Michael A. Langston’s Contributions to Science

Refereed Papers in Journals, Books and Conference Proceedings


33. “Practical In-Place Merging,” *Communications of the ACM* 31 (1988), 348–352, with B.-C. Huang. (A preliminary version of a portion of this paper appeared in publication number 27.)


and Systems (PDCS), Marina Del Rey, California, November, 2003, with F. N. Abu-Khzam and P. Shanbhag.


110. “Combinatorial Genetic Regulatory Network Analysis Tools for High Throughput Transcrip-


233. “Structural and Social Determinants of Health Factors Associated with County-Level Variation in Non-Adherence to Antihypertensive Medication Treatment,” *International Journal of...*


237. “Molecular Subtyping and Outlier Detection in Human Disease Using the Paraclique Algorithm,” *Algorithms* 14 (2021), Special Issue on Biological Knowledge Discovery from Big Data, DOI 10.3390/a14020063, with R. D. Hagan. (A preliminary version of a portion of this paper appeared in publication number 229.)


Conference/Workshop Papers and Abstracts Without a Published Proceedings


336. “Can We Get a Grip on Complexity in Allergy Research?,” *Congress of the European Academy of Allergology and Clinical Immunology*, Vienna, Austria, June, 2006, with L. O. Cardell. *Invited.*


373. “High Throughput Analysis of the Low Dose Radiation Transcriptome,” DOE EPSCoR Program Review Workshop, Oak Ridge National Laboratory, Oak Ridge, Tennessee, 2008, with


418. “Combinatorial Algorithms and Graph Analysis to Process High-Throughput Biological Data to Form Network Models that Describe Emerging Modules for Seasonal Allergic Rhinitis” Workshop on Systems Biology to Personalize Medication and Find Novel Drug Candidates, Heidelberg, Germany, September, 2011. **Invited.**


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454. “Methylation Biomarker Discovery in Age-Related Diseases,” Keystone Symposium on Epigenetic and Metabolic Regulation of Aging and Aging-Related Diseases, Santa Fe, New Mexico, May, 2016, with R. D. Hagan.


473. “Challenges in the Analysis of Heterogeneous Health Sciences Data,” *First Online Conference on Algorithms*, held online, October, 2021. **Invited.**


**Recent Software Releases**

477. CAMDA-Tools, a suite of programs that implement novel combinatorial and graph algorithms for carcinoma detection, prediction and screening

478. ClustalXP, a high-performance parallel version of the popular ClustalW package used for multiple sequence alignment on DNA and protein data

479. GeneWeaver, a curated repository of genomic experimental results with an accompanying tool set for dynamic integration

480. GrAPPA, a web portal designed to simplify the process of high throughput biological data analysis and to provide the lay user with access to highly parallel computational resources

481. Maximal Biclique Enumeration, a set of efficient, scalable and highly innovative improvements over previous efforts to enumerate maximal bicliques in bipartite graphs

482. EntropyExplorer, an R package to augment differential expression with differential Shannon entropy and differential coefficient of variation