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Jinhua Wang, Ph.D.

Summary

Excellent analytical skills in mining genome sequence, microarray expression and proteomics data for gene regulation network, pathway analysis, molecular signature identification, and potential diagnostic marker discovery. Expertise in combing biological and medical knowledge with large scale datasets to develope statistical and bioinformatic tools for data analysis and visualization to meet scientific needs such as generating biological hypotheses and anwsering biological questions.

Exceptional technical knowledge, problem solving and programming skills with expertise in: MatLab, R/Bioconductor/Splus, Perl/bioperl, Genome/SNP databases, Spotfire, C/HTML/SQL/mySQL, and bioinformatics applications (Blast/Blat/GCG/Vector NTI, GO/KEGG/Ingenuity, Phylip/MEGA, data mining tools for microarray etc).

Demonstrated ability to coordinate multidisciplinary projects of molecular biology, biostatistics and computer science. Experience in recruiting, training, supervising junior researchers.

Professional Experiences/Major projects

2007.1- present, NYU cancer institute/Joint disease hospital/NYU cancer genome center Bioinformatics Scientist/Assitant Research Professor. (http://www.med.nyu.edu/nyuci/research/facilities/genomics/contact.html)

2005.1- 2007.1, Bioinformatics Research Scientist, Hartwell Center for Bioinformatics and Biotechnology, St Jude Children's Research Hospital. Memphis TN. (http://www.hartwellcenter.org/)

Cancer genomics project:

1. Characterized potential targets of specific gene transcription and splicing factors through genome level analysis, and deduced a potential transcription and splicing regulation network.

2. Identified candidate alternatively spliced genes as potential bio-markers for cancer diagnosis.

3. Conducted statistical analysis of molecular pathways using gene expression data, and correlation analysis of gene expression profiling data with clinical patient's survival data.

Avian influenza genome project:

Combined the phylogeny analysis of about 300 whole virus genomes with the sequence alignment to characterize in detail the evolution of various virus strains. Also initiated the co-variation analysis of the protein products of the whole virus genome.

2001.9-2004.12 Computational biology (Bioinformatics/Genomics) Postdoc Research Fellow, Cold Spring Harbor Laboratory, NY (http://www.cshl.edu,

http://rulai.cshl.edu)

1. Worked on the project of developing computational techniques for the analysis of alternative pre-mRNA splicing. Designed algorithm to analyze expression data from splicing array, and co-developed ESEfinder program for exonic splicing enhancer identification. Am still working on the improvement of the score matrix for the ESEfinder program.

2. Conducted expression analysis of splicing factors in various human tissues and cell lines using microarray data, this result was correlated with the expression profile analysis of all the human skipping exons, and a regression analysis was performed to understand how the skipping exons are regulated by the combination of different splicing factors.

3. Implemented a comparative analysis of human and mouse genome sequences and the alternatively spliced genes. Compiled a large scale data set of human and mouse promoters, and devised a database for human and mouse conserved sequence elements.

1998.1 – 2001.8 Bioinformatics Graduate Research Projects, multi-institutional collaboration between Bioinformatics Lab in Institute of Biophysics (Chinese Academy of Sciences), Chinese National Human Genome Center in Beijing, and Institute for Biological Sciences in Tokyo. (http://www.ibp.ac.cn, http://www.chgb.org.cn, http://www.sut.ac.jp/labo/research_life.html)

1. Designed the bioinformatics infrastructure and data integration pipeline, completed the sequence assembly and annotation of the genome of Shigella flexneri 2a, (GB: AE005674), performed the whole genome comparison of Shigella flexneri 2a, Ecoli k12 and Ecoli o157 in the Chinese National Human Genome Center in Beijing.

2. Participated in the development of the protein informatics resource at the PIR/JIPID node in Tokyo, particularly worked on protein sequence annotation, and brain tissue proteomics analysis.

Education

2001.9-2004.12, Bioinformatics/Genomics Postdoc Research and Training, Cold Spring Harbor Laboratory, New York

1996.9-2001.8, Ph.D., Computational Biology/Biophysics, Institute of Biophysics, Chinese Academy of Sciences, Beijing, China

1998.3-1999.6, Exchange Student, Protein Informatics Resources (PIR/JIPID) Institute for Biological Sciences, Science University of Tokyo, Tokyo, Japan

1991.9-1996.7, B.S., Nuclear Physics and Technology, Department of Physics, Peking University, Beijing, China

Nov. 2003, Techniques in Gene Microarray Development and Analysis, Jackson Laboratory, Bar Harbor, ME (training course)

Aug. 2001, Parallel computing and super-computer environment, National Computing &Information Center, Beijing, China (training course)

Major Publications

A. Whole genome sequence assembly, annotation, phylogeny analysis, cross-species genome sequence comparison, and sequence motif analysis, promoter analysis. Algorithm developing: developed a mutual information metric for protein co-evolution study, visualization tools for genome comparison.

1. John. Obenauer, P. Mehta, X. Su,. Suraj. Mukatira, D. Finkelstein X,.Xu, *Jinhua. Wang*, J. Ma, Y. Fan, J. Denson, K. Rakestraw, J. Zheng, Z. Zhang, E. Hoffmann, S. Krauss, R. G. Webster and C. W. Naeve. Large scale sequencing of Avian Influenza reveals a novel determinant of virulence. (***Science***, 17 March 2006: 1576-1580.)
2. Zhenyu Xuan, Fang Zhao, *Jinhua Wang*, Gengxin Chen and Zhang MQ Genome-wide promoter extraction and analysis in human, mouse, and rat. ***Genome Biology***, 6-8-R72 2005.
3. Zhenyu Xuan, *Jinhua Wang*, Michael Zhang, Computational comparison of two mouse draft genomes and the human golden path. ***Genome Biology***, 4(1):R1-R10 2003.
4. Jian Yang, *Jinhua Wang*, Zhi-jian Yao, Qi Jin, Yan Shen, Runsheng Chen, GenomeComp: a visualization tool for microbial genome comparison. ***Journal of Microbiology Method***, 54:423-426, 2003
5. Jian Yang, *Jinhua Wang*, Qi Jin, Zhi-Jian Yao, Yan Shen, Runsheng Chen, Identification and characterization of simple sequence repeats in the genomes of *Shigella* species. ***Gene*** 322: 85-92, 2003
6. *Jinhua Wang*, collaboration with Qi Jin, Zhenghong Yuan, Jian Yang, et al. Genome sequence of Shigella Flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157. ***Nucleic Acid Research***. Vol. 30 No.20: 4432-4441, 2002
7. The DNA sequence, annotation and analysis of human chromosome 3. (***Nature***, 440, 1194-1198 (27 April 2006)

B. ChIP-chip data from Agilent/Affy platform, developed protocols for peak finding, peak annotation, target gene selection, repetitive sequence analysis. Data visulization using IGB and Matlab.

8. Chris van Oevelen, Jinhua Wang, Patrik Asp, Qin Yan, William Kaelin, Yuval Kluger, Brian David Dynlacht, A role for mammalian Sin3 in permanent gene silencing. (***Molecular Cell***, 32, 359-370, Nov 7, 2008)
9. Louise V.Wolf, Ying Yang, Jinhua Wang, Qing Xie, Barbara Braunger, Ernst R. Tamm, Jiri Zavadil, Ales Cvekl. Identification of Pax6-dependent gene regulatory networks in the mouse lens. (***PLoS ONE***, 4(1), Jan 2009)

C. Gene expression profiling, DNA copy number analysis, cross-platform data merging. Data integration and correlation analysis of gene expression and copy number variation.

10. Jun J Yang, Deepa Bhojwani, Wenjian Yang, Xiangjun Cai, Gabriele Stocco, Kristine Crews, Jinhua Wang, Debra Morrison, Meenakshi Devidas, Stephen P Hunger, Cheryl L Willman, Elizabeth A Raetz, Ching-hon Pui, William E Evans, Mary V Relling, and William L Carroll. Genome-wide copy number profiling reveals molecular evolution from diagnosis to relapse in childhood acute lymphoblastic leukemia. ***Blood***, Sep 2008; doi:10.1182/blood-2008-06-165027

11. Jiewu Liu, *Jinhua Wang*, Qian Huang, Jason Higdon, Susan Magdaleno, Thomas Curran, Jian Zuo. Gene expression profiles of mouse retinas during the second and third postnatal weeks. (2006 Jul 7; 1098(1):113-25.***Brain Research***) 2006

D. Alternative splicing, research on transcription and splicing coupling through splicing motif analysis, splicing array data and expression data integration. Developed splicing motif analysis method, splicing transcripts database, and splicing form analysis pipeline.

12. Phil Smith, Chaolin Zhang, *Jinhua Wang*, Adrian Krainer, Michael Q. Zhang. An increased specificity score matrix for the prediction of SF2/ASF-specific exonic splicing enhancers. (2006 15(16):2490-2508 ***Human Molecular Genetics)***
13. Hitoshi Suzuki, Yuhong Zuo, *Jinhua Wang,* Michael Zhang, Arun Malhotra and Akila Mayeda. Characterization of RNase R-digested RNA source that consists of lariat and circular RNAs derived from pre-mRNA splicing. (Nucleic Acids Res. 2006; 34(8): e63. Published online 2006 May 8. doi: 10.1093/nar/gkl151. ***Nucl. Acid. Res.)*** 2006
14. *Jinhua Wang*, Phil Smith, Adrian Krainer, Michael Q. Zhang. Distribution of SR Protein Exonic Splicing Enhancer Motifs in Human Protein-Coding Genes. ***Nucl. Acid. Res.*** 33(16):5053-5062 2005
15. Luca Cartegni, *Jinhua Wang*, Zhengwei Zhu, Michael Q. Zhang, Adrian R. Krainer. ESEfinder: A web resource to identify exonic splicing enhancers. ***Nucl. Acid. Res***. 31:3568-3571 2003

Invited Talks

Genome level survey of alternative splicing and cross-species comparison. ***The first joint Cold Spring Harbor Laboratory/Wellcome Trust Conference on Genome Informatics***. NY, USA. May 7-11, 2003 (http://meetings.cshl.edu/meetings/infouk06.shtml)

Network Biology: Concepts, Algorithms and Applications in Cancer Research. ***St Jude Research Workshop Series. TN, USA, Oct. 2006***

Published Abstracts

1, Evolution of gene expression signatures in relapsed childhood acute lymphoblastic leukemia differs based on timing of relapse.
Deepa, Bhojwani, Jinhua Wang, Jun Yang, Debra Morrrison, Meenakshi Devidas, Elizabeth Raetz, Stephan Hunger, Mary Relling, William L. Carroll

2. Gene expression profiling differentiates childhood acute lymphoblastic leukemia in down syndrome versus non-down syndrome patients.
Karen Rabin, Jinhua Wang, Anna Tsimelzon, Debra Morrison, Amos Gaikwad, Laura Hogan, Cassia Rye, Susan Hilsenbeck, Meenakshi Devidas, Nyla Heerema, Andrew Carroll, Giuseppe Basso, William L. Carroll, Andrea Pession, Deepa Bhojwani.

3. Antisnese technology targeting an anti-apoptotic gene improves leukemic cell death in ALL cell lines and mice.
Laura Hogan, David Teachey, Nicole Germino, Gregory Condos, Naomi Moskowitz, Ilna Belitskaya-Levy, Jinhua Wang, Deepa Bhojwani, Mary Relling, Terzah Horton, Puja Sapra, Ivan D Horak, Stephan Grupp, Elizabeth Raetz, William Carroll, Debra Morrison.

4. The unique molecular signatures of modular and superficial spreading

melanoma.
Rose Amy, Jinhua Wang, Pearlman Alex, Doudican N, Hernando-Monge Eva, Goldberg Judy, Orlow, SJ, Polsky D, Ostrer Harry, Osman Iman.

5. Skp2 a prognostic marker and potential theraeutic target in metastatic melanoma.
Guimin Wang, Douglas Hanniford, Amy Rose, Avital Gaziel, Anna Pavlick, Kathy Zhou, Ilana Belitskaya-Levy, Jinhua Wang, Michele Pagano, Eva Hernando, Iman Osman

6.Identification of direct Pax6 target genes in mouse lens, pancreas, and cortex and analysis of their chromatin structure.
Ales Cvekl, Ying Yang, Jinhua Wang, Qing Xie, Louise Wolf, and Jiri Zavadil

7. Integrative analysis of gene regulatory networks underlying nephrotoxic response to aristolochic acid.
Zavadil Jiri, Dickman Kim, Wang Jinhua, Josic David, Grollman A. P.

8. Jinhua Wang, Phil Smith, Adrian Krainer, Michael Zhang, Genome-wide analysis of exonic splicing enhancers with ESEfinder. ***Ninth annual meeting of the RNA society: RNA 2004***, Madison Wisconsin, Jun 1-6, 2004

9. Jinhua Wang, Naoya Hata, XiangDong Fu, Michael Zhang, Searching for tissue specific splicing cis-elements. ***The genome of Homo Sapiens, the 68th CSHL quantitative biology symposium***, NY, USA. Jun 2-7, 2003

10. Hitoshi Suzuki, *Jinhua Wang*, Alison Cooper, Gavin Screaton, Michael Zhang, Akila Mayeda, Nested introns in a long intron. ***Eukaryotic mRNA processing meeting***. (talk) Cold Spring Harbor Lab, NY, Aug. 20-24, 2003

11. Zhenyu Xuan, Fang Zhao, *Jinhua Wang*, Ivo Grosse, Michael Zhang, Mouse Promoter Database. ***The first joint Cold Spring Harbor Laboratory/Wellcome Trust Conference on Genome Informatics***. NY, USA. May 7-11, 2003

Computer Skills

Operating System: Linux, SGI/IRIX, SUN/Solaris, Windows.
Programming Languages: Perl, S-plus/R, C/C++, MatLab etc.
Database System: MySQL, Oracle, biology databases (UCSC genome browser, Ensembl database, TransFac, GeneCards, OMIM, GO, PDB, PIR, GEO, GNF, SNPdb etc.)

Bioinformatics Software Database Developed

1 **ESEfinder sever**. (http://rulai.cshl.edu/tools/ESE/)
2 **Genome Comparison viewer (GenomeComp)**. (http://www.mgc.ac.cn/GenomeComp/)
3 **Database of human and mouse conserved sequence elements.** (http://gene.cshl.org/cgi-bin/gbrowse?source=cse)

Journal Refereeing

Bioinformatics; Nucleic Acid Research; Genomics; Genome Research; Proteomics etc.