Curriculum Vitae

Chaochun Wei

Associate Professor
Department of Bioinformatics and Biostatistics
School of Life Sciences and Biotechnology
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Research interests

- Gene prediction, alternative splicing prediction, regulatory element finding
- Finding and characterization of repeat regions in genomes
- Metagenomics
- High performance computing for bioinformatics

Education

2000-2006	D.Sc. in Computer Science	Washington University in St. Louis, USA
1996-1999	M.E. in Signal and Information Processing	Beijing University, China
1991-1996	B.S. in Mathematics	Beijing University, China

Experience

2008-Present
Associate Professor
Department of Bioinformatics and Biostatistics
Shanghai Jiao Tong University, Shanghai, China
With a joint appointment in
Shanghai Center for Bioinformation Technology

2006-2007
Software Engineer
Microsoft Company , Seattle, WA, USA

2000-2006
Research Assistant in Computational Biology
CSE Department, Washington University in St. Louis, USA

1996-1999
Research Assistant in Signal Processing
Center for Information Science, Beijing University, China

Funding

1. National Basic Research Program of China (973) (2013CB956103, Co-PI, budget ￥1.04M, total budget ￥26M), 2013.1 – 2017.12

   "The degeneration mechanism and recovery potential of coral reefs in South China sea"

2. NSFC Project (61272250, PI, ￥800K), (2013.1-2016.12)

   "Finding and characterization of genes containing repeat regions"

3. NSFC Project (60970050, PI, ￥300K), (2010.1-2012.12)

   "An index measuring gene structure variation and its application on the study of disease susceptibility of genes"

4. National High-Tech R&D Program (863) (2009AA02Z310, PI, ￥1.6 1million), 2009.1-2011.12

   "Metagenomics data collection and analysis system based on the next-generation sequencing technologies"

5. Shanghai Pujiang Program (09PJ1407900, PI, ￥200K), (2009.8-2011.7)

   "Conditional random field theory and its applications in Bioinformatics"

6. Science and Technology Innovation Program of Basic Science Foundation of Shanghai (08JC1416700, PI,￥250K), 2008.10-2010.9

   "Algorithms and system for complex sequence module finding"

Patents
1. "A kit for large scale HPV typing", patent number: ZL200910049555.4.

2. "A GPU-based fast metagenomic sequence classification algorithm", application number: 201110125025.0.

3. "A metagenomics-based unknown pathogen identification system", application number: 2011045266.7.

Software copyright
1. "Metagenome NGS simulation system (NeSSM)", registration number: 2010SR029333

2. "A visualization system for complex subsequence module identification (FlexSA)", registration number: 2010SR057696

3. "A transcription factor binding site prediction system based on conditional random field theory(CTF)", registration number: 2011SR086086

4. "Shigella genome db", registration number: 2011R11L179894

5. "A gene function analysis system for metagenomes", registration number:2011R11L181725

Publications in peer reviewed journals

1. "cGRNB: a web server for building combinatorial gene regulatory networks through integrated engineering of seed-matching sequence information and gene expression datasets", Xu, H., Yu, H., Tu, K., Shi, Q., **Wei, C.**, Li, Y., Li, Y., (2013) ***BMC Systems Biology***, (accepted)

2. "PMRD: a curated database for genes and mutants involved in plant male reproduction", Cui, X., Wang, Q., Yin, W., Xu, H., Wilson, Z., Pan, S., **Wei, C.** and Zhang, D., (2012) *BMC Plant Biology*, **12**:215

3. "Towards biological characters of interactions between transcription factors and their DNA targets in Mammals", Zheng, G., Liu, Q., Ding, G., **Wei, C.***, Li, Y., (2012) *BMC Genomics* ,13:388

4. "CTF: A transcription factor binding site prediction system using conditional random fields", He, Y., Zheng, G., **Wei, C.***, (2012) *BMC Genomics,* 13(Suppl 8):S18

5. "iGepros: An integrated gene and protein annotation server for biological nature exploration", Zheng, G., Wang, H., **Wei, C.***, Li, Y., (2011) *BMC Bioinformatics*, 12(Suppl 14):S6

6. "MetaBinG: Using GPUs to accelerate metagenomic sequence classification", Jia, P., Liu, L., **Wei, C.***, (2011) *PloS ONE*, 6(11): e25353

7. "Analysis of oral microbiota in children with dental caries by PCR-DGGE and Barcoded Pyrosequencing", Ling, Z., Kong, J., Jia, P., **Wei, C.**, Wang, Y., Pan, Z., Huang, W., Chen, H., Xiang, C., (2010) *Microbial Ecology*, 60(3):677-90

8. "The Completion of the Mammalian Gene Collection (MGC), The MGC Project Team. (2009) *Genome Research*, 19:2324-2333

9. "Interactions between gut microbiota, host genetics, and diet relevant to development of metabolic syndromes in mice", Zhang, C., Zhang, M., Wang, S., Han R., Cao, Y., Hua, W., Mao, Y., Zhang X., Pang X., Wei, C., Zhao, G., Chen, Y., Zhao, L., (2010) *ISME J*, 4,232-241

10. "More Than 9,000,000 unique Genes in Human Gut Bacterial Community: Estimating Gene Numbers inside a Human Body", Yang, X., Xie, L. LI, Y. and **Wei, C***. (2009) *PLoS ONE*, 4(6): e6074.

11. "The prediction of interferon treatment effects based on time series microarray gene expression profiles", Huang, T., Tu, K., Shyr, Y, **Wei, C.**, Xie, L. and Li, Y.（2008）, *Journal of Transcriptional Medicine*, 6:44.

12. "ITFP: an integrated platform of mammalian transcription factors", Zheng, G., Tu, K., Yang, Q., Xiong, Y., **Wei, C.**, Xie, L., Zhu, Y. and Li, Y. （2008）*Bioinformatics*, 24(20):2416-2417

13. "The Combination Approach of SVM and ECOC for Powerful Identification and Classification of Transcription Factor", Zheng, G., Qian, Z., Yang, Q., **Wei, C.**, Xie, L., Zhu, Y. and Li, Y.（2008）*BMC Bioinformatics*, 9(1):282.

14. "Using ESTs to Improve the Accuracy of de novo Gene Prediction", **Wei, C.** and Brent, M. R. (2006) *BMC Bioinformatics,* 7:327. **Highly accessed**

15. "PAIRAGON + N-SCAN: A Model-Based Gene Annotation Pipeline", Arumugam, M., **Wei, C.**, Brown, R. H. and Brent, M. R. (2006) *Genome Biology,* 7(Suppl 1): S5.

16. "Closing in on the *C.elegans* ORFeome by Cloning TWINSCAN predictions", **Wei, C.**, Lamesch, P., Arumugam M., Rosenberg, J., Hu, P., Vidal, M., and Brent, M. R. (2005) *Genome Research* 15:577-582. (Reported by *Nature Reviews Genetics* Vol.6 No.5 as "*Research highlight*".)

17. "The Genome Sequence of *Caenorhabditis briggsae*: A Platform for Comparative Genomics", Stein, L. D., Bao, Z., et al. (2003) ***PLoS Biol*** 1(2): E45.

Presentations

1. "NeSSM: Next-generation sequencing simulator for metagenomics", Poster, GIW 2012, Tainan, Taiwan, 2012/12/13

2. "MetaBinG: Using GPUs to accelerate metagenomic sequence classification", Invited talk, ANRRC, Jeju Island, Korea, 2012/10/19

3. "Regulatory element finding by integrating the genomic sequence and epigenetic information", Invited talk, International IRSES meeting, Shanghai, China, 9/10/2012

4. "Using GPUs to accelerate metagenomic sequence classification", Invited talk, ICB, Xi'an, China, 8/19/2012

5. "MetaBinG: a GPU-based fast metagenomic sequence classification system using high-order Markov models", Poster, ISMB, Vienna, Austria, 7/18/2011.

6. "Gene Prediction Methods and Algorithms", Lecture, the 10th Japan-Korea-China Bioinformatics Training Course, Jeju Island, Korea, 5/12/2011.

7. "Bioinformatics for Microbial biology", Lecture, Fudan University, Shanghai, China, 1/13/2011.

8. "Gene Prediction algorithms and systems, and their application for algal genome analysis", Lecture, Top China and Brazil course, Shanghai, China, 7/16/2010.

9. "Gene Prediction and Annotations", Lecture, Next Generation Sequencing Data Analysis Training Course, Fudan University, Shanghai, China, 7/30/2010.

10. "Methods and Algorithms for Gene Prediction", Lecture, the 9th Japan-Korea-China Bioinformatics Training Course, CAS, Shanghai, China, 4/20/2010.

11. "Finding diversity of a microbe community: 16S rRNA or metagenome shotgun sequencing method?", Invited talk, Japan-Korea-China Symposium on Bioinformatics, JST, Tokyo, Japan, 3/1/2010.

12. "Estimation of gene numbers in a human bogy", talk, Symposium "Analysis of complex biological systems", Shanghai Jiao Tong University, Shanghai, China, 8/19/2009.

13. "More than 9,000,000 genes in the human gut bacterial community: Estimation of gene numbers in human", Invited talk, Spring School on Multiscale Methods and Modeling in Biophysics and Systems Biology, Chinese Academy of Science, Shanghai, 5/22/2009.

14. "Estimation of gene numbers in human", Invited talk, the 8th Japan-Korea-China Bioinformatics Symposium, Kyoto University, Kyoto, Japan, 2/28/2009.

15. "Methods and Algorithms for Gene Prediction", Invited talk, the 8th Japan-Korea-China Bioinformatics Training Course, Kyoto University, Kyoto, Japan, 2/27/2009.

16. "Measuring the Impact of Genomic Sequence Variations on Gene Structure Variations", Invited talk, Theory and Applications of Computational Chemistry, Shanghai, China, 9/27/2008.

17. "Using EST to Improve Gene Structure Prediction", Invited talk, Summer Course for Plant Molecular Biology, Shanghai Jiao Tong University, Shanghai, 7/17/2008.

18. "Using EST to Improve Gene Structure Prediction", Invited talk, The Institute of Systems Biology, Seattle, Washington, 7/6/2006.

19. "Integrating EST alignments into TWINSCAN", Poster, Biology of Genomes, CSHL, NY, 5/12/2004.

20. "Experimental Verification of Twinscan Predictions on *C.elegans*", Talk, the 3rd Annual ORFeome Meeting, Boston, MA, 12/3/2003.

21. "Using Gene Prediction to Guide Experiments by Summing Over Consistent Gene Models", Talk, Genome Informatics, CSHL, NY, 5/11/2003.

Teaching

1. "Programming languages for Bioinformatics", Credit 3, Spring 2013

2. "Matlab programming", Credit 2, Spring 2012

3. "Computational Biology", Bioinformatics session, Credit 3, Fall 2011, Fall 2012

4. "Algorithms in Bioinformatics", Credit 3, Fall 2011, Fall 2012

5. "Genomics and Proteomics", Credit 3, Fall 2010

6. "Digital Signal Processing", Credit 3, Fall 2009

7. "Frontier topics in Bioinformatics", Biological Sequence Analysis session, Spring 2009

Mentoring

4 PhD students (1 graduated)

- Guangyong Zheng, 2008-2009, PhD Comittee, Fudan University, now a Research Scientist, CAS

- Huayong Xu, 2010- ，Co-advisor with Prof. Yixue Li, SJTU

- Zhaohui Gu, 2009- , PhD Committee, SJTU

- Zhiqiang Hu, 2010- , Advisor, SJTU

8 Master students (3 graduated)

- Ben Jia, 2011-, Master student, Advisor, SJTU)

- Lu Zeng, 2011-, Master studen, co-adivsor with David Adelson, Adelaide Univeristy, SJTU

- Ting Hou, 2011-, Master student, co-advisor with Prof. Yixue Li, ECUST

- Danfeng Cao, 2012-, Master student, co-advisor with David Adelson, Adelaide University, SJTU

- Jun Xie, 2012-, Master student, Advisor, SJTU

- Liming Xuan, 2010-2012, Master student, co-advisor with Prof. Yixue Li, ECUST, now work for a company in Wuxi, Jiangsu

- Peng Jia, 2009-2011, Master student, co-advisor with Prof. Lei Liu, CAS, now work for an advertisement company, Shanghai,

- Linlin Song (2008-2010, Master student, co-advisor with Prof. Saijuan Chen, SJTU, now work for ICBC, Beijing)

17 undergraduate students (12 graduated)

- Nan Hua, 2012-2013, School of Life Sciences and Biotechnology, SJTU

- Bo Yang, 2012 Summer, School of Life Sciences and Biotechnology, SJTU

- Yiwei Zhou, 2012 Summer, School of Life Sciences and Biotechnology, SJTU

- Xuelian Yu, 2012-2013, School of Life Sciences and Biotechnology, SJTU

- Jie Bi, 2012 Summer, Shool of Life Sciences and Biotechnology, SJTU

- Jia Hou, 2011-2012, Shool of Life Sciences and Biotechnology, SJTU, now in Austrilia

- Chang Huang, 2011-2012, Shool of Life Sciences and Biotechnology, SJTU, now work in Shanghai

- Tao Hu, 2011-2012, Intern, now graudate student at the North Carolina State University, USA

- Linchang Tan, 2011 Summer, Mathematics Department, SJTU, now graduate student at the University of Michigan, USA

- Yujie He, 2010-2011, now graduate student at the department of Computer Science and Engineering, Washington University in St. Louis, USA

- Yupeng He, 2009-2011, now graduate student at University of California, San Diego, USA

- Yuanchun Zhao, 2009-2010, intern, now graduate student at Michigan State University, USA

- Bing He, 2008-2010, now graduate student at the University of Iowa, USA

- Wenjia Wang, 2008-2009, now student at the University Paris Sud (Paris XI), France

- Xing Yang, 2008-2009, now graduate student at Florida International University, USA

- Jie Du, 2008-2009

- Yunfan Cui, 2010, now graduate student at the School of Software, SJTU

12 PRP or summer program students (sophomores or Junior)

- Nicholas Lee, 2012 Summer, Harvard University, USA

- Zixu Ding, 2012, RPR student, School of Life Sciences and Biotechnology, SJTU

- Mai Shi, 2012 Summer, Zhiyuan College, SJTU

- Shiyi Liu, 2012 Summer, School of Life Sciences and Biotechnology, SJTU

- Cheng Sun, 2012 Summer, School of Life Sciences and Biotechnology, SJTU

- Bingqing Shen, 2012 Summer, School of Life Sciences and Biotechnology, SJTU

- Xin Yi, 2012 Summer, School of Life Sciences and Biotechnology, SJTU

- Ming Lin, 2012 Summer, School of Electoric Engineering, SJTU

- Yuanfang Xia, 2012 Summer, School of Electoric Engineering, SJTU

- Cong Xu, 2012 Summer, Zhiyuan College, SJTU

- Danjin Shen, 2012 Summer, Medical School, SJTU

- Mengdi Lu, 2011, PRP student, Undergraduate student, School of Biomedical Engineering, SJTU

- Xufei Wu, 2009, PRP student, Undergraduate student, Physics Department, SJTU

Academic Service

1. Invited reviewer for journals: BMC Bioinformatics, Bioinformatics

2. RECOMB-seq 2013, program committee and session chair, Beijing China, 4/11-12/2013

3. Asia Bioinformatics Institute (ABI, under construction) , member of the working group, 2010-2012

4. EMBO World Practical Course: Computational Biology: from (meta)genomes to phenotype and environment, Shanghai, China, local organizer, 8/16-22/2009

5. Symposium "Analysis of complex Biological Systems", Shanghai Jiao Tong University, organizer, 8/19/2009

6. Multiscale Methods and Modeling in Biophysics and Systems Biology, Chinese Academy of Science, Shanghai, Symposium session chair, 5/22/2009

Committees

1. Major selection advisor committee for undergraduates, School of Life Sciences and Biotechnology, Shanghai Jiao Tong University, member, 2009-2013

2. Graduate student selection committee, the School of Life Sciences and Biotechnology, Shanghai Jiao Tong University, member, 2009-2012

Awards

Shanghai Pujiang Talent Award   (2009)

Gold Award in iGEM competition   (2009)

Excellent Graduate of Beijing University (1996)

Academic Excellence Scholarship   (1995)