forum for scientists of various backgrounds and disciplines to interact to solve biological, health and/or biomedical problems using computational tools. Student research has always been a prominent component of the annual conference, which can be seen in the activities such as student awards, preconference hands-on workshops, and career development activities. Career development is an integral part of MCBIOS' commitment to its trainee members. Professional skills including communication, planning, teamwork, and project management are valued by employers across a wide range of sectors. MCBIOS recognizes that it is important to promote an environment where these skills can be developed and also provide the necessary resources to our trainee members. Furthermore, the career development session offers an enhanced experience to help trainees identify and develop an individualized career plan for themselves. The goals of this session are:

1) To present trainees with a breadth of career-related resources
2) To provide a framework for career trajectory and planning

Topics that will be addressed include: social media for science careers, career options in academia, career options in industry, career lessons learned, career planning, and identifying resources.

Young Scientist Excellence Awards – Day 2: Friday, March 29, 2019 – 8:00 to 9:20 a.m.

MCBIOS Young Scientist Excellence awards program recognizes students and postdoctoral fellows that exhibit scientific excellence in the field of Bioinformatics. Student and postdoctoral fellows go through a rigorous award application and the top five candidates will give an oral presentation in a session dedicated to this award program. In addition to an abstract, participation in this program requires submission of separate description of the innovation of the research and individual contribution to the work being presented. Selection of the top five is based on the evaluation of the award applications first by the MCBIOS board members, and subsequently by a panel of judges (including keynote speakers), for the quality and impact of the research. The quality of the professional presentation is the primary consideration for selection of the award recipients. Applicants with demonstrated multidisciplinary contribution and initiative are given preference during final selection.

Student Mentoring Breakfast- Day 3: Saturday, March 30 – 7:00 to 8:00 a.m.

This year, MCBIOS is implementing a new student-driven initiative which offers an additional opportunity for interactions between faculty members and students. The student mentoring breakfast event offers an opportunity for students to connect with other trainees as well as to have one-on-one discussions with faculty mentors in a casual atmosphere.

Expert Panel

Bioinformatics Education: What's the right curriculum for future translational biomedical data scientists?

Jake Y. Chen, Ph.D.
Professor of Genetics, Computer Science, and Biomedical Engineering
Chief Bioinformatics Officer
Informatics Institute
University of Alabama at Birmingham

Matthew Might, Ph.D.
Professor of Medicine and Computer Science
Founding Director
Hugh Kaul Precision Medicine Institute
University of Alabama at Birmingham

Da Yan, Ph.D.
Assistant Professor of Computer Science
University of Alabama

Ramin Homayouni, Ph.D.
Professor & Director
Population Health Informatics
Beaumont School of Medicine
Oakland University

Roundtable Discussions