MCBIOS XI: Annual Bioinformatics & Computational Biology Conference

MCBIOS XI

ISCB INTERNATIONAL SOCIETY FOR COMPUTATIONAL BIOLOGY

AFFILIATED CONFERENCE

March 06-08, 2014

--- STILLWATER, OKLAHOMA ---

The Wes Watkins Center

From Genome to Phenome: Connecting the Dots

MIDSOUTH COMPUTATIONAL BIOLOGY & BIOINFORMATICS SOCIETY

MCBIOS.ORG

Dear MCBIOS participants,

We are honored and delighted to welcome you to the XIth MidSouth Computational Biology & Bioinformatics Society (MCBIOS) conference on "*Genome to Phenome: Connecting the Dots*" at the Oklahoma State University, Stillwater, USA. We believe we have chosen a venue that guarantees a successful technical conference amid the culture and scenery of Stillwater.

Our technical program is rich and varied with 3 keynote speeches, 1 invited talk and around 125 technical abstracts split between 50 oral and 75 poster presentations. Besides, there are 3 workshops targeted on various aspects of bioinformatics and computational biology. We also expect to provide technical demonstrations, and numerous opportunities for informal networking.

As the organizing committee of MCBIOS-XI, we know that the success of the conference depends ultimately on many people who have worked with us in planning and organizing both the technical program and supporting social arrangements. In particular, we thank the 'MCBIOS Board' for their wise advice and brilliant suggestions on organizing the technical program; the 'Abstract Review Committee' for their thorough and timely reviewing of the abstracts, and our sponsors who have helped us to keep down the costs of this conference. Recognition should go to the 'Local Organizing Committee' members who have all worked extremely hard for the details of important aspects of the conference programs and social activities.

We hope that you will find the conference and your stay both valuable and enjoyable. Welcome to Stillwater, Oklahoma.

Rakesh Kaundal
Conference Chair
(Oklahoma State University,
Stillwater)

Ulrich K. Melcher
Program Chair
(Oklahoma State University,
Stillwater)

Doris Kupfer
Program Chair
(Civil Aerospace
Medical Institute,
Oklahoma City)

Peter R. Hoyt
Workshop Chair
(Oklahoma State University,
Stillwater)

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.

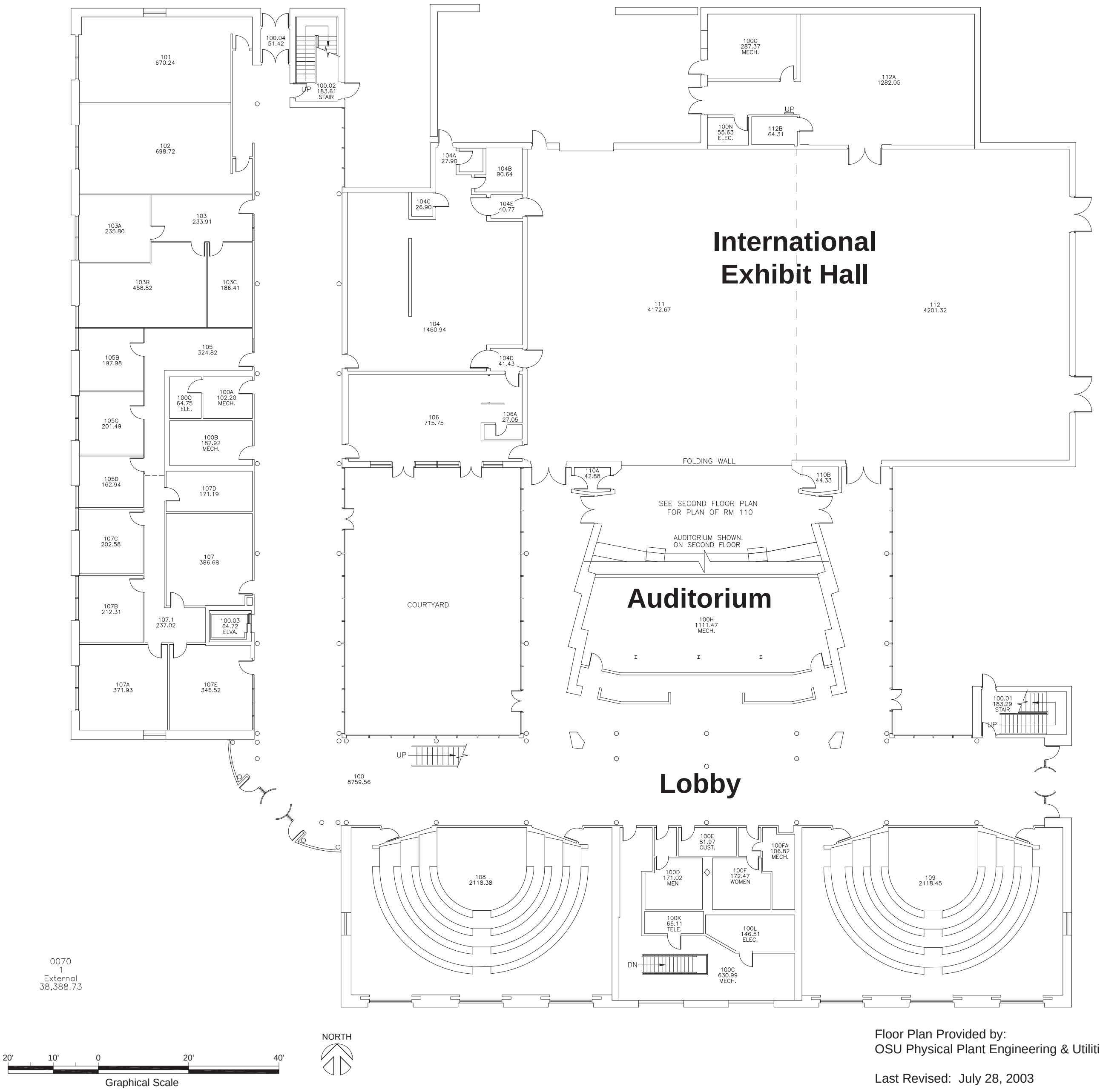
We have a strong orientation toward supporting our student and postdoctoral members.

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).

Major sponsors:

"Funding for this conference was made possible, in part, by the Food and Drug Administration through grant 1R13FD004229-01. The views expressed in written Conference materials or publications and by speakers and moderators do not necessarily reflect the official policies of the Department of Health and Human Services; nor does any mention of trade names, commercial practices, or organization imply endorsement by the United States Government."

First Floor



Floor Plan Provided by:
OSU Physical Plant Engineering & Utilities Services

Last Revised: July 28, 2003

Wes Watkins Center
Oklahoma State University
Stillwater, Oklahoma

Oklahoma State University campus map

For more information on parking, go to http://www.parking.okstate.edu/

Mid-South Computational Biology and Bioinformatics Society (MCBIOS)

XI^{th} Annual Conference

Wes Watkins Center
Oklahoma State University, Stillwater, OK
March 06-08, 2014

Officers

President: Andy D. Perkins, Mississippi State University
Past President: Edward Perkins, US Army Engineer Research and Development Center
President-Elect: Chaoyang (Joe) Zhang, University of Southern Mississippi
Treasurer: Dennis Burian, Civil Aerospace Medical Institute, FAA
Secretary: Debra Knisley, Tennessee State University

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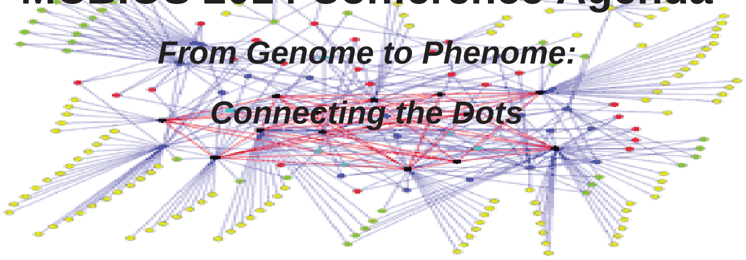
Jonathan Wren, Oklahoma Memorial Research Foundation, OMRF
Rakesh Kaundal, Oklahoma State University, OSU
Cesar Compadre, University of Arkansas for Medical Sciences, UAMS
Roger Perkins, National Center for Toxicology Research, FDA

Local Steering Committee (Oklahoma State University)

Astri Wayadande, NIMFFAB, Entomology & Plant Pathology
Babu Fathepure, Microbiology & Molecular Genetics
Dana Brunson, High Performance Computing Center
Lan Zhu, Statistics
Li Ma, NIMFFAB, Entomology & Plant Pathology
Michael Anderson, Plant & Soil Sciences
Peter Hoyt, Biochemistry & Molecular Biology
Rakesh Kaundal, NIMFFAB, Biochemistry & Molecular Biology
Ramamurthy Mahalingam, Biochemistry & Molecular Biology
Ruchi Verma, Biochemistry & Molecular Biology
Sitanshu S. Sahu, NIMFFAB, Biochemistry & Molecular Biology
Ulrich Melcher, Biochemistry & Molecular Biology

MCBIOS 2014 Conference Agenda



From Genome to Phenome:

Connecting the Dots

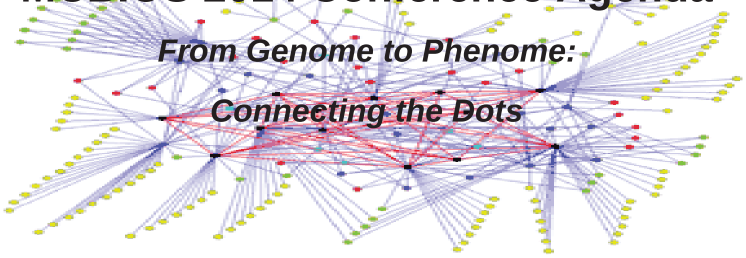
Day 1

Thursday, March 6, 2014

8:00 AM - 10:00 AM	**Registration** (Lobby)
9:30AM - 10:00AM	Coffee / Drinks
10:00 AM - 5:00 PM	**Conference Room** 101/102
	Workshop Chair: Peter Hoyt, OSU
	Next-Generation Sequencing, Bioinformatics Workshop
10:00 AM - 11:00 AM:	Graham Wiley: 12 things to do with a NGS sequencer
11:00 AM - 11:45 AM:	Dana Brunson: Installing software, accessing supercomputers and sharing desktops
11:45 AM - 12:15 PM:	Hoyt: Assembly methods and tools
12:15 PM - 12:45 PM:	**Lunch**
12:45 PM - 3:00 PM:	Hoyt: Assembly hands on exercises
3:00 PM - 3:15 PM:	Break
3:15 PM - 3:45 PM:	Joshua Orvis: Structural annotation of genomic sequences
3:45 PM - 4:15 PM	Functional annotation of predicted proteins
4:15 PM - 5:00 PM	Introduction to metagenomics tools
5:00 PM - 5:30 PM	**Conference Room 101/102**
	ISCB Regional Student Group (RSG) leaders meeting
	Moderator: Shraddha Thakkar
2:00 PM - 6:30 PM	**Registration** (Lobby)
	Poster Set-up: International Exhibit Hall

Note: Posters will be on display for the entire conference.

MCBIOS 2014 Conference Agenda



From Genome to Phenome:

Connecting the Dots

Day 2

Friday, March 7, 2014

7:30 AM - 8:30 AM **Registration** (Lobby); **Poster Set-up** (International Exhibit Hall)

8:30 AM - 8:45 AM **Auditorium, 110**

Welcome and Introductory Remarks:

Andy Perkins, MCBIOS President

Rakesh Kaundal, Conference Chair, Oklahoma State University

Welcome:

Stephen McKeever, Oklahoma Secretary for Science and Technology

8:45 AM - 9:45 AM **Auditorium, 110** **Keynote Address 1**:

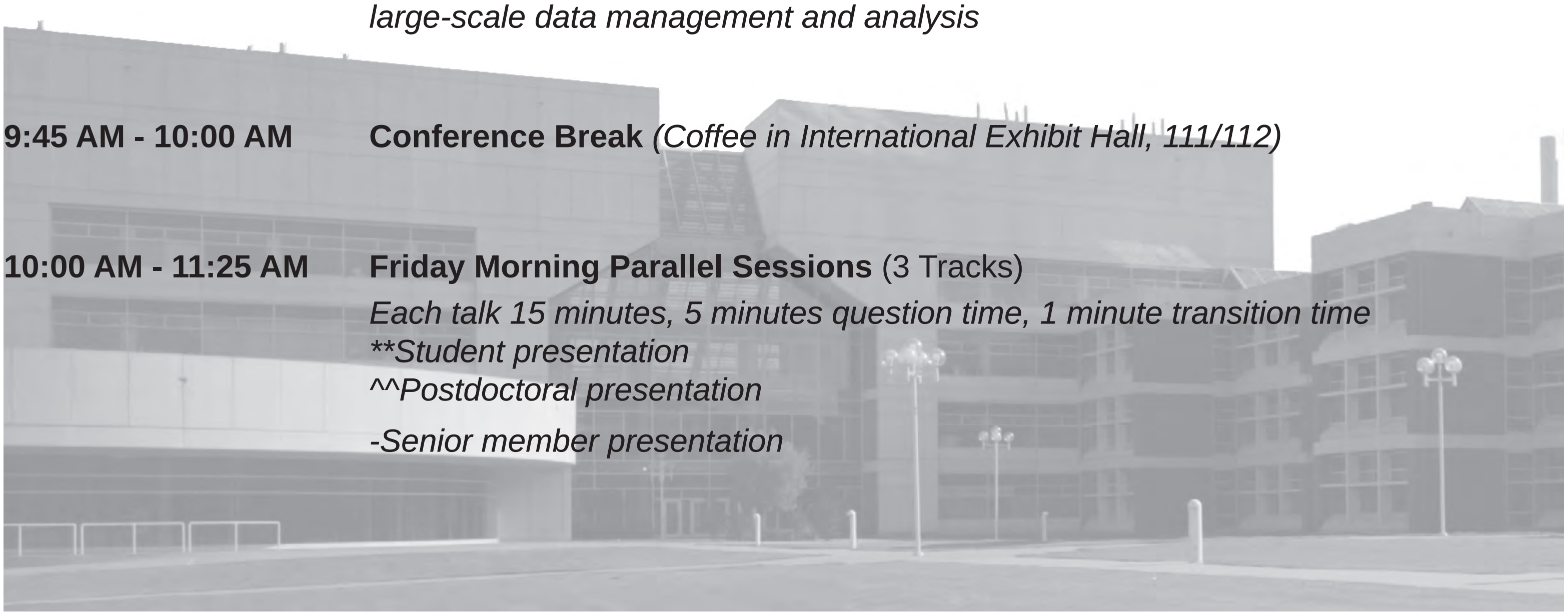
Owen R. White, Professor

Associate Director, Institute for Genome Sciences,

School of Medicine, University of Maryland

Title: *The Human Microbiome Project:*

large-scale data management and analysis



9:45 AM - 10:00 AM **Conference Break** *(Coffee in International Exhibit Hall, 111/112)*

10:00 AM - 11:25 AM **Friday Morning Parallel Sessions** (3 Tracks)

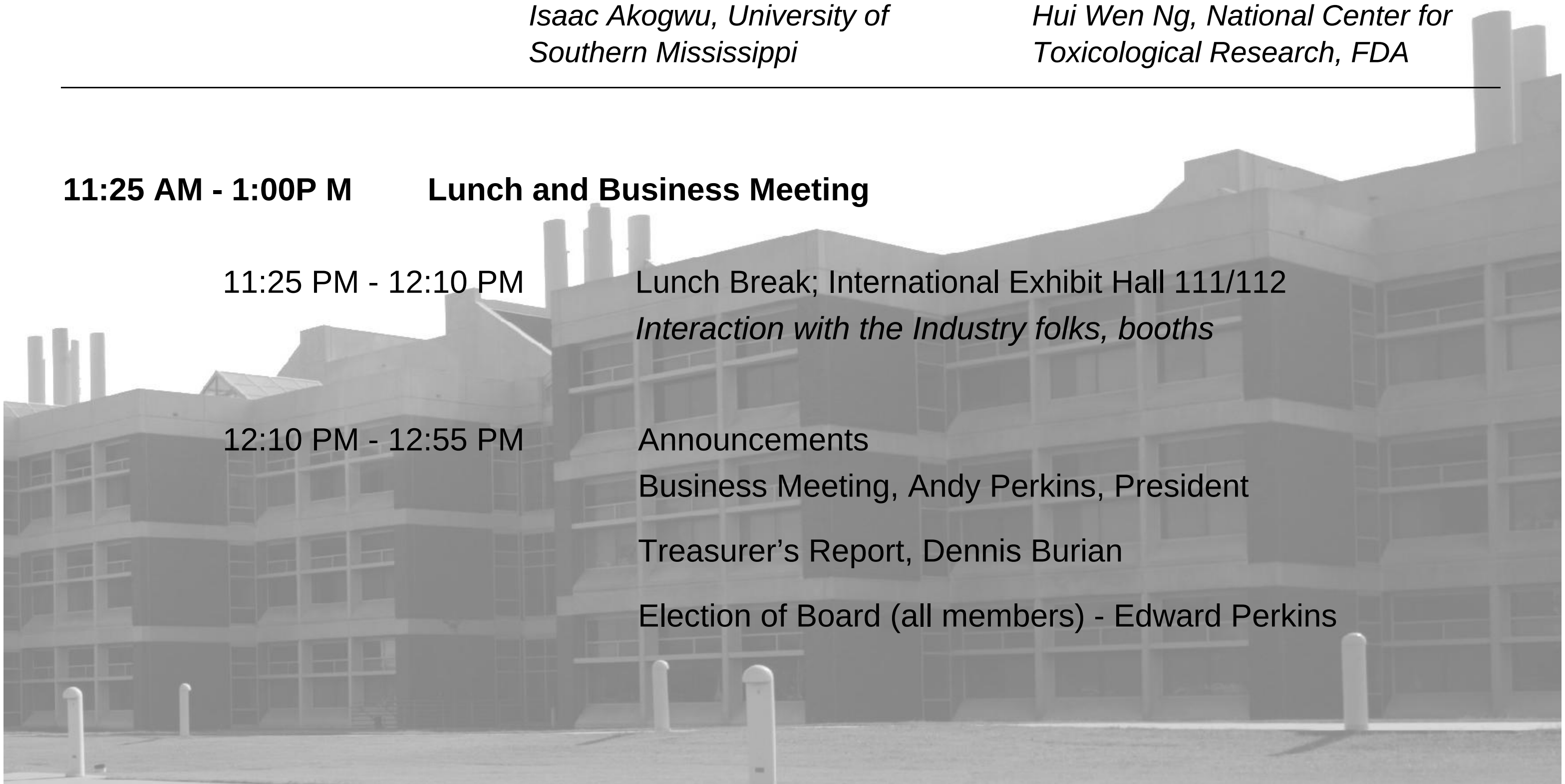
Each talk 15 minutes, 5 minutes question time, 1 minute transition time

***Student presentation*

^^Postdoctoral presentation

-Senior member presentation

Track 1: Auditorium, 110 Topic: *Evolution & Phylogenetics*	**Track 2: Executive Seminar Room, 108** Topic: *NGS Data Analysis*	**Track 3: Executive Seminar Room, 109** Topic: *Molecular Docking*
Session chair: Doris Kupfer Student moderator: Mihir Jaiswal	**Session chair: Michael Anderson** Student moderator: Nathan Cabtree	**Session chair: Rahul Singh** Student moderator: Cory Giles
****Gene Transfers Shaped Evolution of *de novo* NAD+ Biosynthesis in Eukaryotes** *Chad M. Ternes, Oklahoma State University*	****De novo assembly and analysis of the *Staphylococcus agnetis* genome** *Matthew Brian Couger, Oklahoma State University*	****A combined approach using docking and molecular dynamics to predict binding of vitamin E analogues to their transport protein.** *Shraddha Thakkar, University of Arkansas*
****Understanding the evolution of virulence and drug resistance in *Pseudomonas aeruginosa* LESB58** *Mehul Jani, University of North Texas*	****Bermuda: Bidirectional *de novo* assembly of transcripts with low expression and uneven coverage utilizing alternate *de Bruijn* graphs** *Qingming Tang, Toyota Technological Institute, Chicago*	**** Molecular docking to predict potential idiosyncratic drug reactions through interactions between HLA-B*57:01 and drugs** *Heng Luo, University of Arkansas*
****Phylogeny of few freshwater diatoms based on 18S rDNA sequences from Deepor Beel – a Ramsar site of Assam, India** *Lisha Gurung, Gauhati University, Guwahati, India*	****SeqAssist: A Novel Toolkit for Preliminary Analysis of Next-Generation Sequencing Data** *Andrew Maxwell, University of Southern Mississippi*	**** Computer-aided drug design of potential malic enzyme inhibitors for anti-obesity and anti-cancer effects** *Rinku Saha, University of Arkansas*
-Evolutionary Analysis of Papaya Ringspot Virus (PRSV-W) Infecting Cucurbits in the Southern U.S. *Akhtar Ali, University of Tulsa*	****De Novo Assembly and Functional Annotation of Timber Rattlesnake (*Crotalus horridus*) Genome from Next-Generation Sequencing Data** *Isaac Akogwu, University of Southern Mississippi*	**^^ Development of *in silico* model for differentiating estrogen receptor agonists and antagonists based on molecular docking** *Hui Wen Ng, National Center for Toxicological Research, FDA*



11:25 AM - 1:00P M Lunch and Business Meeting

11:25 PM - 12:10 PM	Lunch Break; International Exhibit Hall 111/112 *Interaction with the Industry folks, booths*
12:10 PM - 12:55 PM	Announcements Business Meeting, Andy Perkins, President Treasurer’s Report, Dennis Burian Election of Board (all members) - Edward Perkins

1:00 PM - 2:45 PM **Friday Afternoon Parallel Sessions** (3 Tracks)

Track 1: Auditorium, 110 Topic: *MATLAB workshop*	**Track 2: Executive Seminar Room, 108** Topic: *Data Mining*	**Track 3: Executive Seminar Room, 109** Topic: *Gene Expression*
Session chair: Asawari Samant	**Session chair: Sitanshu S. Sahu** Student moderator: Rinku Saha	**Session chair: Ramamurthy Mahalingam** Student moderator: Shraddha Thakkar
-MATLAB workshop (entire session)	**** MRFalign: Protein Homology Detection through Alignment of Markov Random Fields** *Jianzhu Ma, Toyota Technological Institute, Chicago*	****Probabilistic Topic Modeling on TGP Data Set** *Ming-Hua Chung, National Center for Toxicological Research*
	****Joint Feature Extraction and Classifier Design for ECG Based Biometric Recognition** *Sandeep Gutta, Oklahoma State University*	****Modeling signal transduction pathways involved in determination events of erythropoiesis** *Steven Pennington, Oklahoma State University*
	^^E-probe design for detection of a genetically modified plant pathogen *Serratia marcescens* *Ruchi Verma, Oklahoma State University*	**** Predicting true patterns of gene response to treatments in RNA-Seq-based expression analysis using pairwise comparisons** *Nam Vo, University of Memphis*
	^^ Estimating the Logistic Curve from Incomplete Data: A Comparative Study *Wen Fung Leong, Kansas State University*	****SLDR: A Method to Identify New Gene Regulatory Relationship Candidates** *Zongliang Yue, Indiana University*
	^^Topic Modeling for Cluster Analysis of Large Datasets *Weizhong Zhao, National Center for Toxicological Research, FDA*	**^^ Leveraging the New with the Old: Providing a Framework for the Integration of Historic Microarray Studies with Next Generation Sequencing** *Michael A Bauer, University of Arkansas*

2:45 PM - 2:55 PM Conference Break

2:55 PM - 4:20 PM **Friday Afternoon Parallel Sessions** (2 Tracks)

Track 1: Auditorium, 110 Topic: *Machine Learning*	**Track 2: Executive Seminar Room, 108** Topic: *Host-Pathogen Interactions*
Session chair: Patrick X. Zhao Student moderator: Heng Luo	**Session chair: Dennis Burian** Student moderator: Thomas Hahn
****Biomedical text mining using large-scale distributed machine learning algorithms** *Thomas Hahn, University of Arkansas*	**^^Prediction of Arabidopsis-*Pseudomonas syringae* interactome based on domain and interolog based approaches** *Sitanshu S. Sahu, Oklahoma State University*
****Predicting subtypes of laccases, an important lignin metabolism-related enzyme class, with machine learning** *Tyler Weirick, Oklahoma State University*	**-Characterization of mutation effects on influenza HA–glycan interactions: a computational protocol to structurally simulate binding affinities between influenza virus and host receptors** *Nan Zhao, Mississippi State University*
^^ Improving Protein Fold Recognition by Random Forests *Taeho Jo, University of Missouri*	**-Analysis of Human-HIV Protein-Protein Interaction Networks Using Biological Information Scent-Driven Random Walk** *Rahul Singh, San Francisco State University*
-Prediction of membrane transport proteins and their substrate specificities *Patrick X. Zhao, The Samuel Roberts Noble Foundation*	**-Candidate Stress Responsive Biomolecular Networks in Human Microbiome Reference Genomes** *Shaneka S. Simmons, Jackson State University*

4**:20 PM - 6:20 PM** **Poster Session,** International Exhibit Hall, 111/112

Poster presenters must be present for judging

Snacks available

6:30 PM - 7:30 PM **General Session,** Auditorium, 110

Keynote Address 2:

Vasant G. Honavar, Professor and Edward Frymoyer Chair,
College of Information Sciences and Technology,
Pennsylvania State University

Title: *Towards Predictive Biology: Why big data, although necessary, are not sufficient*

7:30 PM - 8:45 PM **Dinner Session,** International Exhibit Hall, 111/112

8:25 PM - 8:35 PM MCBIOS Board 2015, Election Results

8:35 PM - 8:45 PM Introduction to MCBIOS-XII (2015):
Cesar Compadre, University of Arkansas for
Medical Sciences (UAMS)

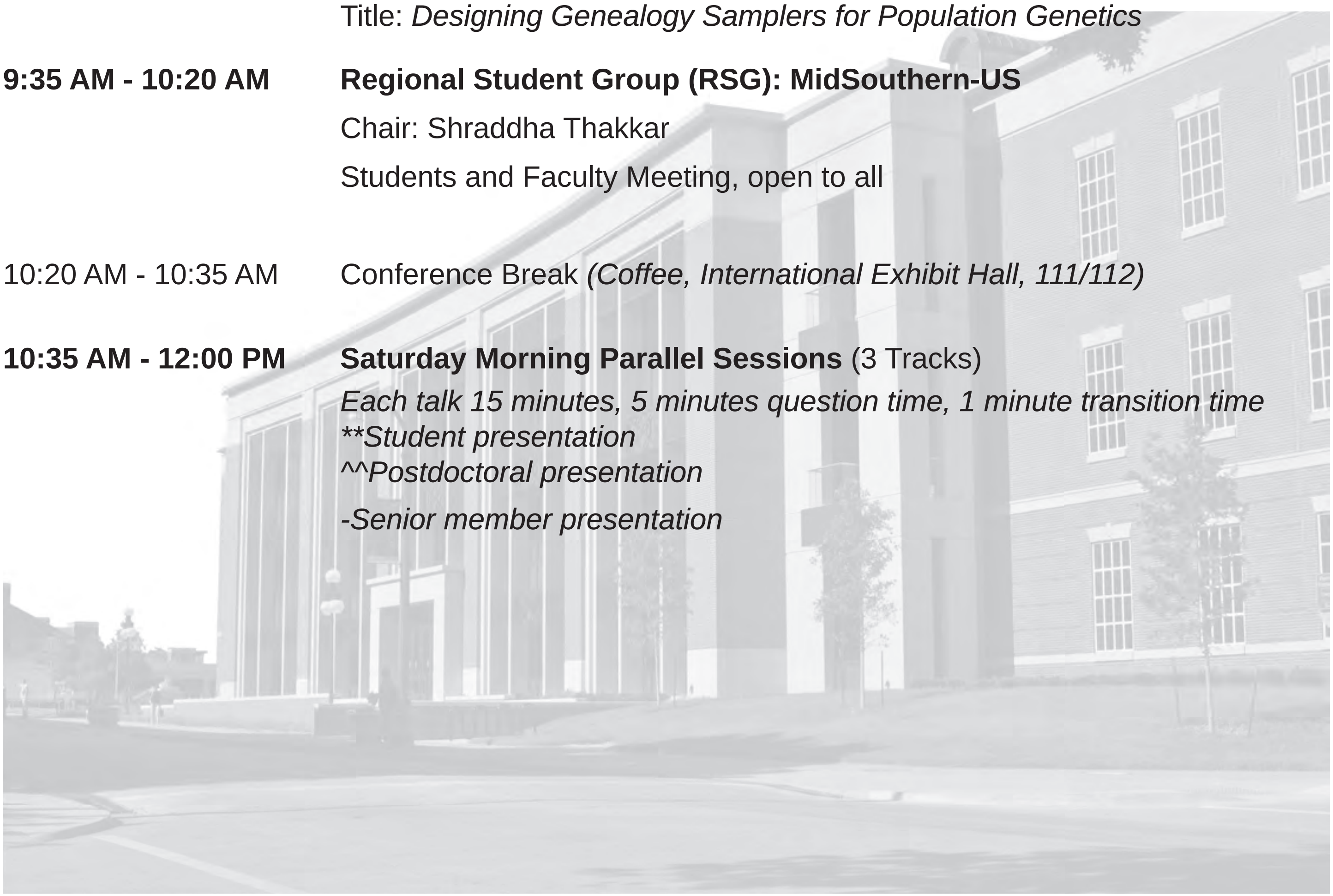
MCBIOS 2014 Conference Agenda

From Genome to Phenome:

Connecting the Dots

Day 3

Saturday, March 8, 2014



7:30 AM - 8:30 AM	Breakfast Business Meeting (Board Members Only)
8:35 AM - 9:35 AM	**General Session,** Auditorium, 110 **Keynote Address 3**: Jody Hey, Professor and Director Center for Computational Genetics and Genomics, Department of Biology, Temple University Title: *Designing Genealogy Samplers for Population Genetics*
9:35 AM - 10:20 AM	**Regional Student Group (RSG): MidSouthern-US** Chair: Shraddha Thakkar Students and Faculty Meeting, open to all
10:20 AM - 10:35 AM	Conference Break *(Coffee, International Exhibit Hall, 111/112)*
10:35 AM - 12:00 PM	**Saturday Morning Parallel Sessions** (3 Tracks) *Each talk 15 minutes, 5 minutes question time, 1 minute transition time* ***Student presentation* *^^Postdoctoral presentation* *-Senior member presentation*

Track 1: Auditorium, 110	**Track 2: Executive Seminar Room, 108**	**Track 3: Executive Seminar Room, 109**
Topic: *Sequencing & Genotyping Technologies*	Topic: *Metagenomics*	Topic: *Protein Structure / Proteomics*
Session chair: Mikhail Dozmorov Student moderator: Christopher Ma	**Session chair: Babu Fathepure** Student moderator: Andrew Maxwell	**Session chair: Ruchi Verma** Student moderator: Robert Pokoo
****SVDisc: A Novel and Integrative Pipeline for Structural Variation Discovery from Genome Re-sequencing Data** *Yan Peng, University of Southern Mississippi*	****Complete Genome Sequence and Analysis of *Edwardsiella Tarda* C07-087** *Hasan C. Tekedar, Mississippi State University*	****Predicting protein contact map using evolutionary and physical constraints by integer programming** *Zhiyong Wang, Toyota Technological Institute, Chicago*
-GSEAserver: Gene Set Enrichment Analysis for *de novo* Transcriptome Assemblies *Jun Li, Samuel Roberts Noble Foundation*	**-Productivity Associated Microbiome in Wheat** *Michael Anderson, Oklahoma State University*	****Protein side-chain prediction with dynamic dependence** *Karl Walker, Arkansas State University*
^^ Identification of Korean population specific SNPs detected by whole genome sequencing *Wenqian Zhang, National Center for Toxicological Research, FDA*	**-Screening metagenomic data for viruses using e-probe diagnostic nucleic acid analysis (EDNA)** *Ulrich Melcher, Oklahoma State University*	****XLPM: X-Linked Peptide Mapping Algorithm** *Mihir Jaiswal, University of Arkansas*
^^Revealing the inherent heterogeneity of human malignancies by variant consensus strategies coupled with cancer clonal analysis *Erich A. Peterson, University of Arkansas*	**-Metagenomic Insight into Bacterial Degradation of Lignin** *Babu Fathepure, Oklahoma State University*	**-Identification of novel alternative splicing biomarkers from breast cancer proteome using RNA-seq** *Fan Zhang, University of North Texas Health Science Center*

12:00 PM - 1:00 PM Conference Lunch; International Exhibit Hall 111/112

Interaction with the Industry folks, booths

Distributed Rattlesnake Genome Annotation Workshop

Point 4 Room, 106

1:00 PM - 2:25 PM **Saturday Afternoon Parallel Sessions** (2 Tracks)

Track 1: Auditorium, 110
Topic: *OMICS Technologies*

Session chair: Jonathan Wren
Student moderator: Fredy Saudale

-Assessing Synergistic Use of Biomarkers and Predictive Models Derived from Microarray and RNA-Seq
Weida Tong, National Center for Toxicological Research, FDA

-miRDisc: A Novel Computational Program for microRNA Discovery from Short Deep Sequencing Reads
Ping Gong, Badger Technical Services, LLC

-Quality evaluation of the extracted ion chromatograph and detected chromatograph peaks from LC/MS-based Metabolomics Data
Wenchao Zhang, Samuel Roberts Noble Foundation

-Haystack, a Web-Based Tool for Metabolomics Research
Stephen C. Grace, University of Arkansas

Track 2: Executive Seminar Room, 108
Topic: *Population & Statistical Genetics*

Session chair: Lan Zhu
Student moderator: Tyler Weirick

-Connecting Genomics and Epigenomics: The Rare Variants' Case
Mikhail Dozmorov, Oklahoma Medical Research Foundation

-Deciphering miRNA - transcription factor feedforward loops to identify drug re-purposing candidates for cystic fibrosis
Zhichao Liu, National Center for Toxicological Research, FDA

-Predicting performance of short-read aligners based on genome complexity
Vinhthuy Phan, University of Memphis

-A Novel Statistical Method for Detecting Natural Selection from Arbitrary Correlated SNP Data
Lan Zhu, Oklahoma State University

2:25 PM - 2:35 PM Conference Break

2:35 PM - 2:55 PM Auditorium, 110 **General Session**

Invited Speaker:

William Slikker, Ph.D., Professor and Director
National Center for Toxicological Research (FDA),
Jefferson, Arkansas
Title: *New Directions for Bioinformatics: Imaging as a Preclinical Assessment Tool*

3:00 PM - 4:15 PM **Awards Ceremony (General Session)**, *Auditorium, 110*

3:00 PM - 4:00 PM	**Announcements**: Students / Postdocs awards; Oral / Poster Best Oral presentation, sponsored by Head of BCMB, OSU Dr. John Gustafson to present the award Thanks (President, MCBIOS), Conclusion
4:00 PM - 4:15 PM	**Photo Session** - Award winners, Groups
4:15 PM - 6:15 PM	**Tour to Stillwater Attractions** (Sheerar Museum, Wrestling Hall of Fame, OSU Museum of Art, etc.): Optional

Please remember to turn in your evaluations!

CONFERENCE KEYNOTES

Keynote Speaker: Dr. Owen R. White, Ph.D.

Owen R. White, Ph.D.
Director Bioinformatics Department
Institute for Genome Sciences (IGS) and Professor of Epidemiology and Public Health at the University of Maryland School of Medicine, Baltimore, Maryland

Owen R. White is the Director of the Bioinformatics department at the Institute for Genome Sciences (IGS) and a Professor of Epidemiology and Public Health at the University of Maryland School of Medicine in Baltimore, Maryland. The IGS Bioinformatics group annotates (or interprets and analyses) the huge strings of sequencing data from genomic and biomedical researchers at the center. Dr. White and the IGS Bioinformatics department are involved in large-scale annotation, ontology development and data sharing. They are the lead institution for the Human Microbiome Project's central data repository or the Data Analysis and Coordination Center (known as the HMP DACC). The HMP was launched by the National Institutes of Health to fuel research into the microbes that live in the various environments of the human body, and to look for correlations between changes in the microbiome and human health. The HMP DACC is the central repository for all HMP data, providing specialized data management and analysis infrastructure to facilitate discoveries about the microbiome.

Dr. White has advanced the use of documenting standard operational procedures, matrix management and employee training practices. His current staff is comprised of 25 people that are similarly engaged in supplying both core services, developing Open Source resources for the community and performing genomic research functions for faculty at IGS. Another critical product of Dr. White's research is to engage other researchers in large-scale interoperation, for annotation, ontology development, and data sharing. The fact that Dr. White was among the second most-cited scientists is a direct reflection of his support for several significant efforts.

Keynote Speaker: Dr. Vasant G. Honavar, Ph.D.

Dr. Vasant G. Honavar, Ph.D.
Professor and Edward Frymoyer Chair Pennsylvania State University
College of Information Sciences and Technology

Dr. Honavar received his Ph.D. in 1990 from the University of Wisconsin–Madison. He is known for his research contributions in artificial intelligence, machine learning, data mining, knowledge representation, neural networks, semantic web, big data analytics, and bioinformatics and computational biology. He has published over 200 research articles as well as edited several books on these topics. His recent work has focused on scalable algorithms for constructing predictive models from large, semantically disparate distributed data, learning predictive models from linked open data, big data analytics, analysis and prediction of protein-protein, protein-RNA, and protein-DNA interfaces and interactions, social network analytics, secrecy-preserving query answering, representing and reasoning about preferences, and causal inference and meta analysis.

During 1990-2013, Dr. Honavar was professor of Computer Science and headed the Iowa State University Artificial Intelligence Research Laboratory. In 2006, he became director of the Iowa State University Center for Computational Intelligence, Learning and Discovery. He was also on the faculty of the interdepartmental graduate programs in Bioinformatics and Computational Biology (serving as Chair during 2003-2005), and Human-Computer Interaction.

During 2010-2013, Dr. Honavar served as a ‘Program Director’ in the Information Integration and Informatics program in the Information and Intelligent Systems Division of the Computer and Information Science and Engineering Directorate of the US National Science Foundation (NSF) where he led the Big Data Program and contributed to several core and cross-cutting programs. He has held visiting professorships at Carnegie Mellon University and at the University of Wisconsin–Madison.

Keynote Speaker: Dr. Jody Hey, Ph.D.

Dr. Jody Hey, Ph.D.
Professor and Director,
Center for Computational Genetics and Genomics, Temple University

Dr. Hey is a renowned Evolutionary Geneticist with a major focus on the understanding of evolutionary mechanisms for the origin of biological taxa. In the 1980s and 1990s, he did research on natural selection and species divergence in fruit flies (Drosophila). More recently he has worked on the development of methods for studying evolutionary divergence, studying cichlid fishes from Lake Malawi, and the divergence process of chimpanzees and human populations. His research on divergence and speciation also led him to study the difficulties of defining species.

Dr. Hey has also conducted mathematical and statistical research in population genetics. He is the author of several popular computer programs used by other biologists to address questions in population genetics. In 2004, Hey and Rasmus Nielsen produced the computer program IM which implements a method for fitting an isolation-with-migration model to a pair of closely related populations or species. For many years, Hey was at Rutgers University before he moved to Temple University in 2013.

In 1998, Hey received a Guggenheim fellowship, and in 2008, he was elected to the presidency of the Society for Molecular Biology and Evolution.

CONFERENCE WORKSHOPS

Workshop 1

Day 1 (*March 6, 2014*):

Title: Working with Next-Generation Sequencing Data: Tools and Techniques

Workshop Chair: Dr. Peter R. Hoyt, Ph.D.

Dr. Peter R. Hoyt, Ph.D.
Director Microarray Core Facility and Bioinformatics Core Facility: BIOinfOSU, Oklahoma State University

Peter Hoyt graduated from the University of Houston with a B.S. in Biology, and followed in 1977 with an M.S. in Marine Microbiology at the University of Houston Marine Science Center where he studied the antibiotic properties of natural bacteriocins in Vibrio and related species relating how they provided for competitive advantages in mixed cultures. After working as a Research Associate at the University of Texas Medical Branch in Galveston, Texas, in 1983 he entered the UTMB Graduate Program in Cell Biology and Human Genetics earning his Ph.D. in Human Genetics and Cell Biology.

His research focused on gene regulation in mice during development specifically contrasting the changes in transcription factor binding to promoters within the albumin/alphafetoprotein complex. In 1988 his work earned him an Alexander Hollaendar Distinguished Postdoctoral Fellowship at the Oak Ridge National Laboratory (ORNL) in Oak Ridge, Tennessee where he studied the genetic regulation and epigenetic effectors of mouse proviral elements, and generated the first transgenic mice with functional genes at ORNL. He served as a National Cancer Institute Training Fellow at ORNL while generating ORNL's first mice with targeted gene knockouts including the oncogenic Evi1 transcription-factor locus demonstrating the role of Evi1 in development of the mesoderm and associated differentiation of tissues during development *in utero*. In 2000, while working at ORNL, Dr. Hoyt joined the faculty at the University of Tennessee in the new Graduate Program of Genome Sciences and Technology. He expanded on his interest in gene expression by forming the first microarray facility at ORNL, and creating high-throughput robotic platforms for purifying DNA, RNAs and proteins. In 2005, his interest in microarray technology brought him to Oklahoma State University as Director of the OSU Microarray Core Facility, and the Bioinformatics Core facility: BIOinfOSU. Dr. Hoyt immediately developed interdisciplinary partnerships and was able to create a Graduate-level Certification Program in Bioinformatics in 2005 and serves as the Graduate Program's Director. His current research interests include determination mechanisms in pluripotent cells leading to differentiation. He also uses comparative genomics to identify antimicrobial resistance genes in bacterial pathogens. As Director of the Bioinformatics Core Facility, he has multiple collaborations across the OSU campus, and statewide. He has developed workshops in Microarray technology, and Bioinformatics, and is currently involved in implementation of new learning technologies at OSU focused on providing online bioinformatics curricula.

Dr. Joshua Orvis

Joshua Orvis is a Bioinformatics Software Engineer at the Institute for Genome Sciences, where he works primarily on single-genome annotation, metagenomics projects, and distributed grid computing infrastructure. He is also a faculty member at Johns Hopkins University, where he teaches three courses in the bioinformatics graduate program.

Dr. Dana Brunson

Dana Brunson is Director of the High Performance Computing Center and is an adjunct associate professor in the Computer Science Department at Oklahoma State University (OSU). She earned her Ph.D. in Numerical Analysis at the University of Texas at Austin in 2005 and her M.S. and B.S. in Mathematics from OSU. In addition, Dana is serving on the committee for OSU's Bioinformatics Graduate Certificate program and is the XSEDE Campus Champion for OSU.

Workshop Agenda:

This workshop will consist of hands-on exercises prepared by Haibao Tang at the J. Craig Venter Institute (JCVI) using Next Generation Sequencing (NGS) data. Online tools will be introduced, but most exercises will be performed on OSU's new super computer: Cowboy. Exercises in recent metabolomics methodologies will be given by Dr. Joshua Orvis (University of Maryland, Institute for Genome Sciences). The workshop will be suitable for beginners. Dr. Dana Brunson of the OSU High-Performance Computing Center will present Basic Linux and Bash scripting commands to facilitate the exercises.

Dr. Joshua Orvis will present structural and functional annotation of single genomes with evidence visualization using tools like Augustus, GeneMark and HMMER3. Following this will be an introduction to metagenomics data analysis tools, including MEGAN5.

Workshop 2

Day 2 (*March 7, 2014*)

Title: MATLAB for Computational Biology Applications

Workshop Chair: Asawari Samant

Asawari Samant
MathWorks Application Engineer

Asawari Samant is a Senior Application Engineer at MathWorks. She has a B.S. and M.S. in chemical engineering. At MathWorks, she primarily supports the pharmaceutical and biotechnology industry, and the computational biology sector.

This workshop will introduce MATLAB as a flexible environment for teaching and research in a wide range of life science applications, including signal processing and image processing, math and optimization, statistics and data analysis and computational biology. In the first half, we will provide an overview of MATLAB as a flexible and powerful tool for data analysis and visualization.

Highlights include:

- Access data from many sources (files, other software, hardware, etc.)
- Use interactive tools for iterative exploration, design, and problem solving
- Automate and capture your work in easy-to-write scripts and programs
- Share your results with others by automatically creating reports
- Build and deploy GUI-based applications

The latter part will focus on the computational biology capabilities starting with the Bioinformatics Toolbox which can be used to read, analyze, and visualize genomic, proteomic, next generation sequencing and microarray data.

This session will also introduce SimBiology, a MATLAB based tool that provides a graphical and programmatic interface for modeling, simulating, and analyzing biochemical pathways and for PK/PD analysis.

Workshop 3

Day 3 (*March 8, 2014*)
Title: The Timber Rattlesnake Genome Project

Workshop Chairs: William S. Sanders, Ph.D.
Ping Gong, Ph.D.

William S. Sanders, *Institute for Genomics, Biocomputing and Biotechnology, Mississippi State University*
E-mail: wss2@igbb.msstate.edu

Ping Gong, *Badger Technical Services, LLC, Engineer Research and Development Center, US Army Corps of Engineers*
E-mail: ping.gong@usace.army.mil

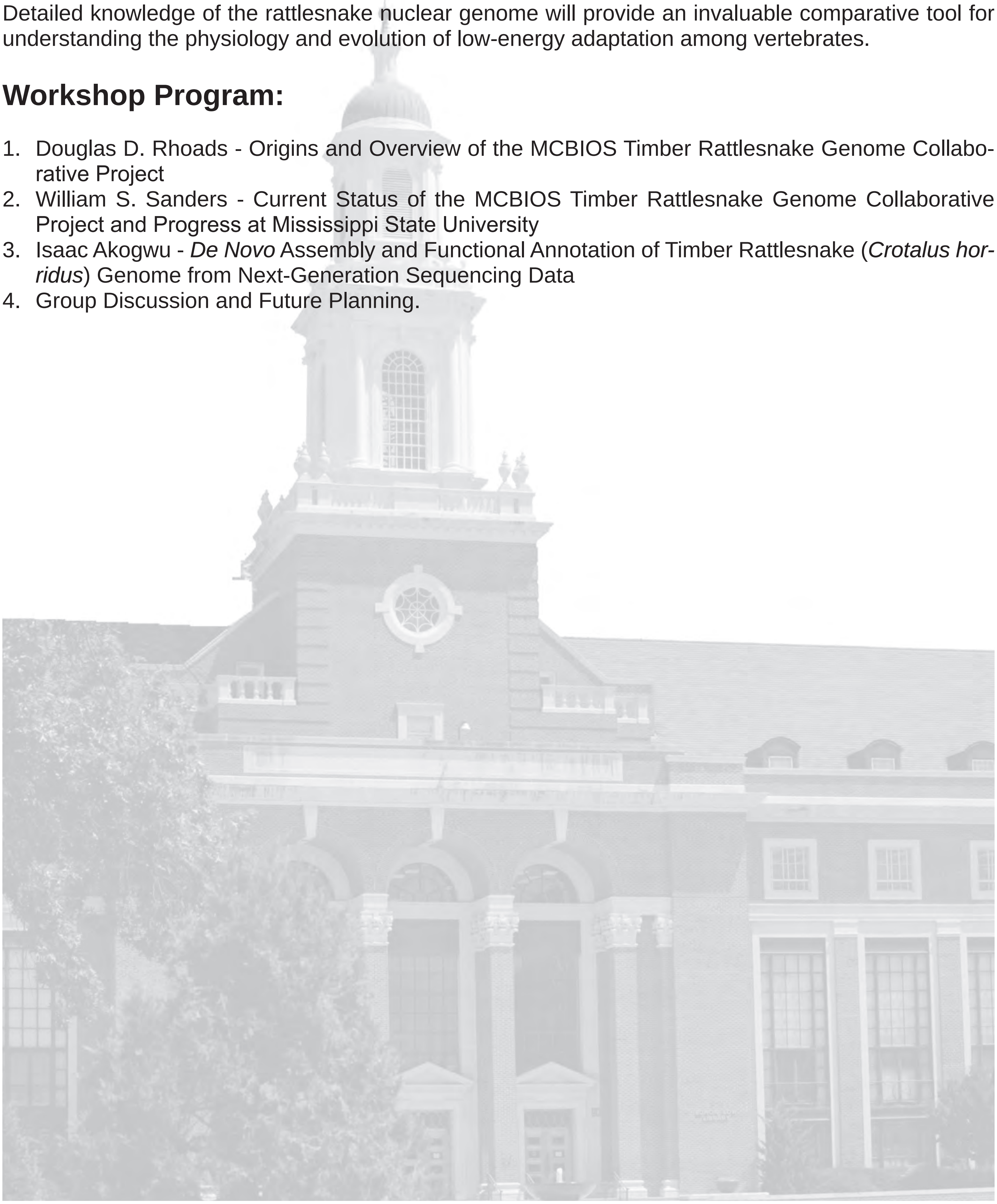
MCBIOS members of all levels are invited to participate in the workshop that serves as a progress review of a community-wide collaborative project to sequence, assemble, and annotate the genome of the timber rattlesnake (*Crotalus horridus*). Both genomic and transcriptomic data were collected using next generation sequencing technologies (Illumina & Roche 454) jointly by Drs. Douglas Rhoads and Steven Beaupreat at University of Arkansas, and Dr. Michael Berumen at King Abdullah University of Science and Technology. These data have been made available to MCBIOS members involved with this project. There are currently three active working groups for this project: (1) Data Management, (2) Genome & Transcriptome Assembly, and (3) Data Mining & Annotation. This workshop also intends to serve as an information session about the project detailing the current status and providing information to new participants on ways they can become involved.

Background:

Rattlesnakes are unique model organisms that facilitate research in a variety of contexts, mostly relating to their general adaptation to low-energy lifestyles. In particular, Rattlesnakes are known for their extremely low standard and resting metabolic rates which reduce their energetic cost of living relative to other similar-sized vertebrates. Low metabolism is facilitated by the ability to down-regulate whole organ systems (e.g. the liver and the digestive tract) when not in use. These organ systems are rapidly up-regulated when needed. Reduced energy requirements make rattlesnakes capable of withstanding starvation bouts of extreme length (up to two years), rendering them a relatively unexplored model of extreme starvation tolerance among vertebrates. As a model of high frequency contraction for the purpose of making noise, the shaker muscle of the rattle of rattlesnakes has been extensively studied and described as a model of muscle specialization. Empirical observations that support the bioenergetic uniqueness of pit vipers, including rattlesnakes, have recently been supported by the discovery of extremely rapid rates of evolution of the mitochondrial genomes of snakes. Together, these separate lines of research firmly establish the rattlesnakes as an important vertebrate model of low-energy adaptation. Detailed knowledge of the rattlesnake nuclear genome will provide an invaluable comparative tool for understanding the physiology and evolution of low-energy adaptation among vertebrates.

Workshop Program:

1. Douglas D. Rhoads - Origins and Overview of the MCBIOS Timber Rattlesnake Genome Collaborative Project
2. William S. Sanders - Current Status of the MCBIOS Timber Rattlesnake Genome Collaborative Project and Progress at Mississippi State University
3. Isaac Akogwu - *De Novo* Assembly and Functional Annotation of Timber Rattlesnake (*Crotalus horridus*) Genome from Next-Generation Sequencing Data
4. Group Discussion and Future Planning.



INVITED PRESENTATIONS

Invited Speaker: William Slikker, Ph.D.

William Slikker, Jr., Ph.D.
Director, National Center for Toxicological Research
Jefferson, AR

Dr. William Slikker, Jr. is the Director of the Food and Drug Administration's (FDA) 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. Dr. Slikker is the past President of the Society of Toxicology (SOT) and Associate Editor for *NeuroToxicology* and *Toxicological Sciences*. He was past Treasurer, SOT and past President of The Academy of Toxicological Sciences. He held committee chairmanships or elected offices in several other scientific societies including the Teratology Society (serving as President); 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. Dr. Slikker has authored or co-authored over 300 publications in the areas of transplancental pharmacokinetics, developmental neurotoxicology, neuroprotection, systems biology, and risk assessment. He has also served on several national/international advisory panels for HESI/ILSI, CIIT Centers for Health Research, EPA, NIEHS, NAS, NIH, and WHO.

MCBIOS: XI

In collaboration with the

International Society of Computational Biology

Students and Faculty Meeting of

Regional Student Group MidSouthern-US

Leaders Meeting - Thursday, 03/06/14, 5:00-5:30 PM
Conference Room 101/102

General Meeting - Saturday, 03/08/14, 9:35-10:20 AM
Auditorium 110

Participants List: Oral Presentations

No.	Presenter	Affiliation	Oral Presentation Title
1	Akogwu, Isaac	University of Southern Mississippi, MS, USA	De Novo Assembly and Functional Annotation of Timber Rattlesnake (*Crotalus horridus*) Genome from Next-Generation Sequencing Data
2	Ali, Akhtar	University of Tulsa, OK, USA	Evolutionary analysis of *papaya ringspot virus* (PRSV-W) infecting cucurbits in the southern united states
3	Anderson, Michael	Oklahoma State University, OK, USA	Productivity Associated Microbiome in Wheat
4	Bauer, Michael A	University of Arkansas for Medical Sciences, AR, USA	Leveraging the New with the Old: Providing a Framework for the Integration of Historic Microarray Studies with Next Generation Sequencing
5	Chung, Ming-Hua	National Center for Toxicological Research (FDA), AR, USA	Probabilistic Topic Modeling on TGP Data set
6	Couger, Matthew Brian	Oklahoma State University, OK, USA	De novo assembly and analysis of the *Staphylococcus agnetis* genome
7	Dozmorov, Mikhail	Oklahoma Medical Research Foundation, OK, USA	CONNECTING GENOMICS AND EPIGENOMICS: THE RARE VARIANTS' CASE
8	Fathepure, Babu	Oklahoma State University, OK, USA	Metagenomic Insight into Bacterial Degradation of Lignin
9	Gong, Ping	Badger Technical Services, LLC, TX, USA	miRDisc: A Novel Computational Program for microRNA Discovery from Short Deep Sequencing Reads
10	Grace, Stephen C.	University of Arkansas at Little Rock, AR, USA	Haystack, a Web-Based Tool for Metabolomics Research
11	Gurung, Lisha	Gauhati University, Guwahati, India	Phylogeny of few freshwater diatoms based on 18S rDNA sequences from Deepor Beel – a Ramsar site of Assam, India

12	Gutta, Sandeep	Oklahoma State University, OK, USA	Joint Feature Extraction and Classifier Design for ECG Based Biometric Recognition
13	Hahn, Thomas	University of Arkansas at Little Rock, AR, USA	Biomedical text mining using large-scale distributed machine learning algorithms
14	Jaiswal, Mihir	University of Arkansas at Little Rock, AR, USA	XLPM: X-Linked Peptide Mapping Algorithm
15	Jani, Mehul	University of North Texas, TX, USA	Understanding the evolution of virulence and drug resistance in *Pseudomonas aeruginosa* LESB58
16	Jo, Taeho	University of Missouri, MO, USA	Improving Protein Fold Recognition by Random Forests
17	Leong, Wen Fung	Kansas State University, KS, USA	Estimating the Logistic Curve from Incomplete Data: A Comparative Study
18	Li, Jun	The Samuel Roberts Noble Foundation, OK, USA	GSEAserver: Gene Set Enrichment Analysis for *de novo* Transcriptome Assemblies
19	Liu, Zhichao	National Center for Toxicological Research (FDA), USA	Deciphering miRNA - transcription factor feed-forward loops to identify drug repurposing candidates for cystic fibrosis
20	Luo, Heng	University of Arkansas at Little Rock, AR, USA	Molecular docking to predict potential idiosyncratic drug reactions through interactions between HLA-B*57:01 and drugs
21	Ma, Jianzhu	Toyota Technological Institute, Chicago, USA	MRFalign: Protein Homology Detection through Alignment of Markov Random Fields
22	Maxwell, Andrew	University of Southern Mississippi, MS, USA	SeqAssist: A Novel Toolkit for Preliminary Analysis of Next-Generation Sequencing Data
23	Melcher, Ulrich	Oklahoma State University, OK, USA	Screening metagenomic data for viruses using e-probe diagnostic nucleic acid analysis (EDNA)
24	Ng, Hui Wen	National Center for Toxicological Research (FDA), AR, USA	Development of *in silico* model for differentiating estrogen receptor agonists and antagonists based on molecular docking

25	Peng, Yan	University of Southern Mississippi, MS, USA	SVDisc: A Novel and Integrative Pipeline for Structural Variation Discovery from Genome Re-sequencing Data
26	Pennington, Steven	Oklahoma State University, OK, USA	Modeling signal transduction pathways involved in determination events of erythropoiesis
27	Peterson, Erich A.	University of Arkansas for Medical Sciences, AR, USA	Revealing the inherent heterogeneity of human malignancies by variant consensus strategies coupled with cancer clonal analysis
28	Phan, Vinhthuy	University of Memphis, TN, USA	Predicting performance of short-read aligners based on genome complexity
29	Saha, Rinku	University of Arkansas at Little Rock, AR, USA	Computer-aided drug design of potential malic enzyme inhibitors for anti-obesity and anti-cancer effects
30	Sahu, Sitanshu S.	Oklahoma State University, OK, USA	Prediction of Arabidopsis-*Pseudomonas syringae* interactome based on domain and interolog based approaches
31	Simmons, Shaneka S.	Jackson State University, MS, USA	Candidate Stress Responsive Biomolecular Networks in Human Microbiome Reference Genomes
32	Singh, Rahul	San Francisco State University, CA, USA	Analysis of Human-HIV Protein-Protein Interaction Networks Using Biological Information Scent-Driven Random Walk
33	Su, Zhenqiang	National Center for Toxicological Research/FDA, USA	Assessing Synergistic Use of Biomarkers and Predictive Models Derived from Microarray and RNA-Seq
34	Tang, Qingming	Toyota Technological Institute, Chicago, USA	Bermuda: Bidirectional *de novo* assembly of transcripts with low expression and uneven coverage utilizing alternate *de Bruijn* graphs
35	Tekedar, Hasan C.	Mississippi State University, MS, USA	Complete Genome Sequence and Analysis of *Edwardsiella Tarda* C07-087
36	Ternes, Chad M.	Oklahoma State University, OK, USA	Gene Transfers Shaped Evolution of *de novo* NAD+ Biosynthesis in Eukaryotes

37	Thakkar, Shraddha	University of Arkansas for Medical Sciences, AR, USA	A combined approach using docking and molecular dynamics to predict binding of vitamin-E analogues to their transport protein
38	Verma, Ruchi	Oklahoma State University, OK, USA	E-probe design for detection of a genetically modified plant pathogen *Serratia marcescens*
39	Vo, Nam	University of Memphis, TN, USA	Predicting true patterns of gene response to treatments in RNA-Seq based expression analysis using pairwise comparisons
40	Walker, Karl	Arkansas State University, AR, USA	Protein Side-chain Prediction with Dynamic Dependence
41	Wang, Zhiyong	Toyota Technological Institute, Chicago, USA	Predicting protein contact map using evolutionary and physical constraints by integer programming
42	Weirick, Tyler	Oklahoma State University, OK, USA	Predicting subtypes of laccases, an important lignin metabolism-related enzyme class, with machine learning
43	Yue, Zongliang	Indiana University, IN, USA	SLDR: A Method to Identify New Gene Regulatory Relationship Candidates
44	Zhang, Fan	University of North Texas Health Science Center, TX, USA	Identification of novel alternative splicing biomarkers from breast cancer proteome using RNA-seq
45	Zhang, Wenchao	The Samuel Roberts Noble Foundation, OK, USA	Quality evaluation of the extracted ion chromatograph and detected chromatograph peaks from LC/MS-based Metabolomics Data
46	Zhang, Wenqian	National Center for Toxicological Research (FDA), AR, USA	Identification of Korean population specific SNPs detected by whole genome sequencing
47	Zhao, Nan	Mississippi State University, MS, USA	Characterization of mutation effects on influenza HA–glycan interactions: a computational protocol to structurally simulate binding affinities between influenza virus and host receptors
48	Zhao, Patrick X.	The Samuel Roberts Noble Foundation, OK, USA	Prediction of membrane transport proteins and their substrate specificities

49	Zhao, Weizhong	National Center for Toxicological Research (FDA), AR, USA	Topic Modeling for Cluster Analysis of Large Datasets
50	Zhu, Lan	Oklahoma State University, OK, USA	A Novel Statistical Method for Detecting Natural Selection from Arbitrary Correlated SNP Data

Participants List: Poster Presentations

No.	Primary Presenter	Affiliation	Poster Title
1	Akgul, Ali	Mississippi State University, MS, USA	Genetic variation analysis in FT1 locus of eastern cottonwood (*Populus deltoides*)
2	Akgun, Devrim	Sakarya University, Hendek, Turkey	OpenMP Accelerated Dynamic Functional Connectivity Analysis on Multicore Computer
3	Aldwairi, Tamer	Mississippi State University, MS, USA	An innovative Computational Approach for Predicting Novel piRNA Clusters in Related Species
4	Ankam, Harish	Texas A&M University-Commerce, TX,USA	A Compact Independent Component Analysis Implementation with Graphical Processing Unit
5	Arick II, Mark	Institute for Genomics, Biotechnology, and Biocomputing, MS, USA	SABRe - Sequence Assembly By Reference
6	Balasubramaniam, Meenakshisundaram	University of Arkansas at Little Rock, AR, USA	Molecular dynamics simulation of Proteins involved in Alzheimer's disease and their role in aggregation
7	Barabote, Ravi	University of Arkansas, AR, USA	16S metagenomics analysis of leaf decomposition
8	Bisgin, Halil	National Center for Toxicological Research (FDA), AR, USA	Exploring Rat Body Map through Topic Modeling
9	Bohra, Kushal	Texas A&M University-Commerce, TX, USA	Software Toolbox for Multivariate Pattern Analysis of Different Brain States from Functional Magnetic Resonance Imaging Data
10	Chavan, Shweta	University of Arkansas for Medical Sciences, AR, USA	Profiling Multiple Myeloma Engraftment Phenomena via an in-vivo SCID Mouse Model and RNA-seq
11	Cheng, Yanbing	Texas A&M University, TX, USA	Comparative genomic analysis of the oxidoreductases involved in lignin degradation in oleaginous fungi *Mucor circinelloides* and *Mortierella alpine*

12	Choudhury, Shuvasish	Assam University, Silchar, India	Genome -Wide Comparative Analysis of Tonoplast Intrinsic Protein (TIP) Genes in Plants
13	Clark, Misti	University of Arkansas at Little Rock, AR, USA	Heart Rate Variation in High Risk vs Low Risk Expectant Mothers
14	Coleman, Jenaelle	Mississippi Valley State University, MS, USA	Pathway and genetic analysis of prostate cancer in African-American males
15	Crabtree, Nathan	University of Arkansas at Little Rock, AR, USA	RNA-Seq: from sequences to knowledge
16	Das, Sunetra	University of Oklahoma, OK, USA	RNA-seq analysis of stage-specific limb regenerates in the fiddler crab, *Uca pugilator*
17	Delongchamp, Robert R.	University of Arkansas for Medical Sciences, AR, USA	Power calculation for genetic association analyses of continuous phenotypes
18	Embry, Stephen C.	University of Arkansas at Little Rock, AR, USA	HayStack: A Webserver for Metabolomic data analysis
19	Esquivel, Johnny	Texas A&M-Commerce, TX,USA	Software for Analyzing Brain's Dynamic Functional Connectivity from Functional Magnetic Resonance Images
20	Fang, Hong	National Center for Toxicological Research (FDA), AR, USA	Exploring the FDA Adverse Event Reporting System (FAERS) to Generate Hypotheses for Monitoring of Disease
21	Farek, Jesse	Mississippi State University, MS,USA	Web-based Visualization of Chicken Gene Expression Data
22	Farek, Jesse	Mississippi State University, MS,USA	Web-based Visualization for Computational Biology Expression Atlases
23	Flores, Heriberto	Texas A&M University-Commerce, TX,USA	Finding Optimal Brain Mappings Using Integer Linear Programming Solvers
24	Gong, Binsheng	National Center for Toxicological Research (FDA), AR, USA	Modulation of Dynamic microRNA Regulation in Rat Liver Treated with Thioacetamide by Integrating Data of microRNA-Seq and mRNA Microarray Expression Profiling
25	Gui, Tina	University of Mississippi,	A Pairwise Feature Selection Method

		MS, USA	for Gene Data Using Information Gain
26	Gupta, Neha	Boston Children’s Hospital, Boston, MA, USA	Biomedical text mining using large-scale distributed machine learning algorithms
27	Hahn, Thomas	University of Arkansas at Little Rock, AR,USA	Graphical multiple sequence alignment tool
28	Hivrale, Vandana	Oklahoma State University, OK, USA	Profiling of abiotic and biotic stress responsive miRNAs in switchgrass using high-throughput sequencing platform
29	Joginipelli, Sravanthi	University of Arkansas at Little Rock, AR, USA	Molecular modeling and *in silico* characterization of mutations associated with multiple drug resistant tuberculosis (MDR-TB) and extensive drug resistant tuberculosis (XDR-TB)
30	Loganantharaj, Rasiah	University of Louisiana, LA, USA	Analysis of desiccation tolerance in *Polypodium polypodioides* by RNA-Seq
31	Kalindamar, S.	Mississippi State University, MS, USA	Identification of *Edwardsiella ictaluri* genes involved in growth
32	Knisley, Debra	East Tennessee State University, TN, USA	Consensus Modeling of Gene Expression Data: An Application to Control versus Cystic Fibrosis Microarray Data
33	Lee, Mikyung	National Center for Toxicological Research (FDA), AR, USA	Application of dynamic topic model to toxicogenomics data
34	Li, Si	University of Southern Mississippi, MS, USA	Deciphering chemically-induced reversible neurotoxicity by reconstructing perturbed pathways from time series microarray gene expression data
35	Lin, Fan	University of Oklahoma, OK, USA	Identification of Grass Cell Wall Synthesis Genes from Correlations between Gene Expression and Cell Wall Composition in Rice

36	Liu, Jie	University of Arkansas at Little Rock, AR,USA	Comparative Analysis of Predictive Models for Liver Toxicity Using ToxCast Assays and Quantitative Structure-Activity Relationships
37	Liu, Sheng	University of Mississippi, MS, USA	Evaluation of Random Forest Based Rule Learning
38	Luo, Heng	University of Arkansas at Little Rock, AR,USA	Microarray analysis of massage effect on rats
39	Ma, Christopher	University of Mississippi, MS, USA	Identification of Cancer Driving Mutations Using a Two-hit Model Assumption
40	Ma, Jianzhu	Toyota Technological Institute, Chicago, USA	Joint sequence variation analysis across multiple protein families reveals more native contacts
41	Ma, Li Maria	Oklahoma State University, OK,USA	Application of High-throughput Sequencing to Assess the Microbial Communities Associated with the Surfaces of Fresh Tomatoes
42	McCullough, Austin	John Brown University, AR, USA	Genomic Annotation of *Drosophila biarmipes* Dot Chromosome Contig 19
43	Nandety, A.	University of Oklahoma, OK, USA	Association Mapping of Cell Wall Enzymatic Digestibility in Switchgrass
44	Pandey, Ravi Shanker	University of North Texas, TX, USA	Understanding plant sex chromosome evolution using an unsupervised composition-based method
45	Pierce, M.D.	Sequencing Solutions, Arkansas State University, AR, USA	GeneSTAR: a Novel Framework for Analyzing Human Transcriptome to Assist with Patient Diagnosis
46	Pitigala, Sachintha	Middle Tennessee State University, TN, USA	Naive Bayes and Support Vector Machines on Small Training Data: An Experimental Study
47	Prade, Rolf	Oklahoma State University, OK, USA	The genome of a thermo tolerant, pathogenic albino *Aspergillus fumigatus*
48	Das, Devashish	Siddaganga Institute of Technology, Karnataka, India	SNiP Snapper: Novel Tool for Genome Variant to Protein Modification Analysis

49	Puli, Phani Kumar	Siddaganga Institute of Technology, Karnataka, India	Finding Mutational sites in drug resistant strain of *Mycobacterium Tuberculosis*: NGS Approach
50	Singh, Kamal	Siddaganga Institute of Technology, Karnataka, India	Natural Variants of AKT1 and their Effect on Inhibitor Binding: an *in silico* analysis
51	Raj, Vinay	University of Arkansas for Medical Sciences, AR, USA	Pathway association analysis of differentially expressed genes in Merkel Cell Carcinoma
52	Rashid, Mamoon	King Abdullah University of Science and Technology, Thuwal, Saudi Arabia	Bioinformatics Pipeline for decontaminating draft assemblies of Single Cell Genomes
53	Reddy, Joseph S.	Mississippi State University, MS, USA	A novel framework for quantifying simultaneous gene expression using RNA-seq
54	Reichley, Stephen	Mississippi State University, MS, USA	Comparative genomic analysis of *Edwardsiella piscicida*, *Edwardsiella piscicida*-like sp. and *Edwardsiella tarda* isolates from fish in the southeastern United States
55	Rinerson, Charles	University of North Texas, TX, USA	NBS-LLR-WRKY identification using nHmmer
56	Saminathan, Thangasamy	West Virginia State University, WV, USA	Genomic Approaches for Appalachian Coal Mine-site Reclamation
57	Sanders, William S.	Mississippi State University, MS, USA	Sequencing, Assembly, and Characterization of the Genome of *Rotylenchulus reniformis*
58	Saxena, Garima	University of North Texas, TX, USA	Impact of Horizontal Gene Transfer in the Evolution of *Galdieria sulphuraria* 074W
59	Saxena, Garima	University of North Texas, TX, USA	Comparison of Machine Learning Algorithms for prioritizing genes intrinsic in various types of cancer
60	Scott II, Edgar	Oklahoma University Health Sciences Center, OK, USA	Divergence of the SigM stress-response regulon and pathogenesis of the *Bacillus cereus sensu lato* group
61	Sharma, Ananya	University of Arkansas, AR, USA	Role of genome organization in bacterial growth

62	Tanti, Bhaben	Gauhati University, Guwahati, India	Molecular docking studies and *in silico* development of inhibitors from Neem (*Azadirachta indica*) against pantothenate synthetase of *Mycobacterium tuberculosis*
63	Thakkar, Shraddha	University of Arkansas for Medical Sciences, AR, USA	Bacterial Communication to Environment: Structure, Function and Evolution of the Spo0B Phosphotransferase
64	Thrash, Adam	Mississippi State University, MS, USA	Probabilistic Assignment of High Throughput Sequence Data in Metatranscriptomic Studies
65	Toby, Inimary	The University of Oklahoma Health Sciences Center, OK, USA	Divergence of protein-coding capacity and regulation in the *Bacillus cereus sensu lato* group
66	Trenfield, Michael	University of North Texas, TX, USA	Predicting origin and terminus of replication in bacteria
67	Urity, Vinoo	University of North Texas, TX, USA	Classifying drug resistance in the NCI60 cancer cell lines based on the mRNA expression levels of the 48 ABC transporters
68	Wayadande, Astri	Oklahoma State University, OK, USA	Characterization of the excreted microbiome from the blow fly, *Phormia regina* (Meigan): The Excretome
69	Weirick, Tyler	Oklahoma State University, OK, USA	LigPred: a comprehensive prediction system for the identification and classification of enzymes related to the synthesis and degradation of lignin
70	Whitlock, Sara	John Brown University, AR, USA	Annotation of *Drosophila biarmipes* Contig 23
71	Wren, Jonathan	Oklahoma Medical Research Foundation (OMRF), OK, USA	Trends in the development of Bioinformatics Resources
72	Yu, Ke	National Center for Toxicological Research (FDA), AR, USA	High daily dose and being a substrate of Cytochrome P450 enzyme are two important predictors of drug-induced liver injury

73	Zhang, Chengcheng	University of Oklahoma, OK, USA	Transcriptomic analysis of four switchgrass genotypes toward revealing the molecular basis of cell wall recalcitrance
74	Zhao, Kangmei	University of Oklahoma, OK, USA	Identification of Regulators in Grass Secondary Cell Wall Biosynthesis via Gene Network Analysis in Rice
75	Zou, Wen	National Center for Toxicological Research (FDA), AR, USA	Developing a pipeline for diversity analysis of *Salmonella fliC* gene from next generation sequencing data

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MCBIOS 2014 Conference Papers

MCBIOS 2014 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** over the 6 years we have data for, which speaks strongly of the impact of MCBIOS and its participants in bioinformatics. The deadline for submission of these papers is **Monday, March 31st, 2014.**

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 15 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 £640** (about $1,016 US at current exchange rates), an amount discounted for this event from the normal $2,190 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 e-mail to the Senior Editor.

Timeline:

March 31, 2014	– Manuscripts should be e-mailed to Jonathan Wren
April 28, 2014	– Reviewers return comments to editors
May 19, 2014	– Revisions due back from authors
June 2, 2014	– Final decisions made on submitted papers by reviewers
June 9, 2014	– Editors notify authors of acceptability of papers
July 4, 2014	– All final manuscript revisions due to editors along with payment of article processing charges due to MCBIOS.

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Theme: "*Emerging Trends in Bioinformatics*"

Hosted by:
University of Arkansas Little Rock,
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National Center for Toxicological Research, FDA
Little Rock, Arkansas (USA)

March 12-14, 2015

Contact Person: Cesar M. Compadre, Ph.D., Professor, College of Pharmacy, University of Arkansas for Medical Sciences, E-mail: compadrecesarm@uams.edu, Phone: 501-686-6493

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