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-
tomic Data,” *Proceedings, RECOMB Satellite Workshop on Systems Biology and Regulatory
Workman, editors), Springer, 150–165.


112. “A Network-Based Analysis of the Late Phase Reaction of the Skin,” *Journal of Allergy and
Clinical Immunology* 118 (2006), 220–225, with M. Adner, B. Andersson, M. Benson, L. O.
Cardell and Å. Torinsson-Naluai.

113. “Parameterized and Exact Computation, Editorial and Introduction to the Special Issue,”

114. “Extracting Gene Networks for Low Dose Radiation using Graph Theoretical Algorithms,”

115. “Detecting Differential and Correlated Protein Expression in Label-Free Shotgun Proteomics,”
Uberbacher, N. C. VerBerkmoes and B. Zhang.

116. “A Network-Based Analysis of Allergen-Challenged CD4+ T Cells from Patients with Al-
lergic Rhinitis,” *Genes and Immunity* 7 (2006), 514–521, with B. Andersson, M. Benson, L.
Carlsson, G. Guillot, M. Jernäs and M. Rudemo.

117. “Computational Analysis of Mass Spectrometry Data Using Novel Combinatorial Methods,”
*Proceedings, ACS/IEEE International Conference on Computer Systems and Applications
(AICCSA)*, Dubai, United Arab Emirates, March, 2006, with A. Fadiel, F. Naftolin, X. Peng,

Symposium on Applied Computing*, Dijon, France, April, 2006, with A. D. Perkins, A. M.
Saxton, J. A. Scharff and B. H. Voy.

119. “A Systems Genetic Analysis of Chronic Fatigue Syndrome: Combinatorial Data Integration
from SNPs to Differential Diagnosis of Disease,” *Proceedings, International Conference for
the Critical Assessment of Microarray Data Analysis (CAMDA)*, Durham, North Carolina,

120. “The Cluster Editing Problem: Implementations and Experiments,” *Proceedings, Interna-
tional Workshop on Parameterized and Exact Computation (IWPEC)*, Zürich, Switzerland,
September, 2006, with F. Dehne, X. Luo, S. Pitre, P. Shaw and Y. Zhang. Proceedings published as *Lecture Notes in Computer Science* 4169 (H. L. Bodlaender and M. A. Langston,
editors), Springer, 13–24.


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


322. “Graph Applications in Systems Genetics,” *AMS Southeast Meeting Session on Discrete Models in Biology*, Johnson City, Tennessee, October, 2005, with E. J. Chesler. **Invited.**


334. “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.


403. “Computation for Large Systems II: Applications and Analysis,” *Winter School in Mathematics and Computational Biology*, University of Queensland, Brisbane, Australia, July, 2010. **Invited.**


416. “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.**


430. “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**

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

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

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

478. 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

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

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