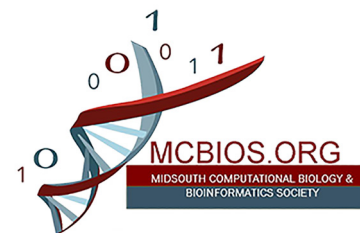


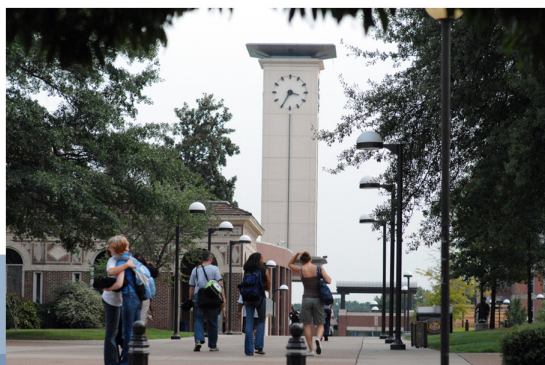
13th Annual MCBIOS: XIII

March 3-5, 2016

MIDSOUTH COMPUTATIONAL BIOLOGY &
BIOINFORMATICS SOCIETY



Hosted by the University of Memphis Bioinformatics Program



Precision Medicine
and
Data Sciences

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Mid-South Computational Biology and Bioinformatics (MCBIOS)
XIII Annual Conference
March 3-5, 2016
FedEx Institute of Technology,
University of Memphis, Memphis, TN

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- **Weida Tong, Ph.D., Speaker Coordinator**
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MCBIOS Mission Statement

The mission of the MidSouth Computational Biology and Bioinformatics Society (MCBIOS) is to foster networking and collaboration, and promote the professional development of our 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
- We have a strong orientation toward supporting our student and postdoctoral members.
- Membership and participation is open to all, though efforts focus on supporting members in the MidSouth region of the United States (Arkansas, Louisiana, Mississippi, Missouri, Oklahoma, Texas).

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MCBIOS 2016 Program Overview

“Precision Medicine & Data Science”

	Day 1, Thursday March 3, 2016		
8:30am-6:30pm	Registration and Poster Set-up “Lobby FedEx Institute”		
9:30am-12:30pm	St. Jude Children’s Hospital tour Bus will leave from FedEx Institute		
2:00pm-2:15pm	Opening Remarks “The Zone”		
2:150pm-3:05pm	Keynote Session I - Mary V. Relling, Pharm.D. Member and Chair, Department of Pharmaceutical Sciences St. Jude Children’s Research Hospital, Memphis, TN “The Zone”		
3:05pm-3:15pm	Break “Lobby FedEx Institute”		
3:15pm-4:35pm	Breakout Session -I miRNA and Toxicogenomics Yuping Wang, Ph.D., National Center for Toxicological Research, FDA “Methodist Presentation Theatre”	Breakout Session -II Targeted Therapies, Systems Biology and Future of the Safety Assessment William B. Mattes, Ph.D., National Center for Toxicological Research, FDA “The Zone”	Breakout Session -III Protein Structure/Function and Biological Networks Jianlin Cheng, Ph.D., University of Missouri “Fish Bowl”- 2 nd Floor
4:35pm-6:30pm	Reception and Mixer “Lobby FedEx Institute”		
	Day 2, Friday March 4, 2016		
9:00am-9:50am	Keynote Session II – Carl E. Cerniglia, Ph.D. Director, Division of Microbiology, National Center for Toxicological Research, U.S. Food and Drug Administration, Jefferson, Arkansas “The Zone”		
9:50am-10:00am	Break “Lobby FedEx Institute”		
10:00am-11:20am	Breakout Session –IV Microbiome: Disease and Drug Resistance Steven Foley, Ph.D., National Center for	Breakout Session -V Predictive toxicology and Chemo-informatics Huixiao Hong, Ph.D., National Center for	Breakout Session -VI Next Generation Sequencing Vinhuy Phan, Ph.D., University of Memphis

	Toxicological Research, FDA “The Zone”	Toxicological Research, FDA and Ping Gong, Ph.D., US Army Corps of Engineers “Methodist Presentation Theatre”	“Fish Bowl” - 2 nd Floor
11:20am-12:30pm	Lunch (Business Meeting and Board Elections) “Holiday Inn Ballroom”		
12:30pm-1:50pm	Breakout Session –VII Machine Learning in Large Data Weida Tong, Ph.D., and Wen Zou, Ph.D., National Center for Toxicological Research, FDA “The Zone”	Breakout Session –VIII Proteomics and Host-pathogen interaction Bindu Nanduri , Ph.D., Mississippi State University “Methodist Presentation Theatre”	Breakout Session –IX Bioinformatics Methodologies Chaoyang Zhang, Ph.D., University of Southern Mississippi “Fish Bowl” - 2 nd Floor
1:50pm-2:00pm	Break “Lobby FedEx Institute”		
2:00pm-3:30pm	Poster Session “Lobby FedEx Institute”		
3:45pm-6:45pm	Workshop –I iPlant Collaborative Jason Williams, Ph.D., <i>Cyverse , Cold Spring Harbor Laboratory</i> “Fish Bowl”- 2 nd Floor	Workshop –II Gene Network and Systems Genetics Robert Williams, Ph.D., <i>University of Tennessee Health Science Center</i> “Methodist Presentation Theatre”	Workshop- III Next Generation Sequencing Analysis Rakesh Kaundal, Ph.D., <i>University of California, Riverside, CA</i> “The Zone”
Day 3, Saturday March 5, 2016			
7:00am-8:30am	Board Business Meeting “Holiday Inn University of Memphis”		
9:00am-9:50am	Keynote Session III Christopher E. Mason, Ph.D. Associate Professor, Department of Physiology and Biophysics, Weill Cornell Medical College, New York, USA “The Zone”		
9:50am-10:00am	Break “Lobby FedEx Institute”		
10:00am-11:20am	Breakout Sessions-X Oncology and Precision Medicine	Breakout Sessions-XI Genomics Mikhail	Breakout Sessions- XII Drug Discovery and Development

	Donald Johann, Ph.D., University of Arkansas Medical Sciences "The Zone"	Dozmorov, Ph.D., Virginia Commonwealth University "Fish Bowl" - 2 nd Floor	Cesar Compadre, Ph.D., University of Arkansas Medical Sciences "Methodist Presentation Theatre"
11:30-12:00pm	Keynote Session IV William Slikker, Jr., Ph.D., Director, National Center for Toxicological Research, FDA, Jefferson, AR The Zone"		
12:00-1:00pm	Awards, Recognitions, Closing and Lunch "Holiday Inn Ballroom"		

MCBIOS 2016 Detailed Program

	Day 1, Thursday March 3, 2016
8:30am-6:30pm	Registration and Poster Set-up "Lobby FedEx Institute"
9:30am-12:30pm	Tour to St. Jude Children's Hospital Bus will leave from FedEx Institute
2:00pm-2:15pm	Welcome and Opening Remarks <ul style="list-style-type: none"> MCBIOS President - Cesar M. Compadre, Ph.D., <i>University of Arkansas for Medical Sciences, Little Rock, AR</i> MCBIOS 2016 Conference Chair - Ramin Homayouni, Ph.D., <i>University of Memphis, Memphis, TN</i> Andrew W. Meyers, Ph.D., <i>Interim VP for Research & Executive Director of University of Memphis Research Foundation, University of Memphis, Memphis, TN</i> "The Zone"
2:15pm-3:05pm	Keynote Session I – Clinical Implementation of Pharmacogenetics in Precision Medicine Mary V. Relling, Pharm.D., <i>Member and Chair, Department of Pharmaceutical Sciences, St. Jude Children's Research Hospital, Memphis, TN</i> "The Zone"
3:05pm-3:15pm	Break "Lobby FedEx Institute"
3:15pm-4:35pm	Breakout Session –I, II, III
	Breakout Session –I : miRNA and Toxicogenomics "Methodist Presentation Theatre" Session Chair- Yuping Wang, MD, Ph.D., DABT, <i>Staff Fellow, U.S. Food and Drug Administration, National Center for Toxicological Research, Jefferson, AR</i> Session Co-Chair - Dan Li, Student, <i>University of Arkansas at Little Rock, Little Rock AR</i>
3:15pm-3:35pm	Session Featured Speaker Evaluation of Toxicogenomics in Advanced Research and Novel Applications Yuping Wang, MD, Ph.D., DABT, <i>Staff Fellow, U.S. Food and Drug Administration, National Center for Toxicological Research, Jefferson, AR</i>
3:35pm-3:50pm	Integration Of MicroRNA-mRNA Interaction Networks With Microarray Data To Increase Experimental Power Bernie Daigle, Ph.D., <i>Assistant Professor, University of Memphis, Memphis, TN</i>
3:50pm-4:05pm	Evaluation of Non-Invasive Micrornas As Biomarkers of Hepatotoxicity; An Update on Translational Acetaminophen Toxicity Biomarkers In Children Xi Yang, Ph.D., <i>Visiting Scientist, Division of Systems Biology, National Center for Toxicological Research, U.S. Food and Drug Administration, Jefferson, AR</i>
4:05pm-4:20pm	MmiRNA-Viewer: A Data Visualization Tool Built to Present The Relationship Between MiRNAs and MRNA's

	Yongsheng Bai, Ph.D., <i>Assistant Professor, Indiana State University, Terre Haute, Indiana</i>
4:20pm-4:35pm	Identification of A Non-Canonical Micro-RNA In An <i>Fgf2</i>-Specific SNP Region Among Breast Cancer Patients Yusuf Nawawi, Student, <i>University of Arkansas for Medical Sciences, Little Rock, Arkansas</i>
	<u>Breakout Session –II: Targeted Therapies, Systems Biology and the Future of Safety Assessment</u> “The Zone” Session Chair - William B. Mattes, Ph.D., DABT , <i>Division Director, Division of Systems Biology, National Center for Toxicological Research, U.S. Food and Drug Administration, Jefferson, AR</i> Session Co-Chair - Nathan Crabtree, Student, <i>University of Arkansas at Little Rock, Little Rock, AR</i>
3:15pm-3:35pm	Session Featured Speaker Targeted Therapies, Systems Biology and The Future of Safety Assessment William B. Mattes, Ph.D., DABT - , <i>Division Director, Division of Systems Biology, National Center for Toxicological Research, U.S. Food and Drug Administration, Jefferson, AR</i>
3:35pm-3:50pm	Identification of Disease Biomarkers Via Integrated Analysis of Longitudinal Clinical and Genomic Data Michelle Lacey, <i>Associate Professor, Tulane University, New Orleans, LA</i>
3:50pm-4:05pm	Exploring The Allosteric Inhibitory Binding Sites For Known Negative Allosteric Modulators Within The Cannabinoid Cb2 Receptor Pankaj Pandey, <i>Post-Doctoral Research Associate, The University of Mississippi, Oxford, MS</i>
4:05pm-4:20pm	Determination of New Biosynthetic Pathways Of Ascorbic Acid Using Bioinformatics Modelling Skylar Connor, <i>Student, University of Arkansas at Pine Bluff, Pine Bluff, AR</i>
4:20pm-4:35pm	PROMISE-ME: A Robust Method For Integrated Analysis of DNA Methylation, Gene Expression, And Multiple Biologically Related Clinical And Pharmacological Outcomes Stan Pounds, <i>Professor, St. Jude Children's Research Hospital, Memphis, TN</i>
	<u>Breakout Session –III Protein Structure/Function and Biological Networks</u> “Fish Bowl”- 2 nd Floor Session Chair - Jianlin Cheng, Ph.D., <i>Associate Professor, University of Missouri, Columbia, MO</i> Session Co-Chair - Ujwani Nukala, Student, <i>University of Arkansas for Medical Sciences, Little Rock, AR</i>
3:15pm-3:35pm	Session Featured Speaker <i>De novo</i> protein conformational sampling using a probabilistic graphical model Jianlin Cheng, Ph.D., <i>Associate Professor, University of Missouri, Columbia, MO</i>
3:35pm-3:50pm	Phylogenetic Tree Construction Using Trinucleotide Usage Profile (Tup)

	Dale Bowman, Ph.D., <i>Assistant Professor, University of Memphis , Memphis, TN</i>
3:50pm-4:05pm	Effective Comparative Analysis of Protein-Protein Interaction Networks By Measuring The Steady State Network Flow Using A Markov Model Hyundoo Jeong, <i>Student, University of Texas A&M, Collage Station, TX</i>
4:05pm-4:20pm	Matrix Linear Models For High Throughput Genetic Screens Śaunak Sen, Ph.D., <i>Professor and Chief of Biostatistics, University of Tennessee Health Science Center, Memphis, TN</i>
4:20pm-4:35pm	A Graph-Theoretic Model of Nucleotide Binding Domain 2 Of The Cystic Fibrosis Transmembrane Conductance Regulator Samuel Kakraba, <i>Student, University of Arkansas at Little Rock, Little Rock, AR</i>
4:35pm-6:30pm	Reception and Mixer "Lobby FedEx Institute"
Day 2, Friday March 4, 2016	
9:00am-9:50am	Keynote Session – II Human Microbiome: Sequencing-Based High-Throughput Omics Technology and Bioinformatics Used in The Assessment of The Safety of Antimicrobial Drug Residues in Food Carl E. Cerniglia, Ph.D., <i>Director, Division of Microbiology, National Center for Toxicological Research, U.S. Food and Drug Administration, Jefferson, Arkansas</i> "The Zone"
9:50am-10:00am	Break "Lobby FedEx Institute"
10:00pm-11:20pm	Breakout Session –IV, V, VI
	Breakout Session –IV: <u>Microbiome: Disease and Drug Resistance</u> "The Zone" Session Chair - Steven Foley, Ph.D., <i>Research Microbiologist, Division of Microbiology, National Center for Toxicological Research, U.S. Food and Drug Administration, Jefferson, Arkansas</i> Session Co-Chair - Caleb Benson, <i>Student, Mississippi State University, Starkville, Mississippi, MS</i>
10:00am-10:20am	Session Featured Speaker The Microbiome And Its Relationship with Antimicrobial Resistance Steven Foley , Ph.D., <i>Research Microbiologist, Division of Microbiology, National Center for Toxicological Research, U.S. Food and Drug Administration, Jefferson, Arkansas</i>
10:20am-10:35am	Silver Nanoparticles: Effect on Intestinal Microbiome and Development of Resistance Sangeeta Khare, Ph.D., <i>Research Microbiologist, Division of Microbiology, National Center for Toxicological Research, U.S. Food and Drug Administration, Jefferson, Arkansas</i>
10:35am-10:50am	Network Based Functional Pan-Genomics: A New Approach To Build Connections Between Genomic Dynamics And Phenotypic Evolution In The Genus Mycobacterium

	Ohgew Kweon, Ph.D., <i>Research Microbiologist, Division of Microbiology, National Center for Toxicological Research, U.S. Food and Drug Administration, Jefferson, Arkansas</i>
10:50am-11:05am	Complete Genome Sequence of Flavobacterium Columnare Strain 94-081 Salih Kumru, <i>Student, Mississippi State University, Starkville, Mississippi</i>
11:05am-11:20am	An Alignment-Based Method For Profiling Microbial Community Using Compressed FM-Index Shanshan Gao, <i>Student, University of Memphis, Memphis, TN</i>
	Breakout Session –V <u>Predictive toxicology and Chemo-informatics</u> “Methodist Presentation Theatre” Session Chair - Huixiao Hong, Ph.D., <i>Senior Scientist, Division of Bioinformatics and Biostatistics, National Center for Toxicological Research, U.S. Food and Drug Administration, Jefferson, AR and</i> Ping Gong, Ph.D., <i>Principle Investigator at Environmental Laboratory, U.S. Army Engineer</i> Session Co-Chair - Kristin McEuen, <i>Student, University of Arkansas at Little Rock, Little Rock, AR</i>
10:00am-10:20am	Session Featured Speaker Predictive Toxicology in Regulatory Science: Endocrine Disruptors Knowledge Base Huixiao Hong, Ph.D., <i>Senior Scientist, Division of Bioinformatics and Biostatistics, National Center for Toxicological Research, U.S. Food and Drug Administration, Jefferson, AR</i>
10:20am-10:35am	Earthworm Toxicogenomics: A 21st Century Approach And Toolbox For Environmental Predictive Toxicology Ping Gong, Ph.D., <i>Principle Investigator at Environmental Laboratory, U.S. Army Engineer</i>
10:35am-10:50am	Quantitative Structure-Activity Relation Study Of Quaternary Ammonium Compounds In Pathogen Control: Computational Methods For The Discovery Of Food Antimicrobials Ethan Rath, <i>Student, Indiana State University, Terre Haute, Indiana</i>
10:50am-11:05am	The Development Of A QSAR Model For Predicting Estrogen Receptor-A Binding Using Large Data Sets HuiWen Ng, Ph.D., <i>Post-Doctoral Associate, Division of Bioinformatics and Biostatistics, National Center for Toxicological Research, U.S. Food and Drug Administration, Jefferson, Arkansas</i>
11:05am-11:20am	Hepatotoxicity And Mitochondrial Toxicity Of FDA Approved Tyrosine Kinase Inhibitors Qiang Shi, Ph.D., <i>Visiting Scientist, Division of Systems Biology, National Center for Toxicological Research, U.S. Food and Drug Administration, Jefferson, AR</i>
	Breakout Session –V I: <u>Next Gen Sequencing</u> “Fish Bowl”- 2 nd Floor Session Chair - Vinhthuy Phan, Ph.D., <i>Associate Professor, University of Memphis,</i>

	<p><i>Memphis, Tennessee</i></p> <p>Session Co-Chair - Samuel Kakraba, <i>Student, University of Arkansas for Medical Sciences, Little Rock, AR</i></p>
10:00am-10:20am	<p>Session Featured Speaker</p> <p>Strategies for efficient partial alignment of reads for DNA/RNA quantification</p> <p>Vinhthuy Phan, Ph.D., <i>Associate Professor, University of Memphis, Memphis, Tennessee</i></p>
10:20am-10:35am	<p>Differentially Expressed Genes In Latitudinal Populations Of Common Sunflower (<i>Helianthus Annuus</i> L.) Are Enriched With Microsatellites</p> <p>Chathurani Ranathunge, <i>Student, Mississippi State University, Starkville, Mississippi</i></p>
10:35am-10:50am	<p>Multiclass Computational Evolution: Benchmark Evalutation And Application To Rna-Seq Biomarker Discovery</p> <p>Nathan Crabtree, <i>Student, University of Arkansas at Little Rock, Little Rock, AR</i></p>
10:50am-11:05am	<p>Fm-Index Based Light-Weight Alignment For Quantification Of Rna-Seq Data</p> <p>Quang Tran, <i>Student, University of Memphis, Memphis, Tennessee</i></p>
11:05am-11:20am	<p>Large-Scale Soybean Genomic Variation Analysis Workflow In Soykb NGS Browser</p> <p>Yang Liu, <i>Student, University of Missouri, Columbia, MO</i></p>
11:20am-12:30pm	<p>Lunch (Business Meeting and Board Elections)</p> <p>"Holiday Inn Ballroom"</p>
12:30pm-1:50pm	<p>Breakout Session –VII, VIII, IX</p>
	<p>Breakout Session –VII <u>Machine Learning in Large Data</u></p> <p>"The Zone"</p> <p>Session Chair- Wen Zou, Ph.D. ,<i>Visiting Scientist, U.S. Food and Drug Administration , National Center for Toxicological Research, Jefferson, AR</i></p> <p>Session Co- Chair- Islam Ebeid, <i>Student, University of Arkansas at Little Rock, Little Rock, AR</i></p>
12:30pm-12:50pm	<p>Session Featured Speaker</p> <p>Of Text and Gene – Analysis of Big Genomics Data with Text Mining Methods</p> <p>Weida Tong, Ph.D. <i>Division Director, Division of Bioinformatics and Biostatistics, National Center for Toxicological Research, U.S. Food and Drug Administration, Jefferson, Arkansas</i></p>
12:50pm-1:05pm	<p>Best Practice In Mining Topics From Regulatory Textual Documents</p> <p>Weizhong Zhao, Ph.D., <i>Post-Doctoral Associate , Division of Bioinformatics and Biostatistics, National Center for Toxicological Research, U.S. Food and Drug Administration, Jefferson, Arkansas</i></p>
1:05pm-1:20pm	<p>High Performance Computing and Data Mining In Bioinformatics</p> <p>Richard Segall, Ph.D., <i>Professor, Arkansas State University, Jonesboro, AR</i></p>
1:20pm-1:35pm	<p>Leveraging Graph Topology and Semantic Context For Pharmacovigilance In Twitter Streams</p> <p>Ryan Eshleman, Ph.D., <i>Research Staff, Biocomputing and Media Research Lab, San Francisco State University, San Francisco, California</i></p>

1:35pm-1:50pm	Successful Classification of Cocaine Dependence Using Brain Imaging: A Machine Learning Approach Mutlu Mete, Ph.D., <i>Associate Professor, University of Texas A&M, Collage Station, TX</i>
	Breakout Session –VIII <u>Proteomics & Host-pathogen interaction</u> “Methodist Presentation Theatre” Session Chair- Bindu Nanduri, Ph.D., <i>Associate Professor, Mississippi State University, Starkville, MS</i> Session Co-Chair- Anagha Gopakumar, <i>Student, Mississippi State University, Starkville, MS</i>
12:30pm-12:50pm	Session Featured Speaker Proteomics and Host-Pathogen Interactions Bindu Nanduri, Ph.D., <i>Associate Professor, Mississippi State University, Starkville, Mississippi</i>
12:50pm-1:05pm	Vdjml – Tools For Capturing The Results Of Inferring Immune Receptor Rearrangements Inimary Toby, Ph.D. , <i>Computational Biologist II , UT Southwestern Medical Cente, Dallas, TX</i>
1:05pm-1:20pm	A Template-Based Protein Structure Reconstruction Method Using Deep Autoencoder Learning Haiou Li, <i>Student , University of Missouri, Columbia, MO</i>
1:20pm-1:35pm	Proteomics of Host and Pathogen To Study The Role of Polyamine Transport In Pneumococcal Virulence In A Mouse Model Aswathy Rai, Ph.D., <i>Post-Doctoral Associate, Mississippi State University, Starkville, Mississippi</i>
1:35pm-1:50pm	Single Model Quality Assessment Using Protein Structural And Contact Information With Machine Learning Techniques Renzhi Cao, <i>Student, University of Missouri, Columbia, MO</i> Un Jung Lee and Tamu
	Breakout Session –IX <u>Bioinformatics Methodologies</u> “Fish Bowl”- 2 nd Floor Session Chair- Chaoyang (Joe) Zhang, Ph.D., <i>Professor, University of Southern Mississippi, Hattiesburg, Mississippi</i> Session Co-Chair - Meenakshisundaram Balasubramaniam, <i>Student, University of Arkansas at Little Rock, Little Rock, AR</i>
12:30pm-12:50pm	Session Featured Speaker New Advances in Inference of Gene Regulatory Networks from Time Series Data Chaoyang (Joe) Zhang, Ph.D., <i>Professor, University of Southern Mississippi, Hattiesburg, Mississippi</i>
12:50pm-1:05pm	The Challenges of Long non-coding RNA Function Prediction Phil Williams, Ph.D., <i>Director, MidSouth Bioinformatics, University of Arkansas at Little Rock, Little Rock, AR</i>
1:05pm-1:20pm	An Integrated Statistical Probe of Error Correction Methods for Next-

	Generation Sequencing Data Isaac Akogwu, <i>Student, University of Southern Mississippi, Hattiesburg, Mississippi</i>
1:20pm-1:35pm	BRIDGES – Biomarkers Reuse In Different Gene Expression Systems Leihong Wu, Ph.D., <i>Post –Doctoral Fellow, Division of Bioinformatics and Biostatistics, National Center for Toxicological Research, U.S. Food and Drug Administration, Jefferson, Arkansas</i>
1:35pm-1:50pm	A framework for evaluating the quality of the personal genomes generated by de novo assembly tools Gokhan Yavas, Ph.D., <i>Computer Scientist, Division of Bioinformatics and Biostatistics, National Center for Toxicological Research, U.S. Food and Drug Administration, Jefferson, Arkansas</i>
1:50pm-2:00pm	Break “Lobby FedEx Institute”
2:00pm-3:30pm	Poster Session “Lobby FedEx Institute”
3:45pm-6:45pm	Workshop – I,II,III Session Chair - Zhichao Liu, Ph.D., <i>Visiting Scientist, U.S. Food and Drug Administration , National Center for Toxicological Research, Jefferson, AR</i>
	Workshop – I iPlant Collaborative Jason Williams, Ph.D., <i>Assistant Director, Cyverse (formerly iPlant Collaborative), DNA Learning Center, Cold Spring Harbor Laboratory</i> “Fish Bowl”- 2 nd Floor
	Workshop – II Gene Network and Systems Genetics Robert Williams, Ph.D., <i>Professor and Director, University of Tennessee Health Science Center, Memphis, TN</i> “Methodist Presentation Theatre”
	Workshop – III Next Generation Sequencing Analysis Rakesh Kaundal, Ph.D., <i>Director, High-Performance Computing, Institute for Integrative Genome Biology, University of California, Riverside, CA</i> “The Zone”
Day 3, Saturday March 5, 2016	
7:00am-8:30am	Board business meeting “Holiday Inn Meeting Room”
9:00am-9:50am	Keynote Session- III Genome, Epigenome, Transcriptome, and Epitranscriptome Landscapes: from single cells, to entire cities, to space Christopher E. Mason, Ph.D. , <i>Associate Professor, Department of Physiology and Biophysics, Weill Cornell Medical College, New York, USA</i> “The Zone”

9:50am-10:00am	Break "Lobby FedEx Institute"
10:00am-11:20am	Breakout Session –X,XI,XII
	Breakout Session –X: <u>Oncology and Precision Medicine</u> "The Zone" Session Chair - Donald J. Johann, Ph.D., <i>Associate Professor, University of Arkansas for Medical Sciences, Little Rock, Arkansas</i> Session Co-Chair- Oluwatosin Oluwadare, <i>Student, University of Missouri, Columbia,MO</i>
10:00am-10:20am	Session Featured Speaker Approaching Precision Oncology with Tissue Proteomics Donald J. Johann, Ph.D., <i>Associate Professor, University of Arkansas for Medical Sciences, Little Rock, AR</i>
10:20am-10:35am	Potential Reuse of Oncologic Drugs For The Treatment Of Rare Diseases Zhichao Liu, Ph.D., <i>Visiting Scientist, U.S. Food and Drug Administration , National Center for Toxicological Research, Jefferson, AR</i>
10:35am-10:50am	Texture Homogeneity Analysis of Lesion Border in Dermoscopy Images For Malignancy Detection Sertan Kaya, <i>Student, Arkansas State University, Jonesboro, AR</i>
10:50am-11:05am	Mode of Action And Biomarker Discovery for Anti-Cancer Natural Products Malia Potts, Ph.D., <i>Post-Doctoral Associate, St. Jude Children's Research Hospital, Memphis, TN</i>
11:05am-11:20am	Procedures for Identifying Biomarkers-Defined Subgroups With Differential Treatment Effect Through Recursive Partitions in Precision Medicine Un Jung Lee, Ph.D., <i>Post-Doctoral Associate, U.S. Food and Drug Administration , National Center for Toxicological Research, Jefferson, AR</i>
	Breakout Session –XI: <u>Genomics</u> "Fish Bowl"- 2 nd Floor Session Chair - Mikhail Dozmorov, <i>Ph.D., Assistant Professor, Virginia Commonwealth University, Richmond, Virginia</i> Session Co-Chair - Haiou Li, <i>Student, University of Missouri, Columbia, MO</i>
10:00am-10:20am	Session Featured Speaker Genome runner Web Server: Regulatory Similarity and Differences Define Functional Impact Of Snp Sets Mikhail Dozmorov, Ph.D., <i>Assistant Professor, Virginia Commonwealth University, Richmond, Virginia</i>
10:20am-10:35am	Missing Data Interpretation For Non-Referenced or Semi-Referenced Genomes Charles Chen, Ph.D., <i>Assistant Professor, Oklahoma State University, Stillwater, OK</i>
10:35am-10:50am	Update On The MCBIOS Timeber -Rattlesnake Genome Project Adam Thrash, <i>Student, Mississippi State University, Starkville, Mississippi</i>
10:50am-11:05am	Comparative Functional Genomics Of Mammalian Sperm Th2b, Regulator Of Sperm Chromatin Dynamics And Male Fertility

	Naseer Kutchy, <i>Student, Mississippi State University, Starkville, Mississippi</i>
11:05am-11:20am	Comparative Genomics Analysis of Aeromonas Hydrophila Strains Hasan Tekedar, <i>Student, Mississippi State University, Starkville, Mississippi</i>
	Breakout Session –XII : Drug Discovery and Development “Methodist Presentation Theatre” Session Chair - Cesar M. Compadre, BS, MS, Ph.D., <i>Professor, Department of Pharmaceutical Sciences, University of Arkansas for Medical Sciences</i> Session Co-Chair- Renzhi Cao, <i>Student, University of Missouri, Columbia ,MO</i>
10:00am-10:20am	Session Featured Speaker Development of the Tocoflexols, a Series of Novel Vitamin E Analogues with Improved Bioavailability Cesar M. Compadre, BS, MS, Ph.D., <i>Professor, Department of Pharmaceutical Sciences, University of Arkansas for Medical Sciences</i>
10:20am-10:35am	Design and Synthesis of selective TF/VIIa Inhibitors Darin E. Jones, Ph.D., <i>Assistant Professor, University of Arkansas at Little Rock, Little Rock, AR</i>
10:35am-10:50am	Liver Toxicity – Understanding of multiple dimensions of Drug-Induced Liver Injury Shraddha Thakkar, Ph.D., <i>Visiting Scientist, U.S. Food and Drug Administration , National Center for Toxicological Research, Jefferson, AR</i>
10:50am-11:05am	Protein Structure-Based Virtual Screening for The Discovery Of Novel CB2 Receptor Agonists Ngoc Luong Nguyen, <i>Student, University of Mississippi, Oxford, MS</i>
11:05am-11:20am	Use of Surface Signature Analysis To Study The Structure Anti-Leukemic Activity Relationship Of Sesquiterpene Lactones Ujwani Nukala, <i>Student, University of Arkansas at Little Rock, Little Rock, AR</i>
11:20am-11:30am	Break “Lobby FedEx Institute”
11:30am-11:55pm	Keynote Session IV Regulatory Implications of Genomics and Bioinformatics for Food and Drug Safety William Slikker, Jr., Ph.D., <i>Director, National Center for Toxicological Research, FDA, Jefferson, AR</i> “The Zone”
12:15pm-1:00pm	Awards, Recognitions, Closing Remarks and Lunch “Holiday Inn Ballroom”

List of Poster Presenters

S.No.	Name	Membership Type	Affiliation	Title
1	Alexander Yu	Student	University of Central Arkansas	Dynamic Voxelization For Virtual Rotator Cuff Surgery
2	Anagha Gopakumar	Student	Mississippi State University	The Role Of Polyamines In Pneumococcal Defense Mechansims Against Oxidative Stress Generated By Hydrogen Peroxide
3	Andrew Maxwell	Student	University of Southern Mississippi	Bayesian Learning In An Underdetermined System Of Gene Regulatory Networks
4	Aswathy Rai	Professional	Mississippi State University	Evaluation Of Host Response During Experimental Bovine Respiratory Disease Using Expression Proteomics
5	Binsheng Gong	Professional	National Center for Toxicological Research/FDA	Landscape Of Circrna Candidates Across 11 Organs And 4 Developmental Stages In Fischer 344 Rat
6	Caleb Benson	Student	Mississippi State University	Gene Expression Analysis Of Wild Type And An Iron-Dependent Transcriptional Regulator Deficient Pneumococci Using Rna-Seq
7	Cameron Walker	Student	University of Arkansas at Pine Bluff	Lcs Based Protein Structure Prediction
8	Chaitanya Mallikanti	Student	SIT India	Mobiprot: A Feasible Tool For Protein Sequence Alignment And Physiochemical Properties On Android Platform
9	Dan Li	Student	University of Arkansas at Little Rock	An Integrative Method For Comprehensively Reconstructing Transcripts
10	Dinum Perera	Professional	Mississippi State University	Advancing Pine Genomics: Identification And Characterization Of Wood Formation Genes From Pinus Taeda BAC Clones
11	Doga Demirel	Student	University of Central Arkansas	Time And Video Analysis Of Virtual Arthroscopic Tear Diagnosis And Evaluation Platform (VATDEP)
12	Edmund Glass	Student	Virginia Commonwealth	Maximizing The Power Of Cell

			University	Type-Specific Differential Expression Detection In Heterogeneous Gene Expression Measures
13	Halil Bisign	Professional	University of Michigan at Flint	A Probabilistic Framework For Identifying Drug-Drug Interactions And Primary Suspect Drugs For Multi-Drug Treatment Settings
14	Hithesh Kumar	Student	SIT India	De Novo Transcriptome Assembly Of Rauwolfia Serpentine Reveals Novel Transcript Related To Alkaloid Biosynthesis And Gene Discovery
15	Hong Fang	Professional	National Center for Toxicological Research/FDA	FDAlable Database: A Rich Resource For Study Of Pharmacogenomics Biomarkers To Facilitate Precision Medicine And Drug Safety
16	Isaac Akogwu	Student	University of Southern Mississippi	BECOW: A Web-Based Bioinformatics Error Correction Workflow Tool For Next Generation Sequence Data Correction
17	Islam Ebeid	Student	University of Arkansas at Little Rock	Visint-X: Visualizing Interactions In Cross-Linked Proteins
18	Itika Arora	Student	Indiana University–Purdue University Indianapolis	Digital Terrain Mapping As A Novel Disease Classification Tool: An Alzheimer’s Disease Case Study
19	Ji-Eun Seo	Student	National Center for Toxicological Research/FDA	Comprehensive Assessment Of Hepatotoxicity Induced By Herbal And Dietary Supplement
20	Jordan Fansler	Student	Oklahoma State University	Spiroplasma Relatedness Through The Investigation Of Viral Inserts
21	Joshua Xu	Professional	National Center for Toxicological Research/FDA	Developing An Intelligent Recognition System For Storage Pest Fragments Contaminating Food Products
22	Kevin Townsend	Student	University of Memphis	Large-Scale Microarray Data Integration For Improved Differential Expression Analysis
23	Khaled Elokely	Professional	Temple University	Model Construction And Validation Of Cannabinoid Receptors For Drug Discovery

24	Kristin McEuen	Student	University of Arkansas at Little Rock	A Bioinformatics Strategy To Enhance Dili Prediction By Integrating Diverse Predictive Models
25	Leihong Wu	Professional	National Center for Toxicological Research/FDA	Investigating The Role Of De Novo Assembly To Discover Single Nucleotide Variations In Human Genome
26	Lizhong Ding	Student	Indiana State University	Discovered Alternative Splicing From Tcga Suggests Across-Cancer Types Alternative Splicing And Regulatory Factor Alteration In These Cancer Types
27	Mais Ammari	Professional	University of Arizona	Hpidb 2.0: Current Updates In Database Content, Interface And Computational Prediction Of Host Pathogen Interactions
28	Manal Nael	Student	University of Mississippi	Design Of New Inhibitors Of Cyclin-Dependant Kinase 5 (Cdk5) For Alzheimer's Disease
29	Meenakshisundaram Balasubramaniam	Student	University of Arkansas at Little Rock	Proteins That Abrogate Aggregation By Blocking Ups Degradation In Neuro-Degenerative Diseases: A Combined Computational And Molecular Biology Approach
30	Minjun Chen	Professional	National Center for Toxicological Research/FDA	Daily Dose And Formation Of Reactive Metabolites Are Associated With The DRESS (Drug Reactions/Rash With Eosinophilia And Systemic Symptoms) Related Drug-Induced Liver Injury
31	Mohamed Aburweis	Student	South Dakota State University	Comparative Study Of The Repetitive Elements In Model Species Genomes
32	Mustafa Bayraktar	Student	University of Arkansas at Little Rock	Convex Hulls Generation And Convergence Of Density Based Skin Lesion Detection
33	Mustafa Bayraktar	Student	University of Arkansas at Little Rock	Left Ventricle Border Tracking To Determine Safe Delivery Trajectory For Transapical Aortic Valve Replacement
34	Mustafa Bayraktar	Student	University of Arkansas at Little Rock	A Framework Proposal For Longitudinal Tumor Response Monitoring

35	Navadon Khunlertgit	Student	University of Texas A&M	Incorporating Topological Information For Predicting Robust Cancer Subnetwork Markers In Human Protein-Protein Interaction Network
36	Neslihan Bisgin	Student	University of Arkansas at Little Rock	Fetal Heart Localization By Magnetic Dipole Fitting
37	Oluwatosin Oluwadare	Student	University of Missouri	Iterative Reconstruction Of Three-Dimensional Models Of Human Chromosomes From Chromosomal Contact Data
38	Prasant Allaka	Student	University of Arkansas at Pine Bluff	Computational Molecular Modeling Simulations Of Three Dimensional Protein Structures Using Data Mining Techniques
39	Rachel Steele	Student	Troy University	A Mitochondrial Genome Of The Timber Rattlesnake (Crotalus Horridus) And A Reptilian Mitochondrial Phylogeny
40	Ramin Homayouni	Professional	University of Memphis	Development Of Literature Aided Bayesian Sparse Generalized Linear Model-Bridging Classification Accuracy And Biological Relevance
41	Richard Segall	Professional	Arkansas State University	Regulation Of Sterol Transport In Response To Aging In Saccharomyces Cerevisiae
42	Runzhi Li	Professional	Zhengzhou University	Multi-Label Support Vector Machine Classification For Intelligent Health Risk Prediction
43	Safak Kalindamar	Student	Mississippi State University	Comparative Reverse Vaccinology Analysis Of Aeromonas Hydrophila M109-119 Genome
44	Samuel Kakraba	Student	University of Arkansas at Little Rock	Effects Of Small Molecules On Protein Aggregation And Paralysis In C. Elegans Strain Expressing A β 1–42 In The Muscle
45	Shanshan Gao	Student	University of Memphis	Analysis Of Optimal Alignment Unfolds Bias In Existing Variant Profiles
46	Sidney Smith	Student	University of Arkansas at Pine Bluff	Peptide Sequence Patterns Related To Omega Angles In Cis Conformation

47	Suguna Devi Sakkiah	Professional	National Center for Toxicological Research/FDA	Identification Of Critical Chemical Features To Differentiate Androgen Receptor Agonists And Antagonists: Pharmacophore Modeling And Molecular Docking
48	Sujoy Roy	Professional	University of Memphis	Prioritization, Clustering And Annotation Of MicroRNA Using Latent Semantic Indexing Of Pubmed Abstracts
49	Suresh Subramani	Professional	National Center for Toxicological Research/FDA	Application Of Dynamic Topic Modeling To Toxicogenomics Data
50	Tanzim Hassan	Student	Mississippi State University	Pan-Cancer Transcriptomic Network Analysis
51	Tina Gui	Student	University of Mississippi	Arm-B: Mining Biclusters With Association Rules In Gene Expression Data Analysis
52	Ujwani Nukala	Student	University of Arkansas at Little Rock	Bams Database- A Database For Bioactive Molecules
53	Vivek Chandramohan	Student	SIT India	Identification And Evaluation Of Potential Lead Compound For Parkinson's Disease By Insilico And Proteomics Approach
54	Xueyuan Cao	Professional	St Jude's Children Hospital	Post: A Framework For Set Based Association Analysis In High Dimensional Genetic Data

List of Oral Presenters

S. No.	Name	Role	Title	Session
1	Adam Thrash	Oral Presenter	Update On The Mcbios Timeber Rattlesnake Genome Project	Breakout Session -11
2	Aswathy Rai	Oral Presenter	Proteomics Of Host And Pathogen To Study The Role Of Polyamine Transport In Pneumococcal Virulence In A Mouse Model	Breakout Session - 8
3	Bernie Daigle	Oral Presenter	Integration Of Microrna-Mrna Interaction Networks With Microarray Data To Increase Experimental Power	Breakout Session -1
4	Bindu Nanduri	Feature Speaker	Proteomics And Host-Pathogen Interactions	Breakout Session - 8
5	Carl Cerniglia	Keynote Speaker	Human Microbiome: Sequencing-Based High-Throughput Omics Technology And Bioinformatics Used In The Assessment Of The Safety Of Antimicrobial Drug Residues In Food	Keynote Speaker - II
6	Cesar Compadre	Feature Speaker	Development Of The Tocoflexols, A Series Of Novel Vitamin E Analogues With Improved Bioavailability	Breakout Session - 12
7	Chaoyang Zhang	Feature Speaker	New Advances In Inference Of Gene Regulatory Networks From Time Series Data	Breakout Session - 9
8	Charles Chen	Oral Presenter	Missing Data Interpretation For Non-Referenced Or Semi-Referenced Genomes	Breakout Session -11
9	Chathurani Ranathunge	Oral Presenter	Differentially Expressed Genes In Latitudinal Populations Of Common Sunflower (Helianthus Annuus L.) Are Enriched With Microsatellites	Breakout Session - 6
10	Christopher Mason	Keynote Speaker	Genome, Epigenome, Transcriptome, And Epitranscriptome Landscapes: From Single Cells, To Entire Cities, To Space	Keynote Speaker - III
11	Dale Bowman	Oral Presenter	Phylogenetic Tree Construction Using Trinucleotide Usage Profile (Tup)	Breakout Session - 3
12	Darin Jones	Oral Presenter	Design And Synthesis Of Selective Tf/Viia Inhibitors	Breakout Session - 12

13	Donald Johann	Feature Speaker	Approaching Precision Oncology With Tissue Proteomics	Breakout Session - 10
14	Ethan Rath	Oral Presenter	Quantitative Structure-Activity Relation Study Of Quaternary Ammonium Compounds In Pathogen Control: Computational Methods For The Discovery Of Food Antimicrobials	Breakout Session - 5
15	Gokhan Yavas	Oral Presenter	A Framework For Evaluating The Quality Of The Personal Genomes Generated By De Novo Assembly Tools	Breakout Session - 9
16	Haiou Li	Oral Presenter	A Template-Based Protein Structure Reconstruction Method Using Deep Autoencoder Learning	Breakout Session - 8
17	Hasan Tekedar	Oral Presenter	Comparative Genomics Analysis Of Aeromonas Hydrophila Strains	Breakout Session - 4
18	Hui Wen Ng	Oral Presenter	The Development Of A Qsar Model For Predicting Estrogen Receptor-? Binding Using Large Data Sets	Breakout Session - 5
19	Huixiao Hong	Feature Speaker	Predictive Toxicology In Regulatory Science: Endocrine Disruptors Knowledge Base	Breakout Session - 5
20	Hyundoo Jeong	Oral Presenter	Effective Comparative Analysis Of Protein-Protein Interaction Networks By Measuring The Steady State Network Flow Using A Markov Model	Breakout Session - 3
21	Inimary Toby	Oral Presenter	Vdjml – Tools For Capturing The Results Of Inferring Immune Receptor Rearrangements	Breakout Session - 8
22	Isaac Akogwu	Oral Presenter	An Integrated Statistical Probe Of Error Correction Methods For Next-Generation Sequencing Data	Breakout Session - 9
23	Jianlin Cheng	Feature Speaker	De Novo Protein Conformational Sampling Using A Probabilistic Graphical Model	Breakout Session - 3
24	Leihong Wu	Oral Presenter	Bridges – Biomarkers Reuse In Different Gene Expression Systems	Breakout Session - 9
25	Malia Potts	Oral Presenter	Mode Of Action And Biomarker Discovery For Anti-Cancer Natural Products	Breakout Session - 10
26	Mary Relling	Keynote Speaker	Clinical Implementation Of Pharmacogenetics In Precision Medicine	Keynote Speaker - I

27	Michelle Lacey	Oral Presenter	Identification Of Disease Biomarkers Via Integrated Analysis Of Longitudinal Clinical And Genomic Data	Breakout Session - 2
28	Mikhail Dozmorov	Feature Speaker	Genomerunner Web Server: Regulatory Similarity And Differences Define Functional Impact Of Snp Sets	Breakout Session -11
29	Mutlu Mete	Oral Presenter	Successful Classification Of Cocaine Dependence Using Brain Imaging: A Machine Learning Approach	Breakout Session - 7
30	Naseer Kutchy	Oral Presenter	Comparative Functional Genomics Of Mammalian Sperm Th2b, Regulator Of Sperm Chromatin Dynamics And Male Fertility	Breakout Session -11
31	Nathan Crabtree	Oral Presenter	Multiclass Computational Evolution: Benchmark Evaluation And Application To Rna-Seq Biomarker Discovery	Breakout Session - 6
32	Ngoc Luong Nguyen	Oral Presenter	Protein Structure-Based Virtual Screening For The Discovery Of Novel Cb2 Receptor Agonists	Breakout Session - 12
33	Ohgew Kweon	Oral Presenter	Network Based Functional Pan-Genomics: A New Approach To Build Connections Between Genomic Dynamics And Phenotypic Evolution In The Genus Mycobacterium	Breakout Session -11
34	Pankaj Pandey	Oral Presenter	Exploring The Allosteric Inhibitory Binding Sites For Known Negative Allosteric Modulators Within The Cannabinoid Cb2 Receptor	Breakout Session - 2
35	Phil Williams	Oral Presenter	The Challenges Of Long Non-Coding Rna Function Prediction	Breakout Session - 9
36	Ping Gong	Oral Presenter	Earthworm Toxicogenomics: A 21st Century Approach And Toolbox For Environmental Predictive Toxicology	Breakout Session - 5
37	Qiang Shi	Oral Presenter	Hepatotoxicity And Mitochondrial Toxicity Of Fda Approved Tyrosine Kinase Inhibitors	Breakout Session - 5
38	Quang Tran	Oral Presenter	Fm-Index Based Light-Weight Alignment For Quantification Of Rna-Seq Data	Breakout Session - 6
39	Renzhi Cao	Oral Presenter	Single Model Quality Assessment Using Protein Structural And	Breakout Session - 8

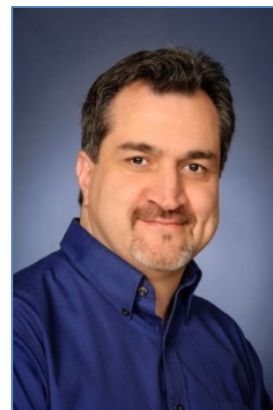
			Contact Information With Machine Learning Techniques	
40	Richard Segall	Oral Presenter	High Performance Computing And Data Mining In Bioinformatics	Breakout Session - 7
41	Ryan Eshleman	Oral Presenter	Leveraging Graph Topology And Semantic Context For Pharmacovigilance In Twitter Streams	Breakout Session - 7
42	Salih Kumru	Oral Presenter	Complete Genome Sequence Of Flavobacterium Columnare Strain 94-081	Breakout Session - 4
43	Samuel Kakraba	Oral Presenter	A Graph-Theoretic Model Of Nucleotide Binding Domain 2 Of The Cystic Fibrosis Transmembrane Conductance Regulator	Breakout Session - 3
44	Sangeeta Khare	Oral Presenter	Silver Nanoparticles: Effect On Intestinal Microbiome And Development Of Resistance	Breakout Session - 4
45	Saunak Sen	Oral Presenter	Matrix Linear Models For High Throughput Genetic Screens	Breakout Session - 3
46	Sertan Kaya	Oral Presenter	Texture Homogeneity Analysis Of Lesion Border In Dermoscopy Images For Malignancy Detection	Breakout Session - 10
47	Shanshan Gao	Oral Presenter	An Alignment-Based Method For Profiling Microbial Community Using Compressed Fm-Index	Breakout Session - 4
48	Shraddha Thakkar	Oral Presenter	Liver Toxicity Knowledge Base (Ltkb): A Comprehensive Database To Understand Multiple Dimensions Of Drug-Induced Liver Injury	Breakout Session - 12
49	Skylar Connor	Oral Presenter	Determination Of New Biosynthetic Pathways Of Ascorbic Acid Using Bioinformatics Modelling	Breakout Session - 2
50	Stan Pounds	Oral Presenter	Promise-Me: A Robust Method For Integrated Analysis Of Dna Methylation, Gene Expression, And Multiple Biologically Related Clinical And Pharmacological Outcomes	Breakout Session - 2
51	Steven Foley	Feature Speaker	The Microbiome And Its Relationship With Antimicrobial Resistance	Breakout Session - 4
52	Ujwani Nukala	Oral Presenter	Use Of Surface Signature Analysis To Study The Structure Anti-	Breakout Session - 12

			Leukemic Activity Relationship Of Sesquiterpene Lactones	
53	Un Jung Lee	Oral Presenter	Procedures For Identifying Biomarkers-Defined Subgroups With Differential Treatment Effect Through Recursive Partitions In Precision Medicine	Breakout Session - 10
54	Vinhthuy Phan	Feature Speaker	Strategies For Efficient Partial Alignment Of Reads For Dna/Rna Quantification	Breakout Session - 6
55	Weida Tong	Feature Speaker	Of Text And Gene – Analysis Of Big Genomics Data With Text Mining Methods	Breakout Session - 7
56	Weizhong Zhao	Oral Presenter	Best Practice In Mining Topics From Regulatory Textual Documents	Breakout Session - 7
57	William Mattes	Feature Speaker	Targeted Therapies, Systems Biology And The Future Of Safety Assessment	Breakout Session - 2
64	William Slikker, Jr.	Keynote Speaker	Regulatory Implications Of Genomics And Bioinformatics For Food And Drug Safety	Keynote Speaker - Iv
58	Xi Yang	Oral Presenter	Evaluation Of Non-Invasive Micrornas As Biomarkers Of Hepatotoxicity; An Update On Translational Acetaminophen Toxicity Biomarkers In Children	Breakout Session -1
59	Yang Liu	Oral Presenter	Large-Scale Soybean Genomic Variation Analysis Workflow In Soykb Ngs Browser	Breakout Session - 6
60	Yongsheng Bai	Oral Presenter	Mmirna-Viewer: A Data Visualization Tool Built To Present The Relationship Between Mirnas And Mrnas	Breakout Session -1
61	Yuping Wang	Feature Speaker	Evaluation Of Toxicogenomics In Advanced Research And Novel Applications	Breakout Session -1
62	Yusuf Nawawi	Oral Presenter	Identification Of A Non-Canonical Micro-Rna In An Fgf2-Specific Snp Region Among Breast Cancer Patients	Breakout Session -1
63	Zhichao Liu	Oral Presenter	Potential Reuse Of Oncologic Drugs For The Treatment Of Rare Diseases	Breakout Session - 10

Ramin Homayouni, Ph.D. – MCBIOS 2016 Conference Chair

Professor of Biology, Director, Bioinformatics Program, FedEx Institute Center for Translational Informatics, University of Memphis, Memphis TN

Dr. Homayouni received a Ph.D. in Biochemistry from University of Houston in 1996 and postdoctoral training in developmental neurobiology at St. Jude Children's Research Hospital in Memphis, TN. In 2001, he became an Assistant Professor in the Department of Neurology at the University of Tennessee Health Science Center, where he also Directed the Center for Genomics Microarray Analysis Core. In 2006, he joined the University of Memphis as an Associate Professor of Biology and Director of Bioinformatics. He is the founding Director of the FedEx Institute Center for Translational Informatics at the University of Memphis. Dr. Homayouni leads an active research team focusing on multiple areas spanning neurodevelopment, neurodegeneration (Alzheimer's disease), genomics and bioinformatics. His research has been funded by a number of federal and private grants and has led to 3 US patent applications and over 54 peer-reviewed journal articles. In 2007, Dr. Homayouni co-founded Quire Inc. (formerly Computable Genomix), a bioinformatics company which develops analytical software for genomic and clinical research.



Shraddha Thakkar, Ph.D. – MCBIOS 2016 Program Chair

Visiting Scientist, Division of Bioinformatics and Biostatistics, National Center for Toxicological Research, U.S. Food and Drug Administration, Jefferson, AR

She received her MSc. degree in Biotechnology from Bangalore University, India and her MS, and Ph.D. degrees in Bioinformatics from the University of Arkansas at Little Rock (UALR)/University of Arkansas for Medical Sciences (UAMS) Joint bioinformatics program. She received her postdoctoral training at the FDA'S National Center for Toxicological Research. Dr. Thakkar is Adjunct Assistant Professor at UAMS College of Pharmacy and Graduate Faculty at UALR. Dr. Thakkar's research interests are on the use of structural and computational techniques for the elucidation of macromolecular mechanisms relevant for drug discovery and toxicity. Along with her expertise in crystallography, Dr. Thakkar has developed strong expertise in macromolecular cloning and expression, and on the use of molecular modeling, QSAR and virtual screening. She has ten research publications, two USA patent applications and many research presentations at national and international meetings. Dr. Thakkar has received multiple research and leadership awards regionally and nationally, including 2012 Genentech Innovation in Biotechnology Award from American Association of Pharmaceutical Scientist (AAPS) and Margret C. Etter Student lecturer award from American Crystallography Association. She is the Vice Chair of Pharmacogenomics Focus group from AAPS and Chair of AAPS Biotech Section Graduate Student Research Awards. She is the founding president of the Regional Student Group – MidSouthernUS the MCBIOS student group. Dr. Thakkar was elected as Board member of the MCBIOS in 2014 and as President Elect in 2015.



Keynote Speakers

Keynote Speaker I

Mary V. Relling, Pharm.D.

*Member and Chair, Department of Pharmaceutical Sciences
St. Jude Children's Research Hospital, Memphis, TN*

Dr. Relling earned her undergraduate B.S. degree from the University Of Arizona College Of Pharmacy and her doctoral degree from the University Of Utah College Of Pharmacy. She completed post-doctoral fellowships with Dr. William Evans at St. Jude and with Dr. Urs Meyer at University of Basel. She joined St. Jude as a faculty member in 1988 and in 2003 was named chair of the Department of Pharmaceutical Sciences. She is also a professor at the University of Tennessee in the Colleges of Medicine and Pharmacy. Her primary interests are in treatment and pharmacogenetics of childhood leukemia and clinical implementation of pharmacogenetic testing. Dr. Relling is Chair of NIH's Pharmacogenomics Research Network and co-founder of CPIC, the Clinical Pharmacogenetics Implementation Consortium. She has published over 300 original scientific manuscripts. She was elected to the Institute of Medicine in 2009.



Keynote Speaker II

Carl E. Cerniglia, Ph.D.

Director, Division of Microbiology, National Center for Toxicological Research, U.S. Food and Drug Administration, Jefferson, Arkansas

Dr. Cerniglia is a Senior Biomedical Research Service (SBRS) Research Microbiologist, Director of the Division of Microbiology at the National Center for Toxicological Research (NCTR), US Food and Drug Administration (FDA) and elected member of the American Academy of Microbiology. He is also an adjunct Professor in the Department of Pharmacology and Toxicology at the University of Arkansas Medical Sciences, Little Rock, AR.

Dr. Cerniglia leads a team at the NCTR that has impacted public health in a variety of research areas including food safety, antimicrobial resistance, environmental biotechnology, nanotechnology, women's health and human intestinal microbiome-host interactions. Dr. Cerniglia's research has resulted in over 400 scientific publications and numerous book chapters and review articles. His research has been frequently highlighted in the scientific and popular press. Dr. Cerniglia has numerous invited presentations at national and international conferences and meetings and is also an ASM Foundation of Microbiology lecturer. The research achievements of Dr. Cerniglia has been recognized by national and international awards from the Food and Drug Administration, American Pharmaceutical Association, International Society of Toxicity Testing, American Society for Microbiology, and American Academy of Microbiology and U.S. Department of Health and Human Services. Dr. Cerniglia was recently awarded the Silver Medal by the World Health Organization for outstanding scientific contribution to the Joint Expert Committee on Food Additives (JECFA) in advancing science-based risk assessments on evaluating the effects of veterinary drug residues and other food contaminants on the human intestinal microbiome, the FDA Lifetime Achievement Award, the FDA Commissioner's Award Merit, the DHHS Outstanding Leader Award and Distinguished Alumnus Award at North Carolina State University.



Keynote Speaker III

Christopher E. Mason, Ph.D.

Associate Professor, Department of Physiology and Biophysics, Weill Cornell Medical College, New York, USA

Dr. Mason, is an associate professor of Computational Genomics at Weill Cornell Medical College. He completed his B.S In Genetics and Biochemistry from University of Wisconsin-Madison and Ph.D. in Genome Evolution and postdoctoral in Neuroscience from Yale University. His laboratory work utilizes computational and experimental methodologies to identify and characterize the essential genetic elements that guide the function of the human genome. He perform research in three principal areas: (1) the functional annotation of the human genome by mutational profiling in families with brain malformations and cancer patients, (2) the examination of the elements that orchestrate the development of the human brain and their evolutionary changes, and (3) the development of models for systems and synthetic biology. Mason Lab uses high-throughput methods to generate cell-specific molecular maps of genetic, epigenetic, and transcriptional activity and we use them to create multi-dimensional molecular portraits of development and disease. He also develops algorithms to detect, catalog and functionally annotate variants in the genetic pathways that control developmental processes. He has more than 130 publications.

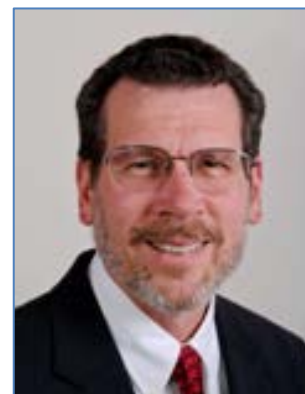


Keynote Speaker IV

William (Bill) Slikker, Jr., Ph.D.

Center Director, National Center for Toxicological Research, U.S. Food and Drug Administration, Jefferson, Arkansas

Dr. William Slikker, Jr. is the Director of FDA's National Center for Toxicological Research (NCTR). He received his Ph.D. in Pharmacology and Toxicology from the University of California at Davis in 1978. Dr. Slikker holds Adjunct Professorships in the Departments of Pediatrics, and Pharmacology and Toxicology at the University of Arkansas for Medical Sciences. He has held committee chairmanships or elected offices in several scientific societies, including the Teratology Society (serving as President) and the American Society for Pharmacology and Experimental Therapeutics (Chair, Developmental Pharmacology Section and member of the Program Committee) and co-founder and past President of the MidSouth Computational Biology and Bioinformatics Society. He is currently Associate Editor for NeuroToxicology and Toxicological Sciences. He is the past President of The Academy of Toxicological Sciences, the Society of Toxicology and the recipient of the 2014 George H. Scott Memorial Award from The Toxicology Forum. Dr. Slikker has authored or co-authored over 300 publications in the areas of transplacental pharmacokinetics, developmental neurotoxicology, neuroprotection, systems biology, and risk assessment. He has also served on several national/international advisory panels for the International Life Sciences Institute (ILSI)/Health and Environmental Sciences Institute (HESI), Chemical Industry Institute of Toxicology (CIIT) Centers for Health Research, Environmental Protection Agency (EPA), National Institute of Environmental Health Sciences (NIEHS), National Academy of Sciences (NAS), National Institutes of Health (NIH) and World Health Organization (WHO).



Workshop Speakers

Workshop Speaker I

Robert Williams, Ph.D.

Professor and Director, University of Tennessee Health Science Center, Memphis, Tennessee

Robert (Rob) W. Williams received a BA in neuroscience from UC Santa Cruz (1975) and a Ph.D. in physiology at UC Davis with Leo M Chalupa (1983). He did postdoctoral work in developmental neurobiology at Yale with Pasko Rakic and moved to the University of Tennessee in 1989. He is chair of the Department of Genetics, Genomics and Informatics at UTHSC. Williams holds the UT Oak Ridge National Laboratory Governor's Chair in Computational Genomics. He was a past president of the International Society for Behavioural and Neural Genetics and founding director of the Complex Trait Community (www.complextait.org). He is editor-in-chief of *Frontiers in Neurogenomics*, and serves on the editorial boards of *Genes, Brain & Behavior*, *Neuroinformatics*, *Mammalian Genome*, *Molecular Vision*, *European Journal of Anatomy*, *Alcohol*, *BiomedCentral Neuroscience*, *the Journal of Biomedical Discovery and Collaboration*, and *Behavior Genetics*. One of Williams' more notable contributions is in the field of systems genetics and expression genetics (eQTL analysis). He and his research group have built GeneNetwork (www.genenetwork.org), an online resource and suite of gene mapping code that is used widely by the genetics and molecular.



Workshop Speaker II

Jason Williams, Ph.D.

Assistant Director, Cyverse (formerly iPlant Collaborative), DNA Learning Center, Cold Spring Harbor Laboratory

Jason Williams is Assistant Director – External Collaborations of Cold Spring Harbor Laboratory's DNA Learning Center and the CyVerse Education, Outreach, and Training Lead – Based out of Cold Spring Harbor Laboratory, his background is in plant molecular biology. Jason organizes, manages, and instructs at more than a dozen annual bioinformatics workshops, conferences, and events.



Workshop Speaker III

Rakesh Kaundal, Ph.D.

Director, High-Performance Computing, Institute for Integrative Genome Biology, University of California, Riverside

Rakesh Kaundal is the Director of High-Performance Computing | Bioinformatics Facility at the Institute for Integrative Genome Biology (IIGB / CEPCEB), University of California, Riverside. His major role is to lead / manage the UCR's HPC infrastructure, supervise informatics staff, instruct bioinformatics workshops and develop data analysis pipelines for high-throughput data analysis, including data from next generation sequencing (NGS) technologies. His research interests and expertise include the

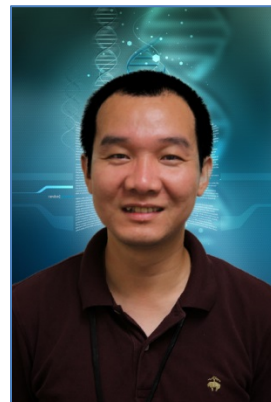


development of computational approaches, bioinformatics systems, and integrated databases to support fundamental research in agriculture, molecular biology and life sciences. For more details, please visit <http://bioinfo.ucr.edu/>.

Zhichao Liu, Ph.D., Session Chair

Visiting Scientist, Division of Bioinformatics and Biostatistics, National Center for Toxicological Research, U.S. Food and Drug Administration, Jefferson, AR

Dr. Liu received his Ph.D. degree from Nankai University, China. Currently, he is a Visiting Scientist in Division of Bioinformatics and Biostatistics (DBB), National Center of Toxicological Research (NCTR), U.S. Food and Drug Administration (FDA). In past ten years, he led or took part in several cutting-edge projects from both industry and academia. Recently, Dr. Liu focused on developing the standard pipeline to balance the efficacy and safety in drug repositioning and drug safety areas. The goal aims at providing the standard *in silico* pipeline for drug repositioning and early drug safety detection by retrieving, integrating and organizing the information from chemical, biological and clinical spaces, which help industry to seek for the optimal route to accelerate the drug development efficacy from advanced regulatory sciences perspective.



Feature Speaker and Breakout-Session Chair

Breakout Session –I miRNA and Toxicogenomics

Yuping Wang, MD, PhD, DABT - Feature Speaker and Session Chair

Staff Fellow, Division of Bioinformatics and Biostatistics, National Center for Toxicological Research, U.S. Food and Drug Administration, Jefferson, AR

Dr. Yuping Wang has broad educational background and working experiences from molecular biology, toxicology and medical science. In addition, Dr. Wang has been certified by American Board of Toxicology (DABT). Over more than twenty years working actively in the field of toxicology, she has participated in multiple projects focusing on carcinogenicity and liver toxicities associated with FDA approved drugs or environmental chemicals. These research results have been published in many peer-reviewed publications in prestigious journals. The most current research for Dr. Wang is focusing on to perform high quality research to achieve goals of identifying biomarkers, build knowledge bases, create software solutions, etc. that can be used to a) prevent and/or identify early stage disease and/toxicity, b) assist FDA reviewers in the performance of their jobs and c) advance global alliances. Specifically, as the PI, Dr. Wang has initiated projects to explore the roles of miRNAs in putative mechanisms of drug induced liver injury (DILI) and as potential biomarkers (DILI). More recently, Dr. Wang has established a broad collaboration with experts in the clinical toxicology, physicians and computational science to conduct systematically assess risks to identify the safety signals from electronic medical records (EMRs) and FDA Adverse Events Reporting System (FAERS) for the minority populations and to assess potential drug property/class – patients' interaction in contributing DILI in humans.



Breakout Session –II Targeted Therapies, Systems Biology and Future of the Safety Assessment

William B. Mattes, Ph.D., DABT - Feature Speaker and Session Chair

Division Director, Division of Systems Biology, National Center for Toxicological Research, U.S. Food and Drug Administration, Jefferson, AR

Dr. Mattes is the Director of the Division of Systems Biology, part of the FDA's National Center for Toxicological Research in Jefferson, Arkansas. The Division pursues a wide range of research that uses and develops innovative tools for assessing pharmaceutical safety and advancing public health. He has been an independent consultant as well as Director of Toxicology at the Critical Path Institute where he developed and directed the Predictive Safety Testing Consortium (PSTC), a collaboration of 16 of the world's major pharmaceutical companies, with FDA and EMEA advisors, with the goal of qualifying new biomarkers for drug safety in a regulatory setting. This work resulted in the establishment of a formal process of biomarker qualification for the FDA and EMEA, and FDA/EMA/PMDA qualification of new biomarkers of kidney injury. Dr. Mattes also developed the COPD Biomarkers Qualification Consortium, serving as its Senior Director and overseeing interactions with the FDA. Dr. Mattes other positions included senior scientific director of Toxicogenomics at Gene Logic, Associate Director of Toxicogenomics and Group Leader of Genetic Toxicology at Pharmacia Corp, Kalamazoo, MI, Group Leader of Experimental Toxicology and Metabolism at Ciba Pharmaceuticals, Summit, NJ, and Group Leader of Molecular and Cellular Toxicology, Ciba-Geigy Agricultural Chemical Division, Farmington, CT. Dr. Mattes received his BA from the University of Pennsylvania and PhD in biological chemistry from the University of Michigan, Ann Arbor. He did his postdoctoral training in biochemistry at the Johns Hopkins University, and was a staff fellow at the National Cancer Institute, the National Institutes of Health (NCI/NIH). In 1997 Dr. Mattes became a diplomate of the American Board of Toxicology. Dr. Mattes chaired the subcommittee that established a public toxicogenomics database at the European Bioinformatics Institute. His research interests include bioinformatics and data analysis, cross-species comparisons of molecular responses, as well as group dynamics that lead to successful collaboration between scientists and changes in scientific policy. He also currently fills the guitar chair for the group Jazzicology at the American College of Toxicology annual meeting.



Breakout Session –III Protein Structure/Function and Biological Networks

Jianlin Cheng, Ph.D. - Feature Speaker and Session Chair

Associate Professor, University of Missouri, Columbia, Missouri

Dr. Jianlin Cheng received his PhD in computer science from the University of California – Irvine in 2006. He is currently an associate professor in the Computer Science Department at the University of Missouri - Columbia. His research focuses on protein structure and function prediction, genome structure modeling, and biological network modeling. Dr. Cheng has authored or co-authored 91 journal articles and dozens of bioinformatics software tools. His research has been supported by NIH, NSF, DoE, and University of Missouri. He is a recipient of a 2012 NSF CAREER award.



Breakout Session –IV Microbiome: Disease and Drug Resistance

Steven Foley, Ph.D. - Feature Speaker and Session Chair

Research Microbiologist, Division of Microbiology, National Center for Toxicological Research, U.S. Food and Drug Administration, Jefferson, Arkansas

Dr. Steven Foley is a Research Microbiologist in the Division of Microbiology at FDA's National Center for Toxicological Research (NCTR) in Jefferson, Arkansas. Dr. Foley earned his B.S. in Zoology and his Ph.D. in Cellular and Molecular Biology/Infectious Diseases from North Dakota State University in Fargo. After completing his Ph.D., he completed a postdoctoral fellowship with FDA's Center for Veterinary Medicine. He also served as an Assistant Professor at the University of Central Arkansas and an Associate Research Scientist with the Marshfield Clinic Research Foundation prior to joining NCTR.



Dr. Foley's research interests are largely in the fields of bacterial pathogenesis and antimicrobial resistance among foodborne pathogens and understanding the distribution of microbial populations in FDA-regulated products. Specific areas of interest include understanding the distribution of enteric pathogens and their virulence and antimicrobial resistance factors in food production environments. By understanding the distribution mechanisms of pathogens, we may be able to develop interventions to reduce the spread of pathogenic microorganisms from food sources to humans. He is also interested in the development of methods to better understand the contribution of plasmid encoded genes to enhanced bacterial function. Plasmids are capable of horizontal gene transfer, which could facilitate the spread of antimicrobial resistance and increased virulence among bacteria leading to more difficult to treat infections. Thus a more comprehensive understanding of plasmid genetics and associated physiology should ultimately lead to improved public health.

Breakout Session –V Predictive Toxicology and Chemo-Informatics

Huixiao Hong, Ph.D. - Feature Speaker and Session Chair

Senior Scientist, Division of Bioinformatics and Biostatistics, National Center for Toxicological Research, U.S. Food and Drug Administration, Jefferson, Arkansas

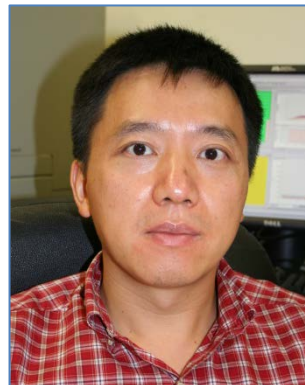
Dr. Huixiao Hong is a senior Scientist at National Center for Toxicological Research (NCTR), US Food and Drug Administration (FDA), Arkansas, USA, working on the scientific bases for regulatory application and development of genomics biomarkers. Before joining the FDA, he was the Manager of Bioinformatics Division at Z-Tech, an ICFI company, at NCTR. He held a Research Scientist position at Sumitomo Chemical Company in Japan. He was a visiting scientist at National Cancer Institute (NCI) at National Institutes of Health (NIH). He was also an Associated Professor and the Director of Laboratory of Computational Chemistry at Nanjing University in China. He published more than 140 scientific papers and served as Editor-in-Chief, Executive Editor and Editorial Board member for more than 10 peer-reviewed journals and as reviewer for more than 20 peer-reviewed journals. He received his Ph.D. from Nanjing University in China and did post-doctoral research at Maxwell Institute in Leeds University in England.



Ping Gong, Ph.D. –Session Chair

Principle Investigator at Environmental Laboratory, U.S. Army Engineer Research and Development Center, Vicksburg, Mississippi

Dr. Gong is a Principle Investigator at Environmental Laboratory, U.S. Army Engineer Research and Development Center. His main research interest centers around developing and applying novel and integrated genomics, genetic engineering, bioinformatics and computational biology approaches to address a wide spectrum of environmental problems, particularly in discovering novel biomarkers, elucidating the toxicological mode of action at the molecular level, predicting herbicide resistance and chemical toxicity, and engineering CRISPR-Cas9-mediated gene drive for invasive species control. He received a B.S. degree in Environmental Biology and Ecology from Peking University and a Ph.D. in Ecotoxicology from the Institute of Applied Ecology, Chinese Academy of Sciences. Prior to joining ERDC-EL, Dr. Gong worked in the Biotechnology Research Institute of National Research Council (Canada), Swedish University of Agricultural Sciences, Technical University of Berlin (Germany), and Chinese Academy of Sciences. He has published over 70 research papers in toxicogenomics, bioinformatics, computational biology, ecotoxicology, risk assessment and regulatory toxicology.

**Breakout Session –VI Next Generation Sequencing****Vinhthuy Phan, Ph.D. - Feature Speaker and Session Chair**

Associate Professor, University of Memphis, Memphis, Tennessee

Dr. Vinhthuy Phan is an associate professor of Computer Science at the University of Memphis. He received his undergraduate education at Brandeis University in Mathematics and Computer Science, and did his graduate studies at Stony Brook University in New York, where he received his Ph.D. in 2003. Dr. Phan's research interest lies in the interdisciplinary area of computing and molecular biology. His current research, supported by the National Science Foundation, focuses on developing computational methods to analyze next-generation sequencing data to detect genetic variants, gene expression and abundance of microbial genomes in metagenomic samples.

**Breakout Session –VII Machine Learning in Large Data****Weida Tong, Ph.D. - Feature Speaker**

Division Director, Division of Bioinformatics and Biostatistics, National Center for Toxicological Research, U.S. Food and Drug Administration, Jefferson, Arkansas

Dr. Tong is a gifted computational chemist with broad expertise that spans the entire spectrum of computational methods in molecular modeling and bioinformatics applied to systems biology, predictive toxicology, and knowledge management. He is internationally recognized for his leadership in the areas of computer modeling and bioinformatics, serves as a Science Advisory Board (SAB) member for the Netherlands Toxicogenomics Center, and as a SAB member for the EU Framework Project on CarcinoGenomics. Weida received his B.S. in Chemistry (1983) and his Ph.D. in



Polymer Chemistry (1990) from Fudan University in China. Weida's efforts and leadership qualities have made a significant impact within FDA and worldwide. He has supervised the FDA-led community-wide MicroArray Quality Control Consortium, analyzing technical performance and practical utility of emerging molecular technologies; and coordinated the development of the Liver Toxicity Knowledge Base to address public health concerns related to drug-induced liver injury. He played a major leadership role in the conception, design, and development of numerous computational tools in bioinformatics, chemoinformatics, computational toxicology, biostatistics, and systems biology. His work and creativity have public health impacts in predictive systems toxicology and risk assessment. His research (>200 publications) is cataloged in eminent peer-reviewed journals

Wen Zou, Ph.D. - Session Chair

Visiting Scientist, Division of Bioinformatics and Biostatistics, National Center for Toxicological Research, U.S. Food and Drug Administration, Jefferson, Arkansas

Dr. Zou received her B.S. in Microbiology, M.S. in Molecular Microbiology from Shandong University in China, and Ph.D. degree in Biochemistry and Molecular Microbiology from Kyoto University in Japan. She completed her postdoctoral experience in Oncology at McGill University in Canada, and in Food Safety in NCTR/USFDA. She is now a visiting scientist in Division of Bioinformatics and Biostatistics in NCTR/USFDA. Her primary research is in the areas of: 1) microbial next-generation sequencing data analysis and data mining; 2) safety signal detection of FDA Spontaneous Reporting Systems (SRs); and 3) studies on topic modeling for knowledge discovering of big datasets.



Breakout Session –VIII Proteomics and Host Pathogen Interaction

Bindu Nanduri, Ph.D. - Feature Speaker and Session Chair

Associate Professor, Mississippi State University, Starkville, Mississippi

Dr. Bindu Nanduri received her PhD in Biochemistry and Molecular Biology from the University of Arkansas for Medical Sciences, Little Rock in 1998. She is currently an associate professor in the Department of Basic Sciences, College of Veterinary Medicine at Mississippi State University. Nanduri's research focuses on identifying polyamine dependent mechanisms in pneumococcal pneumonia, developing host-pathogen interaction database resources for agricultural systems, and structural and functional annotation of genomes. Dr. Nanduri has co-authored 58 journal articles and her research has been supported by NIH, NSF, USDA, and Mississippi State University.



Breakout Session –IX Bioinformatics Methodologies

Chaoyang (Joe) Zhang, Ph.D. - Feature Speaker and Session Chair

Professor, University of Southern Mississippi, Hattiesburg, Mississippi

Dr. Zhang joined the Department of Computer Science at the University of Southern Mississippi as an assistant professor in 2003. He received my Ph.D. at Louisiana Tech University in 2001 and was a research assistant professor in the Department of Computer Science at the University of Vermont from 2001 to 2003. he was the Director of School of Computing from July 2008 to June 2014. Currently I am a professor in computer science in the School of Computing. Research interests include 1) High performance computing (parallel computing, distributed



computing and grid computing applications and algorithms). 2) Computational biology and bioinformatics (microarray data analysis, classification and gene network reconstruction) 3) Information technology (Web-based information retrieval, machine learning and data mining) 4) Imaging and visualization (3D image reconstruction, information visualization and inverse problems) 5) Data analysis and modeling.

Breakout Session –X Oncology

Donald J. Johann, MS, MD - Feature Speaker and Session Chair

Associate Professor, University of Arkansas for Medical Sciences, Little Rock, Arkansas

Dr. Johann is a physician/scientist and associate professor at UAMS and Director of Informatics at the Myeloma Institute for Research and Therapy. His scientific focus concerns the application of advanced molecular profiling and high-throughput technologies for the characterization of molecular alterations in cancer cells. Areas of emphasis include next-gen sequencing (NGS), high-resolution identity-based mass spectrometry (proteomics), laser capture microdissection (LCM), bioinformatics, and cancer biology. Previously, he was an assistant investigator at the National Cancer Institute (NCI), Center for Cancer Research (CCR), Medical Oncology Branch in Bethesda, MD. Prior to attending medical school he worked as an engineer for the Unisys Corporation for six years, where he directed a team of five engineers on projects involving avionic software design and instrumentation. During this time he also earned a graduate degree in computer science with distinction from Hofstra University. Dr. Johann received his M.D., from Case Western and received a graduate with distinction honors for Computer Applications in Medicine. Following residency he then became a postdoctoral research fellow at the NIH/NCI Lab of Pathology, under the mentorship of Dr. Lance Liotta, with a focus on clinical proteomics. He was twice selected for an AACR Scholar-in-Training Award for research work involving novel bioinformatics. Medical Oncology/Hematology fellowships were completed at NIH in the NCI and NHLBI. He has authored ~40 publications and contributed to three patents.

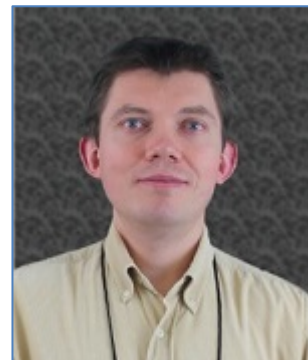


Breakout Session –XI Genomics

Mikhail Dozmorov, Ph.D. - Feature Speaker and Session Chair

Assistant Professor, Virginia Commonwealth University, Richmond, Virginia

Dr. Dozmorov received his Ph.D. in Medical Biophysics from Göthenburg University at Göthenburg, Sweden. He also have master's degree in Microelectronics, Moscow Institute of Electronic Technology (Technical University) from Russia. He has Over 10 years of bioinformatics research in Cancer, Immunology, and Neurobiology, with focus on genomics. He has Extensive experience in sequencing technologies and 'omics' data analysis. He is Assistant Professor in the department of biostatistics at Virginia Commonwealth University. His research interests are Bioinformatics, computational genomics and epigenomics, microarray and next-generation sequencing data analysis, gene ontology and signaling pathway analysis, genome-wide association studies, machine learning and data mining, ENCODE, TCGA, GEO and other databases, integrative analysis of high-throughput genomic assays, 3D structure of the human genome, personalized medicine,



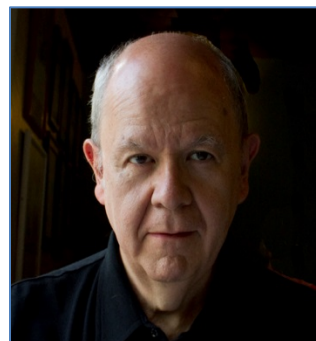
complex diseases and aging. - See more at: <http://www.biostatistics.vcu.edu/mikhail-g-dozmorov/#sthash.OAog9QPi.dpuf>

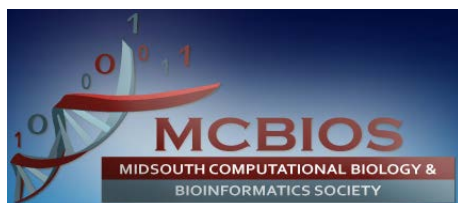
Breakout Session –XII Drug Discovery and Development

Cesar M. Compadre, BS, MS, Ph.D. - Feature Speaker and Session Chair

Professor, Department of Pharmaceutical Sciences, University of Arkansas for Medical Sciences

Dr. Cesar M. Compadre is a professor at the Department of Pharmaceutical Sciences, of the University of Arkansas for Medical Sciences. He received his BS Pharm from National University of Mexico, 1977, MS from National University of Mexico, 1980, and Ph.D. from University of Illinois, Chicago, IL in 1985. He has extensive research experience on the development of bioactive compounds based on naturally occurring compounds, and on the use of molecular modeling in drug design and structure-activity studies. He has published over 85 publications and co-authored more than 70 patents related to the development of bioactive compounds. He is also the developer of one FDA approved antimicrobial technology, which is commercially used, and he is also co-founder of Tocol Pharmaceuticals, a company focused in the development of enhanced vitamin-E analogues. Dr. Compadre has a BSPharm degree, and obtained his Ph.D. degree in medicinal chemistry and pharmacognosy, from the University of Illinois at Chicago. He conducted postdoctoral research on structure-activity relationships studies using molecular modeling at the University of Illinois working with Dr. John M. Pezzuto and at Pomona College working with Professor Corwin Hansch. Additionally, he had a sabbatical experience at NASA Ames Research Center in computer modeling. Dr. Compadre is past-chair of the Board of the Arkansas Science and Technology Authority, and chair of the board of the Coalition for a Tobacco Free Arkansas. He also serves at the Board of MCBIOS where he is currently the Chair-elect. As an educator Dr. Compadre, regularly teaches graduate and professional courses at the University of Arkansas for Medical Sciences and has directed over 20 graduate students, and post-doctoral trainees. Dr. Compadre is founding faculty of the joint UALR/UAMS bioinformatics program. Dr. Compadre has extensive research collaborations with many scientists locally, nationally and internationally.





MCBIOS 2016 Conference Proceedings

MCBIOS 2016 presenters who had their poster or platform abstracts accepted for presentation are eligible to submit a **full paper** on the work they presented to be considered for formal, peer-reviewed publication in the conference proceedings. The proceedings will appear in a special issue of *BMC Bioinformatics*. **Past MCBIOS Proceedings have yielded an average impact factor of 5.17** (2006-12), which speaks strongly of the impact of MCBIOS and its participants in bioinformatics. The deadline for submission of these papers is **Friday, April 30th, 2016**.

[*BMC Bioinformatics*](#) is an open access, peer-reviewed journal that considers articles on all aspects of the development, testing and novel application of computational and statistical methods for the modeling and analysis of all kinds of biological data, as well as other areas of computational biology. Submissions must be within this scope of interest and represent original work. **Important note:** Like last year, BMC has requested that we restrict acceptance to the top 14 papers. As such, MCBIOS will officially recognize a **best paper** from among those submitted and highlight it in the MCBIOS Proceedings editorial. This best paper will also be eligible to be recognized in the Highlights Track for the 2015 ISMB Proceedings.

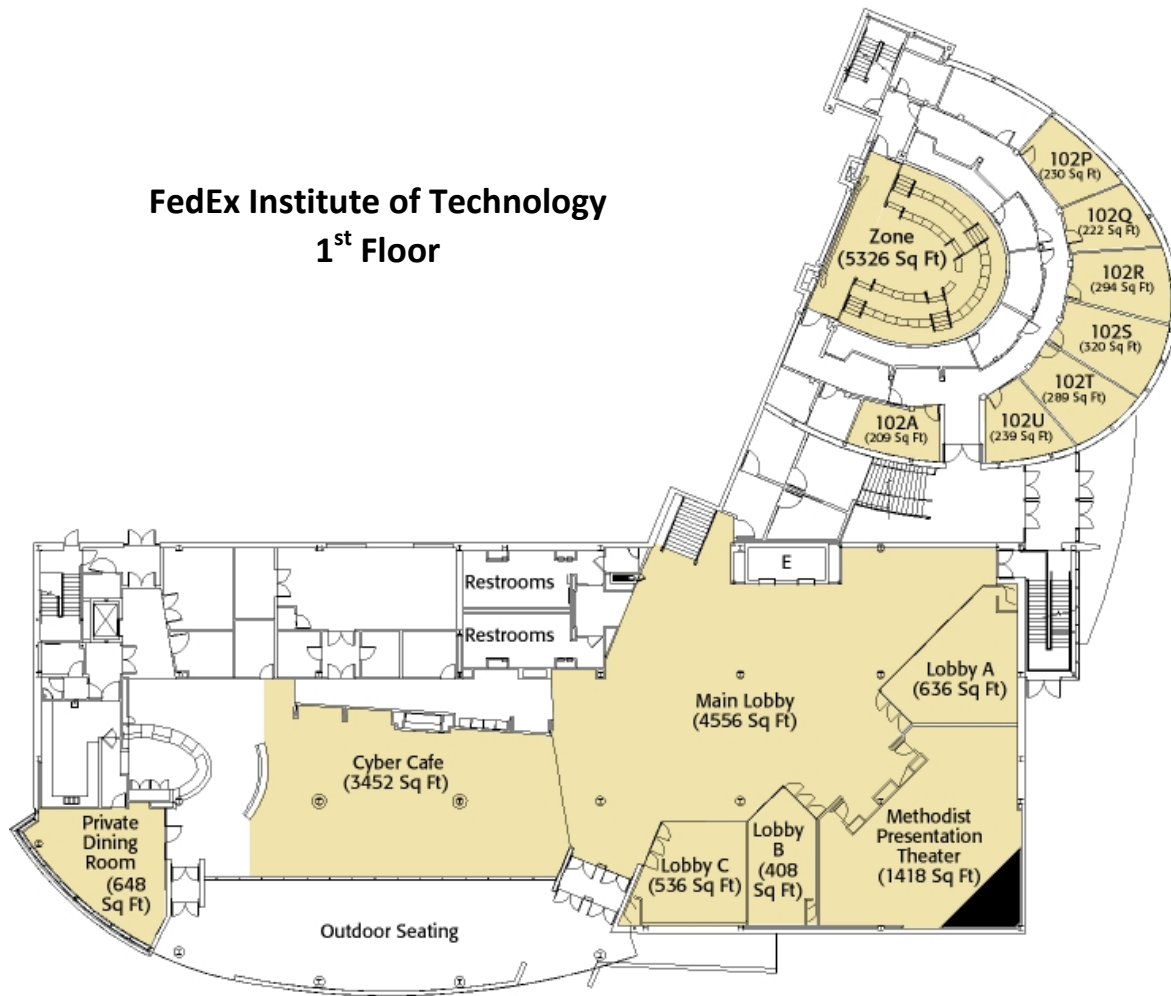
Specific formatting instructions for Proceedings papers can be found on their website (<http://www.biomedcentral.com/info/authors/instprepdoc>). Note that this is a different web address than the one for their regular papers. Authors of accepted papers will be asked to **pay an article processing charge of £715** (about \$1,052 USD at current exchange rates), an amount discounted for this event from the normal \$2,145 charge. Because this is a special issue, fee waivers and institutional discounts do not apply.

If you intend to submit a paper, please send your tentative title/abstract to the Senior Editor, (Jonathan-Wren@OMRF.org) as soon as possible to enable us to better plan for reviews, paper handling, etc. Papers should be submitted by email to the Senior Editor.

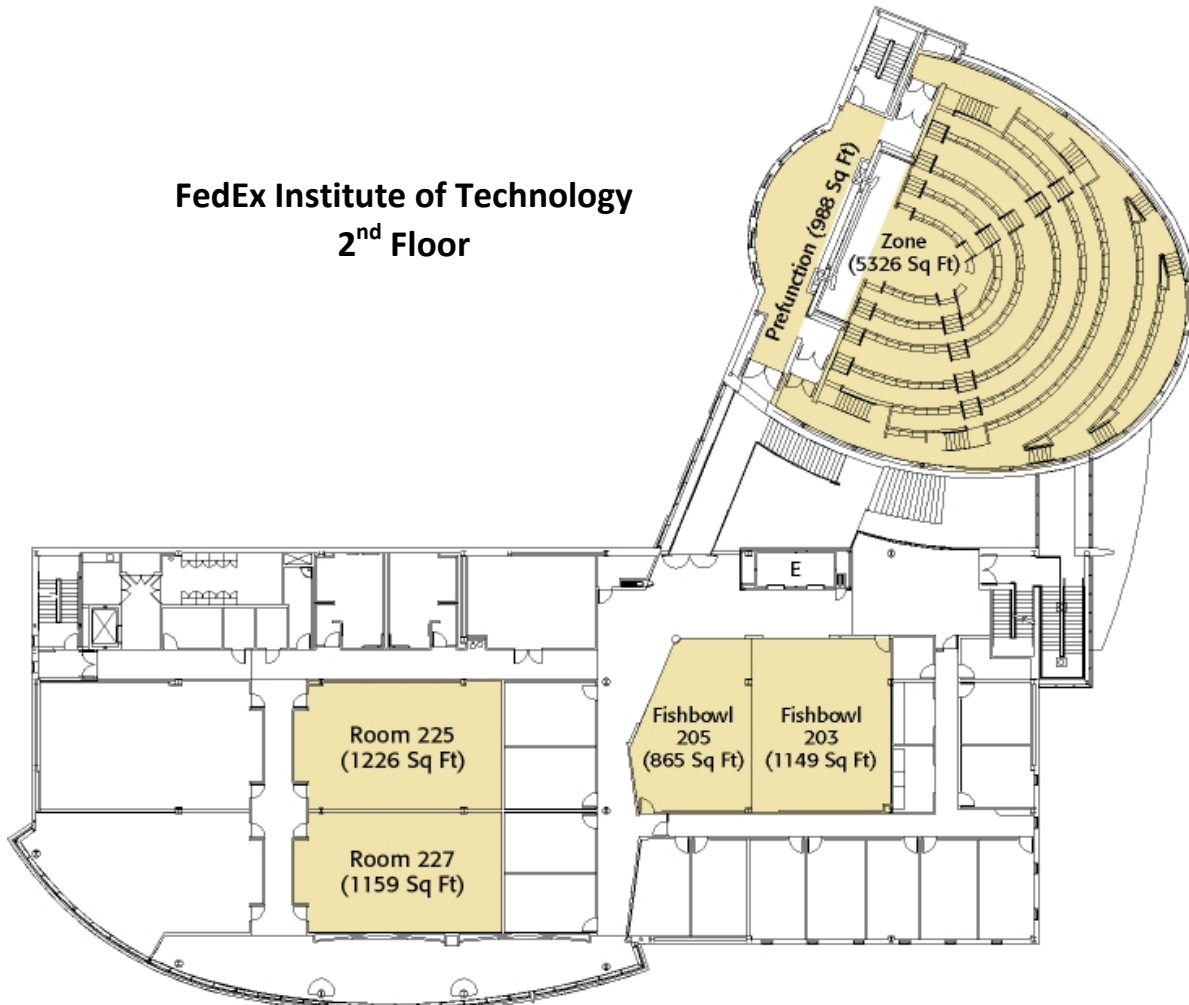
Timeline:

- | | |
|----------------|---|
| April 30, 2016 | – Manuscripts should be <u>e-mailed</u> to Jonathan Wren |
| May 23, 2016 | – Reviewers return comments to editors |
| June 13, 2016 | – Revisions due back from authors |
| June 26, 2016 | – Final decisions made on submitted papers by reviewers |
| July 3, 2016 | – Editors notify authors of acceptability of papers |
| July 28, 2016 | – All final manuscript revisions due to editors along with payment of article processing charges due to MCBIOS. |

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