

## BIOGRAPHICAL SKETCH

### **Xiaoqiu Huang**

Associate Professor, Department of Computer Science  
226 Atanasoff Hall, Iowa State University, Ames, IA 50011

#### **a. Professional Preparation**

- Changsha Institute of Technology (China)      Computer Science      B.S., 1982.
- Pennsylvania State University                      Computer Science      M.S., 1989.
- Pennsylvania State University                      Computer Science      Ph.D., 1990.

#### **b. Appointments**

- 2001-Pres. Associate Professor, Department of Computer Science, Iowa State University, Ames, IA.
- 1999-2000. Principal Scientist, Paracel, Inc., Pasadena, CA.
- 1999-2000. Associate Professor, Keck Graduate Institute of Applied Life Sciences, Claremont, CA.
- 1996-1999. Associate Professor, Department of Computer Science, Michigan Technological University, Houghton, MI.
- 1996-1997. Visiting Faculty, The Institute for Genomic Research, Rockville, MD.
- 1990-1996. Assistant Professor, Department of Computer Science, Michigan Technological University, Houghton, MI.

#### **c. Publications**

##### **(i) A list of up to 5 publications most closely related to the proposed project**

1. Huang, X., Yang, S.-P., Chinwalla, A., Hillier, L., Minx, P., Mardis, E. and Wilson, R. (2006) Application of a Superword Array in Genome Assembly, *Nucleic Acids Research*, 34: 201-205.
2. Huang, X., Wang, J., Aluru, S., Yang, S.-P. and Hillier, L. (2003) PCAP: A Whole Genome Assembly Program, *Genome Research*, 13: 2164-2170.
3. Huang, X. and Madan, A. (1999) CAP3: A DNA Sequence Assembly Program, *Genome Research*, 9: 868-877.
4. Huang, X., Adams, M.D., Zhou, H. and Kerlavage, A.R. (1997) A Tool for Analyzing and Annotating Genomic Sequences, *Genomics*, 46(1): 37-45.
5. Huang, X. (1992) A Contig Assembly Program Based on Sensitive Detection of Fragment Overlaps, *Genomics*, 14:18-25.

##### **(ii) A list of up to 5 other significant publications**

1. Huang, X. and Brutlag, D.L. (2007) Dynamic Use of Multiple Parameter Sets in Sequence Alignment, *Nucleic Acids Research*, 35: 678-686.
2. Wang, J. and Huang, X. (2005) A Method for Finding Single-Nucleotide Polymorphisms with Allele Frequencies in Sequences of Deep Coverage, *BMC Bioinformatics*, 6: 220.
3. Ye, L. and Huang, X. (2005) MAP2: Multiple Alignment of Syntenic Genomic Sequences, *Nucleic Acids Research*, 33: 162-170.
4. Huang, X. and Zhang, J. (1996) Methods for Comparing a DNA Sequence with a Protein Sequence, *Computer Applications in the Biosciences*, 12: 497-506.
5. Huang, X. and Miller, W. (1991) A Time-efficient, Linear-Space Local Similarity Algorithm, *Advances in Applied Mathematics*, 12: 337-357.

#### **d. Synergistic Activities**

1. Program Committee Member, 11th International Conference on Intelligent Systems for Molecular Biology, June, 2003.
2. Core Faculty Member, Laurence H. Baker Center for Bioinformatics and Biological Statistics, Iowa State University.

3. Faculty Member, Interdisciplinary Graduate Program in Bioinformatics and Computational Biology, Iowa State University.

**e. Collaborators & Other Affiliations**

**(1) Collaborators and Co-Editors**

Srinivas Aluru (Iowa State University), Volker Brendel (Iowa State University), Douglas Brutlag (Stanford University), Kun-Mao Chao (National Taiwan University), Jianjun Chen (University of Chicago), Asif Chinwalla (Washington University, St. Louis), Hui-Hsien Chou (Iowa State University), Natsuhiko Futamura (Wright State University), Xun Gu (Iowa State University), LaDeana Hillier (Washington University, St. Louis), Tao Jiang (University of California, Riverside), Steven Jones (Michael Smith Genome Sciences Centre), Yaw-Ling Lin (Providence University), Elaine Mardis (Washington University, St. Louis), Patrick Minx (Washington University, St. Louis), Geo Pertea (The Institute for Genomic Research), Darren Platt (Joint Genome Institute), John Quackenbush (Dana-Farber Cancer Institute), Jianmin Wang (Roswell Park Cancer Institute), Rene Warren (Michael Smith Genome Sciences Centre), Richard Wilson (Washington University, St. Louis), Shiaw-Pyng Yang (Washington University, St. Louis), Liang Ye (Washington University, St. Louis).

**(2) Graduate and Postdoctoral Advisors**

Webb Miller (Pennsylvania State University).

**(3) Thesis Advisor and Postgraduate-Scholar Sponsor**

The total number of graduate students advised: 12 (9 M.S. and 3 Ph.D.)

The total number of postdoctoral scholars sponsored: 0

Ankit Agrawal (Iowa State University), Dimitrios Evmorfopoulos (unknown), Douglas Haanpaa (Cybernet Systems), Haining Lin (The Institute for Genomic Research), Jin Lin (Oracle), Mini Nadupparambil (unknown), Jin Qian (SeeBeyond Technology), Lijie Tu (unknown), Jianmin Wang (Roswell Park Cancer Institute), Paul Wiedemeier (Columbia College of Missouri), Liang Ye (Washington University, St. Louis), Hao Zhou (The Jackson Lab).