

BIOGRAPHICAL SKETCH: HUI-HSIEN CHOU, Iowa State University, 503 Science II Hall
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(i) PROFESSIONAL PREPARATION

B.S., Chemical Engineering, 1984, Ming-Chih Institute of Technology, Taipei, Taiwan
B.S., Computer Science, 1989, National Taiwan University, Taipei, Taiwan
Ph.D., Computer Science, 1996, University of Maryland, College Park, Maryland
Postdoctoral Fellow, Bioinformatics, 1996–98, The Institute for Genomic Research, Rockville,
Maryland

(ii) APPOINTMENTS

2005 – Present Associate Professor, Iowa State University, Ames, Iowa
1999 – 2005 Assistant Professor, Iowa State University, Ames, Iowa
1998 – 1998 Research Scientist, Celera Genomics Corporation, Rockville, Maryland
1996 – 1997 Lecturer, Dept. of Computer Science, University of Maryland at College Park

(iii) PUBLICATIONS (selected; 5 most closely related to the proposed project; 5 other relevant)

Five Publications Most Closely Related:

Young-Su Seo, Malinee Sriariyanun, Li Wang, Janice Pfeiff, Jirapa Phetsom, Ye Lin, Ki-Hong Jung, Hui-Hsien Chou, Adam J Bogdanove and Pamela C Ronald. A two-genome microarray for the rice pathogens *Xanthomonas oryzae pv. oryzae* and *X. oryzae pv. oryzicola* and its use in the discovery of a difference in their regulation of hrp genes. *BMC Microbiology*, 8(1):99, 2008.

Hui-Hsien Chou. Computational Design of Whole Genome Microarrays. In Srinivas Aluru, editor, *Handbook of Computational Molecular Biology*. ISBN 1584884061. CRC Press, Boca Raton, FL, 2005.

Hui-Hsien Chou, An-Ping Hsia, Denise L. Mooney, and Patrick S. Schnable. PICKY: Oligo Microarray Design for Large Genomes. *Bioinformatics*, 20:2893–2902, Nov. 2004.

Song Li and Hui-Hsien Chou. LUCY2: an interactive DNA sequence quality trimming and vector removal tool. *Bioinformatics*, 20:2865–2866, Nov. 2004.

Hui-Hsien Chou and Michael H. Holmes. DNA Sequence Quality Trimming and Vector Removal. *Bioinformatics*, 17:1093–1104, Dec. 2001.

Five Other Significant Publications:

Scott Emrich, Li Li, Tsui-Jung Wen, Marna Yandean-Nelson, Yan Fu, Ling Guo, Hui-Hsien Chou, Srinivas Aluru, Daniel Ashlock, and Patrick Schnable. Nearly identical paralogs (NIPs): implications for maize (*Zea mays* L.) genome evolution. *Genetics*, 175(1): 429–439, 2007.

Philip M. Maher, Hui-Hsien Chou, Elizabeth Hahn, Tsui-Jung Wen, and Patrick S. Schnable. GRAMA: Genetic mapping analysis of temperature gradient capillary electrophoresis (TGCE) Data. *Theoretical and Applied Genetics*, 113(1):156–162, June 2006.

Hui-Hsien Chou. VECT: an automatic visual Perl programming tool for nonprogrammers. *BioTechniques*, 38:615–621, April 2005.

Song Li and Hui-Hsien Chou. UBVIZ: Explore Biochemical Pathways in 3-D Space. *BioTechniques*, 38:540–542, April 2005.

Eugene W. Myers, Granger G. Sutton, Art L. Delcher, Ian M. Dew, Dan P. Fasulo, Michael J. Flanigan, Saul A. Kravitz, Clark M. Mobarry, Knut H. J. Reinert, Karin A. Remington, Eric L. Anson, Randall A. Bolanos, Hui-Hsien Chou, Catherine M. Jordan, Aaron L. Halpern, Stefano Lonardi, Ellen M. Beasley, Rhonda C. Brandon, Lin Chen, Patrick J. Dunn, Zhongwu

Lai, Yong Liang, Deborah R. Nusskern, Ming Zhan, Qing Zhang, Xiangqun Zheng, Gerald M. Rubin, Mark D. Adams, and J. Craig Venter. A Whole-Genome Assembly of *Drosophila*. *Science*, 287:2196–2204, March 24, 2000.

(iv) BIOINFORMATIC SOFTWARE DEVELOPMENT

The PI has created many bioinformatic software tools and made them freely available to academic scientists from his lab website <http://ww.complex.iastate.edu>. All tools are readily executable on many different computing platforms and most are also available in source code format to the users. A partial listing of these software tools is given below:

- PICKY, an optimal oligo microarray design tool for large genomes. PICKY is an efficient oligo microarray design tool for large genomes. Oligos designed by PICKY are computationally optimized to guarantee the best specificity, sensitivity and uniformity under the given design parameters. PICKY has been used to design the NSF rice oligo microarray (DBI-0313887) as well as several other arrays for different species including maize, cotton, *Arabidopsis*, *Xanthomonas oryzae pv oryzae*, *Xanthomonas oryzae pv oryzicola*, etc.
- VECT, an automatic Perl programming tool for non-programmers. VECT stands for “Visual Extraction and Conversion Tool” and is developed to assist biologists with very limited computer science background to create bioinformatic solutions without having to master a programming language. Programming using VECT is achieved by visually performing the desired data extraction, conversion, and output composition tasks. These tasks are then automatically compiled by VECT into an executable Perl program to solve problems.
- LUCY2, an interactive DNA quality trimming and vector removal tool. LUCY2 is a new DNA sequence quality trimming and contaminant removal tool based on the command-line based LUCY1 also developed by the PI previously. With LUCY2, users can set parameters, trim multiple DNA sequences obtained from DNA sequencing machines, and visualize the trimming results all within an integrated, easy-to-use graphical user interface.
- UBVis, biochemical pathway visualization in 3-D space. UBVis is designed to make it easier to understand biochemical pathways. Users can visualize and interact with pathways from the KEGG website (<http://www.genome.jp/kegg>) in 3-D space, and browse all related web pages within one window. With UBVis’ built-in networking capability, pathway data are obtained directly from KEGG’s website and automatically presented on-screen, allowing users to view more recent versions of the KEGG biochemical pathway data than KEGG’s manually drawn 2-D figures allowed.

Through many years of continuous improvement and end-user support, these software tools are gradually gaining popularity. For example, searching the following sample phrases “oligo microarray design”, “automatic Perl programming”, “DNA quality trimming” or “TGCE data analysis” on Google routinely returns the download websites or publications for these tools at the top of the result pages, indicating their popularity for a variety of scientific computations.

(v) COLLABORATORS & OTHER AFFILIATIONS

Graduate Advisors

James A. Reggia, University of Maryland at College Park

Postdoctoral Advisor

Granger G. Sutton III, The Institute for Genomic Research

Collaborators and Coauthors

See the attached combined conflict of interest list in the Single Copy Document section.