

Curriculum Vitae

Chaochun Wei

Professor, Associate Chair
Department of Bioinformatics and Biostatistics
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Research interests

- Finding functional elements in genomes
 - Gene prediction, alternative splicing prediction
 - Regulatory element finding
 - Finding and characterization of repeat regions in genomes
 - Pan-genome analysis
- 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

2016-Present	Professor
2014-Present	Associate Chair of Department
2008-2015	Associate Professor Department of Bioinformatics and Biostatistics Shanghai Jiao Tong University, Shanghai, China
2008-Present	Group Leader, 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. Medicine and Engineering joint project (YG2017ZD01, co-PI, ¥750K) 2018.1-2020.12
“Data analysis platform for big omics data from gastric cancer considering complex cancer phenotypes and microbiome diversity”
2. NSFC Project (61472246, PI, ¥800K), 2015.1-2018.12
" Finding and characterizing complex structure sequence modules in metagenomes"
3. National High-Tech R&D Program (863) (2014AA02502, Co-PI, budget ¥650K, total budget ¥7.2M), 2014.1-2017.12
“Key technologies for microbial genomic data integration and analysis”
4. 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”
5. NSFC Project (61272250, PI, ¥800K), (2013.1-2016.12)
“Finding and characterization of genes containing repeat regions”
6. 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”
7. 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”
8. Shanghai Pujiang Program (09PJ1407900, PI, ¥200K), (2009.8-2011.7)
“Conditional random field theory and its applications in Bioinformatics”
9. 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”, patent number: ZL201110125025.0.
3. “A metagenomics-based unknown pathogen identification system”, application number: 2011045266.7.

4. "A fluorescence imaging system and image analysis method", application number: 201510186113.X.
5. "A fluorescence image analysis system", application number: 201520237179.2.
6. "A nucleic acid sequence amplification primer design system and its application", application number: 20150559179.9.
7. "A fast isothermal identification system for *Cronobacter sakazakii*", application number: 201510556917.4.
8. "A fast isothermal identification system for *Salmonella*", application number: 201610767608.6.
9. "A kit for fast isothermal identification of *Listeria monocytogenes*", application number: 201610767426.9.
10. "A fast isothermal identification system for *Bacillus cereus*", application number: 201610767579.3.
11. "A fast isothermal identification system for *Vibrio cholera o1*", application number: 201610767491.1.
12. "A fast isothermal identification system for *Vibrio vulnificus*", application number: 201610767402.3.
13. "A fast isothermal identification method for *Cronobacter sakazakii*, primers and their applications", application number: 201610767389.1.
14. "A fast isothermal identification method for *Staphylococcus aureus Rosenbach*, primers and their applications", application number: 201610767576.X
15. "A fast isothermal identification method for *Vibrio Parahaemolyticus*, primers and their applications", application number: 201610780447.4
16. "A fast isothermal identification method for *Yersinia pseudotuberculosis*, primers and their applications", application number: 201610767506.4
17. "A fast isothermal identification method for *Listeria monocytogenes*, primers and their applications", application number: 201610767436.2
18. "A fast isothermal identification method for *Bacillus cereus*, primers and reagent kit", application number: 201610780460.X
19. "A fast isothermal identification method for *Vibrio cholera O1*, primers and reagent kit", application number: 201610780456.3
20. "A fast isothermal identification method for *Staphylococcus aureus*, primers and reagent kit", application number: 201610767557.7
21. "A fast isothermal identification method for *Vibrio vulnificus*, primers and their applications", application number: 201610780421.X
22. "A fast isothermal method for simultaneously identification of *Vibrio cholerae* and *Vibrio vulnificus*, primers and reagent kit", application number: 201610780489.8
23. "A fast isothermal identification method for *Yersinia enterocolitica*, primers and reagent kit", application number: 201610767671.X

24. “A fast isothermal identification method for *Shigella*, primers and reagent kit”, application number: 201610767703.6
25. “A fast isothermal identification method for *Vibrio vulnificus*, primers and reagent kit”, application number: 201610780407.X
26. “A fast isothermal identification method for *Vibrio parahaemolyticus*, primers and reagent kit”, application number: 201610780425.8
27. “A fast isothermal identification method for *Yersinia pseudotuberculosis*, primers and reagent kit”, application number: 201610780457
28. “A fast isothermal identification method for *Slomonella*, primers and reagent kit”, application number: 201610780485. X

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
6. “Logistic regression based protein lysine acetylation sites prediction system”, registration number: 2015SR171889
7. “An integrated gene and protein annotation system for biological feature exploring”, registration number: 2015SR171886

Publications in peer reviewed journals

1. “MetaBinG2: a fast and accurate metagenomic sequence classification system for samples with many unknown organisms”, Qiao, Y., Jia, B., Hu, Z., Sun, C., Xiang, Y., **Wei, C.***, *Biology Direct*, 2018, (accepted)
2. “In silico analysis of endogenous siRNAs associated transposable elements and NATs in *Schistosoma japonicum* reveals their putative roles during reproductive development”, Giri, B., Ye, J., Chen, Y., **Wei, C.***, Cheng, G.*, *Parasitology Research*, 2018 (accepted)
3. “Genome-wide analysis of the association of transposable elements with gene regulation suggests that Alu elements have the largest overall regulatory impact”, Zeng, L., Pederson, S., Cao, D., Qu, Z., Hu, Z., Adelson, D.*, **Wei, C.***, *Journal of Computational Biology*, 2018 (accepted)
4. “Novel sequences, structural variations and gene presence variations of Asian cultivated rice”, Hu, Z., Wang, W., Wu, Z., Sun, C., Li, M., Lu, J., Fu, B., Shi, J., Xu,

- J., **Wei, C.***, Li, Z.*, *Scientific Data*, 2018 (accepted)
5. “Dosage compensation in the process of inactivation/reactivation during both germ cell development and early embryogenesis in mouse”, Li, X., Hu, Z., Yu, X., Ma, B., Zhang, C., **Wei, C.***, and Wu, J.*, *Scientific Reports*, 2017, 7:3729.
 6. “EUPAN enables pan-genome studies of a large number of eukaryotic genomes”, Hu, Z., Sun, C., Lu, K., Chu, X., Zhao, Y., Lu, J., Shi, J., **Wei, C.***, *Bioinformatics*, 2017, 23(15):2408-2409
 7. “Widespread of Horizontal Gene Transfer in the Human Genome”, Huang, W., Tsai L., Li, Y., Hua, N., Sun, C., **Wei, C.***, *BMC Genomics*, 2017, 18:274
 8. “RNA virus receptor Rig-I monitors gut microbiota and inhibits colitis-associated colorectal cancer”, Zhu, H., Xu, W., Hu, Z., Zhang, H., Shen, Y., Lu, S., **Wei, C.***, Wang, Z.*, *J. of Experimental & Clinical Cancer Research*, 2017, 36:2.
 9. “R PAN: Rice Pan-genome Browser for ~3,000 rice genomes”, Sun, C., Hu, Z., Lu, K., Zhao, Y., Lu, J., Zheng, T., Wang, W., Shi, J., Zhang, D., Li, Z., **Wei, C.***, *Nucleic Acids Research*, 2017, 45(2): 597-605.
 10. "Revealing missing human protein isoforms based on *ab initio* prediction, RNA-seq and proteomics", Hu, Z., Scott, H., Qin, G., Zheng, G, Chu, X., Xie, L., Adelson, D., Oftedal, B., Venugopal, P., Babic, M., Hahn, C., Zhang, B., Wang, X., Li, N., **Wei, C.***, *Scientific Reports*, 2015, 5:10940
 11. "MOST+: a *de novo* motif finder combining genomic sequence and heterogeneous genome-wide signatures", Zhang, Y., He, Y., Zheng, G., **Wei, C.***, *BMC Genomics*, 2015, 16(Suppl 7):S13
 12. "Whole genome sequencing of six dog breeds from continuous altitudes reveals adaption to high-altitude hypoxia", Xiao, G. et al., *Genome Research*, 2014, 24(8)1308-15.
 13. "L AceP: lysine acetylation sites prediction using logistic regression classifier", Hou, T., Zheng, G., Zhang P., Jia, J., Li, J., Xie, L., **Wei, C.***, Li, Y., 2014, *PLoS ONE*, 9(2): e89575
 14. "NeSSM: a Next-generation Sequencing Simulator for Metagenomics", Jia, B., Cai, K., Xuan, L., **Wei, C.***, 2013, *PLoS ONE*, 8(10):e75448.
 15. “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*, 7(Suppl 2):S7
 16. “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
 17. “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

18. “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
19. “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
20. “MetaBinG: Using GPUs to accelerate metagenomic sequence classification”, Jia, P., Liu, L., **Wei, C.***, (2011) *PLoS ONE*, 6(11): e25353
21. “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
22. “The Completion of the Mammalian Gene Collection (MGC), The MGC Project Team. (2009) *Genome Research*, 19:2324-2333
23. “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
24. “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.
25. “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.
26. “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
27. “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.
28. “Using ESTs to Improve the Accuracy of de novo Gene Prediction”, **Wei, C.** and Brent, M. R. (2006) *BMC Bioinformatics*, 7:327. **Highly accessed**
29. “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.
30. “Closing in on the *C. elegans* ORFeome by Cloning TWINSKAN 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**”.)
31. "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. “The rice pan-genome: gene presence/absence variation derived from >3000 rice genomes”, Net4FS, Montpellier, France, October 16, 2017

2. "RPAN: the rice pan-genome browser", Breakthrough Highlight Oral Presentation, ISMB 2017, Prague, Czech Republic, 7/24/2017
3. "MetaBinG2: a fast and accurate metagenomics sequence classification method for samples with many unknown organisms", Oral Presentation, CAMDA, ISMB, 2017, Prague, Czech Republic, 7/23/2017
4. "The rice pan-genome: gene presence/absence variation derived from >3000 rice genomes", Oral Presentation, the 15th Japan-Korea-China Bioinformatics Symposium, Seoul, Korea, 6/21/2017
5. "The rice pan-genome: gene presence/absence variation derived from >3000 rice genomes", Net4FS, Shanghai, China, 11/08/2016
6. "How many protein isoforms are encoded in the human genome?", EBI, Cambridge, UK, 7/16/2015
7. "EUPAN: a large-scale pan-genome analysis pipeline for eukaryotic large genomes", Dublin, Ireland, 7/12/2015-7/14/2015
8. "MOST+: A motif finding approach combining genomic sequence and heterogeneous genome-wide signatures", Poster, ISMB2013, Berlin, German, 2013/7/23
9. "Finding functional elements in genomes with statistical models", Lecture, the 11th Japan-Korea-China Bioinformatics Training Course, 6/18/2013
10. "NeSSM: Next-generation sequencing simulator for metagenomics", Poster, GIW 2012, Tainan, Taiwan, 2012/12/13
11. "MetaBinG: Using GPUs to accelerate metagenomic sequence classification", Invited talk, ANRRC, Jeju Island, Korea, 2012/10/19
12. "Regulatory element finding by integrating the genomic sequence and epigenetic information", Invited talk, International IRSES meeting, Shanghai, China, 9/10/2012
13. "Using GPUs to accelerate metagenomic sequence classification", Invited talk, ICB, Xi'an, China, 8/19/2012
14. "MetaBinG: a GPU-based fast metagenomic sequence classification system using high-order Markov models", Poster, ISMB, Vienna, Austria, 7/18/2011.
15. "Gene Prediction Methods and Algorithms", Lecture, the 10th Japan-Korea-China Bioinformatics Training Course, Jeju Island, Korea, 5/12/2011.
16. "Bioinformatics for Microbial biology", Lecture, Fudan University, Shanghai, China, 1/13/2011.
17. "Gene Prediction algorithms and systems, and their application for algal genome analysis", Lecture, Top China and Brazil course, Shanghai, China, 7/16/2010.
18. "Gene Prediction and Annotations", Lecture, Next Generation Sequencing Data Analysis Training Course, Fudan University, Shanghai, China, 7/30/2010.
19. "Methods and Algorithms for Gene Prediction", Lecture, the 9th Japan-Korea-China Bioinformatics Training Course, CAS, Shanghai, China, 4/20/2010.

20. "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.
21. "Estimation of gene numbers in a human body", talk, Symposium "Analysis of complex biological systems", Shanghai Jiao Tong University, Shanghai, China, 8/19/2009.
22. "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.
23. "Estimation of gene numbers in human", Invited talk, the 8th Japan-Korea-China Bioinformatics Symposium, Kyoto University, Kyoto, Japan, 2/28/2009.
24. "Methods and Algorithms for Gene Prediction", Invited talk, the 8th Japan-Korea-China Bioinformatics Training Course, Kyoto University, Kyoto, Japan, 2/27/2009.
25. "Measuring the Impact of Genomic Sequence Variations on Gene Structure Variations", Invited talk, Theory and Applications of Computational Chemistry, Shanghai, China, 9/27/2008.
26. "Using EST to Improve Gene Structure Prediction", Invited talk, Summer Course for Plant Molecular Biology, Shanghai Jiao Tong University, Shanghai, 7/17/2008.
27. "Using EST to Improve Gene Structure Prediction", Invited talk, The Institute of Systems Biology, Seattle, Washington, 7/6/2006.
28. "Integrating EST alignments into TWINSKAN", Poster, Biology of Genomes, CSHL, NY, 5/12/2004.
29. "Experimental Verification of Twinscan Predictions on *C. elegans*", Talk, the 3rd Annual ORFeome Meeting, Boston, MA, 12/3/2003.
30. "Using Gene Prediction to Guide Experiments by Summing Over Consistent Gene Models", Talk, Genome Informatics, CSHL, NY, 5/11/2003.

Teaching

1. "Omics big data", Credit 3, Spring 2017, 2018
2. "Advanced Bioinformatics", Credit 3, Spring 2012-2015
3. "Programming languages for Bioinformatics", Credit 3, Spring 2013-2016, Credit 2, Spring 2017, 2018
4. "Matlab programming", Credit 2, Spring 2012
5. "Computational Biology", Bioinformatics session, Credit 3, Fall 2011- 2016
6. "Algorithms in Bioinformatics", Credit 3, Fall 2011 – 2016, Spring 2018
7. "Genomics and Proteomics", Credit 3, Fall 2010
8. "Digital Signal Processing", Credit 3, Fall 2009
9. "Frontier topics in Bioinformatics", Biological Sequence Analysis session, Spring 2009

Mentoring

7 PhD students, 13 Master students, 22 undergraduate thesis students, 19 intern students

7 PhD students (4 graduated)

- Guangyong Zheng, 2008 - 2009, PhD Committee Member, Fudan University, now a Research Scientist, CAS
- Huayong Xu, 2010 - , Co-advisor with Prof. Yixue Li, SJTU
- Zhaohui Gu, 2009 -2015, PhD Committee Member, SJTU. Now a postdoc in St. Judy Children's Hospital, USA
- Zhiqiang Hu, 2010 - 2016, Advisor, SJTU
- Ben Jia, 2014 -, Advisor, SJTU
- Zhongqu Duan, 2015-, Co-advisor, first advisor Hongyu Zhao, SJTU-Yale Joint Center for Biostatistics
- Huimin Lu, 2017-, Advisor, SJTU

14 Master students (11 graduated)

- Fazhe Yan, 2017-, Master student, Advisor, SJTU
- Wenmin Zhang, 2016 -, Master student, Advisor, SJTU
- Yuyang Qiao, 2015 - 2018, Master student, Advisor, SJTU
- Cheng Sun, 2014 - 2017, Master student, Advisor, SJTU, now a PhD student in University of Michigan, USA
- Jingyuan Lu, 2014 -, Master student, Advisor, SJTU
- Xuling Yu, 2013 - 2016, Master student, Advisor, SJTU
- Ben Jia, 2011 - 2014, Master student, Advisor, SJTU, now a PhD student in SJTU
- Lu Zeng, 2011 - 2014, Master student, co-advisor with David Adelson, Adelaide University, SJTU, now a PhD student in Adelaide University, Australia
- Ting Hou, 2011 - 2014, Master student, co-advisor with Prof. Yixue Li, ECUST, now a PhD student in ECUST.
- Danfeng Cao, 2012 - 2015, Master student, co-advisor with David Adelson, Adelaide University, SJTU
- Jun Xie, 2012 - 2015, 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)

29 undergraduate independent study students (29 graduated)

- Fazhe Yan, 2016-2017, School of Life Sciences and Biotechnology, SJTU, graduate student in SJTU
- Yuanyuan Xi, 2016-2017, School of Life Sciences and Biotechnology, SJTU, admitted to a Sweden graduate school
- Jiannan Ye, 2016-2017, Zhiyuan College, SJTU, graduate student in SJTU
- Humin Lu, 2016-2017, School of Life Sciences, NJAU, graduate student in SJTU
- Yichen Si, 2015-2016, Zhiyuan College, SJTU, now a graduate student in North Carolina State University, USA.
- Wenze Huang, 2014-2016, School of Life Sciences and Biotechnology, SJTU, now a graduate student in Tsinghua University, China
- Liangjie Liu, 2013-2016, School of Life Sciences and Biotechnology, SJTU.
- Jiayao Wang, 2013 - 2015, School of Electronic Engineering, SJTU, now a graduate student in Indiana University, USA
- Jinyuan Lu, 2013 - 2014, Zhiyuan College, SJTU, now a graduate student in SJTU
- Mai Shi, 2013 - 2014, Zhiyuan College, SJTU, now a graduate student in Chinese University of Hong Kong
- Cheng Sun, 2013 - 2014, School of Life Sciences and Biotechnology, SJTU, now a graduate student
- Hailing Wang, 2013 - 2014, School of Life Sciences and Biotechnology, SJTU, now a graduate student in Hong Kong University
- Zixu Ding, 2013 - 2014, School of Life Sciences and Biotechnology, SJTU, now a graduate student in Carnegie Mellon University, USA
- Nan Hua, 2012 - 2013, School of Life Sciences and Biotechnology, SJTU, now a graduate student in the University of Southern California, USA
- Bo Yang, 2012 Summer, School of Life Sciences and Biotechnology, SJTU, then a graduate student in Hong Kong University
- Xueling Yu, 2012 - 2013, School of Life Sciences and Biotechnology, SJTU, now a graduate student in SJTU
- Jie Bi, 2012 Summer, School of Life Sciences and Biotechnology, SJTU, now a graduate student at Shanghai Tech
- Jia Hou, 2011 - 2012, School of Life Sciences and Biotechnology, SJTU, now in Australia
- Chang Huang, 2011 - 2012, School of Life Sciences and Biotechnology, SJTU, now work in Shanghai

- Tao Hu, 2011 - 2012, Intern, now a graduate student at the North Carolina State University, USA
- Linchang Tan, 2011 Summer, Mathematics Department, SJTU, now a 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 a graduate student at University of California, San Diego, USA
- Yuanchun Zhao, 2009 - 2010, intern, now a graduate student at Michigan State University, USA
- Bing He, 2008 - 2010, now a graduate student at the University of Iowa, USA
- Wenjia Wang, 2008 - 2009, now a student at the University Paris Sud (Paris XI), France
- Xing Yang, 2008 - 2009, last seen as a graduate student at Florida International University, USA
- Jie Du, 2008 - 2009
- Yunfan Cui, 2010, last seen as a graduate student at the School of Software, SJTU

19 PRP or other intern program students

- Kuangchen Lu, 2014-, PRP, School of Life Sciences and Biotechnology, SJTU
- Siyuan Ma, 2015-2017, School of Life Sciences and Biotechnology, SJTU, exchange to Yale University
- Yulong Li, 2014 summer, Zhiyuan College, SJTU
- Lillian Tsai, 2014 Summer, Harvard University, USA
- 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
- Yiwei Zhou, 2012 Summer, School of Life Sciences and Biotechnology, SJTU, then a graduate student in Chinese Academy of Science
- Ming Lin, 2012 Summer, School of Electric Engineering, SJTU
- Yuanfang Xia, 2012 Summer, School of Electric 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. *Scientific Reports* (IF 4.26), Editorial Board Member, 2016/8 -
2. *BMC Bioinformatics, Bioinformatics*: Invited reviewer for journals
3. *ICIBM* 2016, Conference committee panel, Huston, Texas, USA, 12/8-10/2016
4. *ICIBM* 2015, Conference committee panel, Indianapolis, IN, USA, 11/13-15,2015
5. *ICIBM* 2014, Conference committee panel, San Antonio, Texas, USA, 12/4-6/2014
6. *BioMed Research International* (IF 2.88), Editorial Board Member, 2013/5 - 2014.12
7. *RECOMB-seq* 2013, Conference committee panel and session chair, Beijing China, 4/11-12/2013
8. Shanghai Association of Bioinformatics, Committee member, 2013/10 -.
9. Asia Bioinformatics Institute (ABI, under construction), member of the working group, 2010 - 2012
- 10.EMBO World Practical Course: Computational Biology: from (meta)genomes to phenotype and environment, Shanghai, China, local organizer, 8/16-22/2009
- 11.Symposium “Analysis of complex Biological Systems”, Shanghai Jiao Tong University, organizer, 8/19/2009
- 12.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-
2. Graduate student recruiting committee, the School of Life Sciences and Biotechnology, Shanghai Jiao Tong University, member, 2009-

Awards

- | | |
|---|--------|
| Excellence in Teaching, Shanghai Jiao Tong University | (2015) |
| Chenxing Scholar, Shanghai Jiao Tong University | (2013) |
| New Century Excellent Talents, Minister of Education, China | (2013) |
| Shanghai Pujiang Talent Award | (2009) |

Gold Award in iGEM competition

(2009, 2014, 2015, 2016)

Excellent Graduate of Beijing University

(1996)