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.


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


287. “Algorithmic Applications of the Immersion Order,” *Slovenian International Conference on Graph Theory*, Lake Bled, Slovenia, June, 1995, with B. C. Plaut. **Invited.**


333. “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.


374. “Combinatorial Analysis of High-Throughput Transcriptomic Biological Data (Keynote Lecture),” *International Conference for Young Computer Scientists*, Zhang Jia Jie, China, November, 2008. **Invited.**


386. “High-Throughput Computation Can Help Identify Key Molecular Response Networks in Allergic Disease,” *Congress of the European Academy of Allergology and Clinical Immunology*, Warsaw, Poland, June, 2009. **Invited.**


429. “Effect of Genetic Diversity of Collaborative Cross Mice on Intestinal Microbial Communities and their Association with Disease Related Traits in Mice,” Complex Trait Community


**Recent Software Releases**

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

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

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

477. 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

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

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