

Introduction

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Introduction

MCBIOS 2009 was held February 20–21, 2009 at the Hunter Henry Center in Starkville, Mississippi on the Mississippi State University campus. The conference was hosted by the four research universities in Mississippi comprising the Mississippi Computational Biology Consortium – Jackson State University (JSU), Mississippi State University (MSU), the University of Mississippi (UM), and the University of Southern Mississippi (USM). Dr. Dawn Wilkins of UM and Dr. Susan Bridges of MSU served as conference co-chairs. Keynote speakers were Dr. Laura Elnitski, Head of the Genomic Functional Analysis Section at the National Human Genome Research Institute (NHGRI), Howard Cash, President and CEO of Gene Codes Corporation, and Dr. Cathy Wu, Director of the Protein Information Resource (PIR).

Dr. Raphael Isokpehi of JSU organized a panel discussion entitled Careers in Computational Biology and Bioinformatics: Perspective from Employers and Students. Panelists were Dr. Ed Perkins of the U.S. Army

Engineering Research and Development Center, Robert Cottingham of Oak Ridge National Laboratory (ORNL), Dr. Doris M. Kupfer, Federal Aviation Administration, James C. Fuscoe, FDA National Center for Toxicological Research, and Cynthia Jeffries, student intern at ORNL. Over 40 student and faculty attendees also participated in the Speed Networking event organized by Dr. Isokpehi and featured in a recent *Science Careers* article [1]. Each person in the event spent 3 minutes talking to twenty other participants in the two hour session providing students an opportunity to interact with employers and with students from other universities in the region.

Dr. Bindu Nanduri and Dr. Andy Perkins, both of MSU managed the setup, judging, and scoring of 80 posters. Monetary awards were provided by Dr. Ed Perkins. Student poster award winners were: first place – Eric Morales of the University of New Orleans (UNO), second place Teresia Buza of MSU, third place – Prashanti Manda of MSU and honorable mention to

Amanda Alba of the UNO, Surya Saha of MSU and Sudhir Chowbina of the Indiana University School of Informatics. Student winners for oral presentations were: first place – Enis Afgan of the University of Alabama at Birmingham, second place – Lipi R. Archarya of UNO, and third place – Anastasia Chueva of Mississippi Valley State University.

Proceedings summary

Thirty-two papers from the 2009 conference were submitted to be considered for inclusion in this supplement, and of them a total of 20 were accepted (62.5% accept rate), making this year's Proceedings the most stringent to date. The number of submitted papers exceeded that of the 2008 MCBIOS Proceedings [2-20]. As in prior conferences, we strove to be inclusive yet rigorous in the peer-review process, so that the end result is both high quality and reflective of the work presented. Papers generally fell into five categories:

Systems biology

A means of better understanding how systems work and interconnect as opposed to the traditional approach of isolating subcomponents and focusing on them is called Systems Biology and has become an increasingly active area of study in bioinformatics [21-34]. Andrey Ptitsyn offers a systems biology approach to the analysis of microarray data [35], partitioning gene expression space into a multi-dimensional taxonomy. Differences between "taxa" are then studied using biological pathway analysis software to associate gene expression patterns with specific phenotypes. For example, the application identifies a link between glycine metabolism aberrations and metabolic biomarkers for metastatic prostate cancer.

Gao *et al.* [36] describe an approach to better integrate data from disparate sources to reach better conclusions about biological response to stimulus than could be obtained from any of the component sources alone. Their study combined the Gene Ontology (GO) with microarray data using a bigraph data structure and associated algorithms.

Chowbina *et al.* address data integration from a different perspective[37], describing a technical resource for regulatory, signaling and biochemical reactions in human biomolecular pathways. Their resource, Human Pathway Database (HPD), integrates several existing resources to provide a web interface to access approximately one thousand pathways.

Zhang *et al.* present text empirics in the context of the PathBinder system [38]. Text empirics refers to properties

of texts that are derived by examining the texts themselves. It differs from the machine learning approach in that derived properties are manually curated and presented as facts that system builders can use when they are designing their systems.

OMICS

"OMICS" is a broad category, based on the fact that fields of study for biological entities often end with the suffix "omics" (e.g., transcriptomics, proteomics) [39-45]. Pendarvis *et al.* [46] describe the creation of a workflow system to analyze mass spectrometry replicate datasets to generate a list of identified proteins and expression changes and link them to biological knowledge. Because it is compliant with proteomic data submission guidelines, users can readily publish data to public proteomic data repositories.

Mete *et al.* [47] present a novel digital image analysis approach to the automated evaluation of angiogenesis in Liver Cancer. The method identifies regional, morphological and fractal features and helps measure microvessel density on digitized images of liver tumor sections. Their results show agreement between automated calculations and manual counting of microvessels.

Microarray studies

Microarrays have long been a subject of bioinformatics analysis not only for better understanding transcription, but also as a model for large-scale analysis of genetic behavior [48-56]. Van Den Berg *et al.* compared gene annotation enrichment tools for functional modeling of agricultural microarray data [57], a category that is underrepresented among current tools. Chavan *et al.* describe Network Analysis Toolbox in R (NATbox), which provides a menu-driven GUI for modeling and analysis of functional relationships inferred from gene expression profiles. It is suited for interdisciplinary researchers and biologists with minimal programming experience who would like to use systems biology approaches without delving into the algorithmic aspects, and can be a useful demonstration/teaching tool.

Perkins and Langston [59] identify a means of effectively selecting thresholds for gene expression on microarrays by identifying "cliques" or subgroups of co-expressed genes. Roughly, the idea being that individual measurements are prone to error, but when a gene is seen co-expressed with other genes, then this reinforces the validity of the expression being biologically significant.

Li *et al.* [60] investigate inter- and intra-platform consistency of microarray measurements. Using pathway

data as a guide for identifying biologically consistent results, the authors demonstrate that highly consistent biological information can be generated from different microarray platforms.

Genomic analysis

T.J. Jankun-Kelly and colleagues present a method to visually explore conserved domains on Multiple Sequence Alignments [61], simultaneously communicating the relative similarity of proteins across species and the differences in how function is expressed via conserved domains. It quickly identifies conserved domains and allows both macro (sequence-long) and micro (small amino-acid neighborhood) views.

Xu *et al.* [62] report the results of an extensive comparative genomics analysis of plant lignin biosynthesis gene families. Lignin is a major component of plant cell walls and appears to be the major cause of cell wall recalcitrance in energy production. Their analysis confirms that, among the species analyzed, the first complete lignin biosynthesis pathway appeared in moss. The major expansion of biosynthesis families occurred after the divergence of monocots and dicots and duplicated genes had many different fates. They conclude that transgenic lignin modification strategies to bioenergy feedstock may only be successful between closely related species.

T. Buza *et al.* report a method of automated functional annotation of the chicken genome, improving both the breadth and quality of annotation of genes [63]. The method can facilitate functional annotation of other microarrays via an Array GO Mapper (AGOM) tool to help researchers quickly retrieve corresponding functional information.

Zhou *et al.* [64] develop CPTRA (Cross-Platform Transcriptome Analysis) to analyze Next Generation Sequencing based on Transcriptome profiling in species with limited genome information.

Miscellaneous

Garcia-Reyero *et al.* [65] study gene expression in fathead minnows (*Pimephales promelas*) in well-characterized sites adjacent to sewage treatment plants and find short-term exposure to effluents were able to induce a site-specific gene expression pattern in the fathead minnow gonad and liver and to affect fish sexual behavior.

There are several other papers published in the supplement but, for space, are not summarized here: Chen and

Johnson [66], Bright *et al.* [67], Zollanvari *et al.* [68] and Malone *et al.* [69].

Future meetings

MCBIOS 2010 will be held in Jonesboro, Arkansas, and hosted by Arkansas State University and the Arkansas Biosciences Institute. Daniel Berleant of University of Arkansas at Little Rock is the 2009–2010 President of MCBIOS and will be chair of MCBIOS 2010. Ulisses Braga-Neto of Texas A&M University is the new President-elect of the society. See <http://www.MCBIOS.org> for information regarding MCBIOS and future meetings. MCBIOS is a regional affiliate of the International Society for Computational Biology <http://www.ISCB.org>.

Competing interests

The authors declare that they have no competing interests.

Authors' contributions

All authors served as co-editors for these proceedings, with JDW serving as Senior Editor. All authors helped write this editorial.

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