Zhibin Huang

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Education

University of Georgia	Athens, GA
Ph.D. Student, Computer Science (GPA 3.8/4.0)	Jan. 2007 - Present

Research Interests: Computational Biology, Machine Learning,
Image Processing and Statistical Pattern Recognition

Huaqiao University	Fujian, P.R.China
M.S. Computer Science	2000 - 2003

Research Interests: Machine Learning, Image Processing and Pattern Recognition
Excellent Graduate Scholarship of Huaqiao University, Dec. 2002

Huaqiao University	Fujian, P.R.China
B.S. Computer Science	1996 - 2000

Excellent Student Scholarship of Huaqiao University, Dec. 1997, Dec. 1998, Mar. 2000

Research & Projects

Fast and accurate search for ncRNA in genomes by their structures (including pseudoknots)   Aug. 2007 - Present

➢ Searching genomes for non-coding RNAs (ncRNAs) by their secondary structure has become an important goal for bioinformatics. For pseudoknot-free structures, ncRNA search can be effective based on the covariance model and CYK-type dynamic programming. However, the computational difficulty in aligning an RNA sequence to a pseudoknot has prohibited fast and accurate search of arbitrary RNA structures. Our work, RNATOPS, introduced a graph model for RNA pseudoknots and proposed to solve the structure–sequence alignment by graph optimization. Given k candidate regions in the target sequence for each of the n stems in the structure, we could compute a best alignment in time $O(ktn)$ based upon a tree width t decomposition of the structure graph. However, to implement this method to programs that can routinely perform fast yet accurate RNA pseudoknot searches, we need novel heuristics to ensure that, without degrading the accuracy, only a small number of stem candidates need to be examined and a tree decomposition of a small tree width can always be found for the structure graph. Test result shows that RNATOPS can do fast searches on prokaryotic and eukaryotic genomes for specific RNA structures of medium to large sizes, including pseudoknots, with high sensitivity and high specificity.

➢ RNATOPS software package download http://www.uga.edu/RNA-Informatics/?f=software&p=RNATOPS

➢ RNATOPS-W website: http://128.192.76.182:8080/rnatops-w/

Automatic Vehicle License Plate Recognition System   June. 2003 - June. 2003

➢ Responsible for major research, architecture design and system implementation.

➢ Detection of vehicle license plate is very important in Vehicle License Plate Recognition System. In this project, a novel classifier fusion-based detection algorithm is proposed. After locating candidate license plate regions, features of these regions are extracted for the optimal feature subset by exhaustive search strategy. Based on classifier fusion theory, Simple Average (SA) method is compared with two Weighted Average (WA) methods. Experimental results show that after reducing the dependency of features, SA method works better. The most three important features of the license plate regions are obtained in the experiment and our algorithm can be applied in real-time applications and robust in filtering out false plate regions.

Publication

➢ Wang,Y., **Huang,Z**., Wu,Y., Malmberg,R., and Cai,L. RNATOPS-W: A Web Server for RNA Structure Searches of Genomes, Bioinformatics, March 5, 2009.

➢ **Huang, Z.**, Wu, Y., Robertson, J., Feng, L., Malmberg, R., and Cai, L. Fast and accurate search for non-coding RNA pseudoknot structures in genomes, Bioinforamtics, 2008 24(20):2281-2287.

➢ Xiaosong Wang, Haitao Zhao, Qingwen Xu, Weibo Jin, Changning Liu, Huagang Zhang, **Zhibin Huang**, Xinyu Zhang, Yu Zhang, Dianqi Xin, Andrew J. G. Simpson, Lloyd J. Old, Yanqun Na, Yi Zhao and Weifeng Chen, HPtaa database-potential target genes for clinical diagnosis and immunotherapy of human carcinoma, Journal of Nucleic Acids Research, 2006, Jan 1;34(Database issue):D607-12.

➢ **Zhibin Huang**, et, al, Classifier Fusion-Based Vehicle License Plate Detection Algorithm, The Second International Conference on Machine Learning and Cybernetics (ICMLC2003), Xi-an, China, Nov 2003, 2984-2989.