

ZHENG LIU

3397 Idaho St. Riverside, CA, 92507 (951)-743-7157 zliu@cs.ucr.edu <http://www.cs.ucr.edu/~zliu>

ACADEMIC DEGREES

University of California, Riverside
Ph.D. in Computer Science and Engineering August, 2006
M.S. in Computer Science and Engineering June, 2004

HuaZhong University of Science and Technology, China
B.E. in Computer Science and Engineering July, 2000

RESEARCH INTERESTS & COMPUTER SKILLS

Data analysis and data mining, algorithm design, and software development in bioinformatics
Programming & Scripting: C, C++, Java, Excel VBA, PHP, Perl, JavaScript, CGI, CSS, HTML
Tools & Packages: MySQL, MATLAB, R, BLAST, CLLUSTW, ImaGene, Bioconductor
Platforms: Windows, Linux and Unix

EXPERIENCE

Research Assistant **2001 - present**
Computer Science, Plant Pathology **University of California, Riverside**

- Study microbial communities through oligonucleotide fingerprinting of rRNA genes. Research topics include genomic sequence analysis, microarray data analysis, and gene function prediction.
- Design algorithms for combinatorial biological problems arising from project, e.g., string matching, sequence alignment, and fingerprint assembly
- Develop statistical methodologies for analyzing correlated discrete or continuous biological data. Have designed a modified Bayes rule to classify microarray data with improved performance.
- Develop several software packages for processing hybridization microarray data.
- Construct web-based Mysql database to manage experimental data, develop and maintain website for project (<http://alglab1.cs.ucr.edu/OFRG>)
- Train new project members, organize regular project meetings and present research progress.

Instructor **Summer 2006**
Computer Science **University of California, Riverside**

- Lectured an upper-level undergraduate class. Responsibilities include composing a syllabus, assigning homework, and preparing quizzes, final exams for students and supervise teaching assistant.

Research Intern **Summer 2005**
Cheminformatics **Genomics Institute of the Novartis Research Foundation**

- Studied gene functions based on in situ hybridization images of mouse brain. Developed statistical and computational methodologies for analyzing gene expression data.
- Designed an image processing algorithm for estimating the mobility of metastatic tumor cells in order to assist pharmaceutical drug design projects.

Teaching Assistant **2002 – 2003**
Computer Science **University of California, Riverside**

- Five quarters TA experience with undergraduate computer science courses. Gave lectures in laboratories and guided students in their laboratory work. Designed and graded course projects.

PUBLICATIONS

- [1] D.R. Jeske, **Z. Liu**, E. Bente, J. Borneman. (2006) Classification Rules that Includes Neutral Zones and their Application to Microbial Community Profiling. *To appear in Communications in Statistics - Theory and Methods*. Vol. 36(10).
- [2] E. Bent, B. Yin, A. Figueroa, J. Ye, Q. Fu, **Z. Liu**, D. Jeske, T. Jiang, and J. Borneman. (2006) Development of a 9,600 Clone Procedure for Oligonucleotide Fingerprinting of rRNA Genes: Utilization to Compare Four Different Soil DNA Extraction Methods. *Journal of Microbiological Methods* Vol. 67(1), 171-180.
- [3] X. Chen, L. Liu, **Z. Liu**, and T. Jiang. (2006) On the Minimum Common Integer Partition Problem. *In Proceedings of the 6th Conference on Algorithms and Complexity (CIAC'06)*, 236-247.
- [4] C. Collins, J. Hong, L. Sapinoso, Y. Zhou, **Z. Liu**, K. Micklash, P. Schultz and G. Hampton. (2006) A Small Interfering RNA Screen for Modulators of Tumor Cell Motility Identifies MAP4K4 as a Promigratory Kinase. *In Proceedings of the National Academy Sciences, USA*. Vol. 103(10), 3775-3780.
- [5] D.R. Jeske, **Z. Liu**, E. Bente, and J. Borneman. (2006) Classification Boundaries that Includes Neutral Zones and their Application to Microbial Community Gene Expression Experiments. *To appear on the 5th Annual Hawaii International Conference on Statistics, Mathematics and Related Field*.
- [6] **Z. Liu**, X. Chen, J. Borneman, and T. Jiang. (2005) A fast algorithm for approximate string matching on gene sequences. *In Proceedings of the 16th Annual Symposium on Combinatorial Pattern Matching (CPM'05)*, LNCS 3537, 79-90.
- [7] **Z. Liu**, J. Borneman, and T. Jiang. (2005) A software system for gene sequence database construction based on fast approximate string matching. *International Journal of Bioinformatics Research and Applications*, Vol. 1(3), 273-291.
- [8] **Z. Liu**, J. Borneman, and T. Jiang. (2004) A software system for gene sequence database construction. *In Proceedings of the 26th Annual International Conference of the IEEE Engineering in Medicine and Biology Society (EMBC'04)*, 2797-2800.
- [9] A. Figueroa, **Z. Liu**, R. Mancini-Jones, J. Borneman, and T. Jiang. (2004) Building phylogenetic trees from binary oligonucleotide fingerprint vectors. *Proc. IEEE EMBC'04*, 2844-2847.
- [10] L. Valinsky, A. Scupham, G.D. Vedova, **Z. Liu**, A. Figueroa, K. Jampachaisri, B. Yin, E. Bent, R. Mancini-Jones, J. Press, T. Jiang, and J. Borneman. (2004) Oligonucleotide Fingerprinting of Ribosomal RNA Genes (OFRG). In G. A. Kowalchuk, F. J. de Bruijn, I. M. Head, A. D. L. Akkermans, J. D. van Elsas (ed.) *Molecular Microbial Ecology Manual* (2nd ed.). Kluwer Academic Publishers, Dordrecht, the Netherlands, 569-585.

Submitted

- [11] **Z. Liu**, S.F. Yan, J. Walker, T. Zwingman, T. Jiang, J. Li, Y. Zhou. Study of Gene Function Based on Spatial Co-expression in a High-resolution Mouse Brain Atlas. *Submitted to BMC Neuroscience*.

BIO-RELATED WORKSHOPS AND COURSES

Workshop on Sequence Analysis toward System Biology Institute of Pure and Applied Mathematics, UCLA	January 2006
Workshop on Biological Data Analysis with R and Bioconductor Bioinformatics Core, Center for Plant Cell Biology, UC Riverside Advances	October 2004
Workshop on GenBank, Molecular Biology Resources and Tools National Center for Biotechnology Information (NCBI), City of Hope, CA.	October 2003
Bioinformatics and Genomics Genetics, Genomics and Bioinformatics (GGB) Graduate Program, UC Riverside	Winter 2003
Probability and Statistical Theory Statistics Department, UC Riverside	Winter 2003