

Chengqi Wang, PhD

CONTACT INFORMATION

Genomics Program
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RESEARCH INTERESTS

My research focuses on understanding how the biological systems that underlie healthy life and disease react to variations in their makeup (genetic variation, for example) or their environment (drugs, for example). I employ statistical inference (MCMC and Bayesian modeling, for example) and machine learning to discover patterns in large datasets (multi-omics data, for example), understand mechanisms, and act upon predictive and causal relationships to, ultimately, address questions in genomics and molecular medicine.

APPOINTMENTS

8/2020-present	Research Assistant Professor , University of South Florida, College of Public Health, Tampa, FL.
8/2014-8/2020	Research Associate , University of South Florida, College of Public Health, Tampa, FL.
7/2012-7/2014	Postdoctoral Fellow , Beijing Institute of Genomics (BGI), Chinese Academy of Sciences.

EDUCATION

2012	Ph.D. in Cheminformatics/Bioinformatics, Lanzhou University, China. Area of Concentration: Protein Structure Prediction by Using Machine Learning Algorithms.
2006	B.S. School of Chemical Engineering, Lanzhou University, China.

AWARDS AND HONORS

2/2021	COPH internal award, University of South Florida, Tampa, FL.
1/2020	First Place Team, Data Science Hackathon, University of South Florida, Tampa, FL.
1/2019	First Place Team (Team leader, Data Visualization Team) NIH Data Science Hackathon, University of South Florida, Tampa, FL.
6/2018	Outstanding Poster Single Cell Genomics Symposium, University of South Florida, Tampa, FL.

MANUSCRIPT REVIEW

Genomics Proteomics and Bioinformatics
BMC Genomics
BMC Supplements
Frontiers in Genetics
Scientific Reports
Journal of Cellular Physiology
Journal of Genetics and Genomic
IEEE/ACM Transactions on Computational Biology and Bioinformatics
Plos ONE
Current Pharmaceutical Design
Meta Gene
Journal of Bioinformatics and Computational Biology
Journal of Bioinformatics, Computational and Systems Biology
International Journal of Data Mining and Bioinformatics
Current Bioinformatics
Advances in Bioinformatics
Heliyon

TEACHING

8/2020	Director and Instructor , Applied Computational Genomics (3 credit) Florida, Tampa, FL. <u>Course Description</u> : Hands-on training, along with an introduction to basic concepts in using popular tools and techniques for genome, transcriptome, epigenome, and microbiome
2/2021, 9/2020, 2/2020, 2/2019, 9/2018	Director and Instructor , Linux and R tutorials, RNA-seq Data Analysis Workshop. Genomics Program, University of South Florida, Tampa, FL. <u>Course Description</u> : Foundational Linux command and R programming, basic statistical concept and data visualization.
3/2020, 11/2020	Director and Instructor , R tutorials, Microbiome Data Analysis Workshop. Genomics Program, University of South Florida, Tampa, FL. <u>Course Description</u> : R programming, basic statistical concept and data visualization in microbiome 16S analysis.
2018 (Spring)	Teaching Assistant , Quantitative Genomics and Genetics. Genomics Program, University of South Florida, Tampa, FL.

COMPUTATIONAL SKILL

Machine learning, Deep learning, Markov Chain Monte Carlo (MCMC), Bayesian modeling, Data mining, Python, Perl, R, C++, Linux system administration and shell script.

INVITED PRESENTATIONS (last 5 years only)

1. **Wang C.** Unraveling the epigenome of the human malaria parasite *Plasmodium falciparum*. Oral Presentation, American Society of Tropical Medicine and Hygiene 68th Annual Meeting, National Harbor, MD. Nov 2019.

2. **Wang C.** From the first genome-sequences to the 4D nucleosome: Integrating fast-moving omics technologies to understand biology and human disease. Invited Oral Presentation, USF Genomics Forum, Genomic Program, University of South Florida, Tampa, FL. Nov 2018.
3. **Wang C.** Human malaria parasite genome is configured into linearly organized gene co-expression modules. Poster Presentation, Single Cell Genomics Symposium, Tampa, FL. May 2018.
4. **Wang C.** Harnessing the power of big data to decode the genomic landscape of the malaria parasite. Invited Oral Presentation, USF Genomics Symposium, Genomic Program, University of South Florida, Tampa, FL. May 2017.
5. **Wang C.** Lean and mean machines – using genomics and epigenomics to understand human malaria parasite genome regulation. Invited Oral Presentation, Global Health Seminar Series, University of South Florida, Tampa, FL. Nov 2016.
6. **Wang C.** Bridging epigenetic and genetic controls in malarial antigenic variation with evolutionarily conserved noncoding elements. Oral Presentation, American Society of Tropical Medicine and Hygiene 64th Annual Meeting, Philadelphia, PA. Oct 2015.

PUBLICATIONS

A. Peer-reviewed Journal Paper

(*indicates co-first author)

1. Si Y, Zeng W, Li N, **Wang C**, Siddiqui F, Zhang J, Pi L, He X, Zhao L, Wang S, Zhao H, Li X, Yang Q, Miao J, Yang Z, Cui, L. In Vitro susceptibility of Plasmodium falciparum isolates from the China–Myanmar border area to piperazine and association with candidate markers. *Antimicrob Agents Chemother.* 2021; (Accepted)
2. **Wang C**, Gibbons J, Adapa DR, Oberstaller J, Liao X, Zhang M, Adams JH, Jiang RHY. The human malaria parasite genome is configured into thousands of co-expressed linear regulatory units. *Journal of genetics and Genomics.* 2020; 47: 513-521
3. Gibbons J, Qin J, Malla P, Wang Z, Brashear A, **Wang C**, Miao J, Adams JH, Kim K, Jiang RHY, Cui L. Lineage-specific expansion of Plasmodium falciparum parasites with *pfhrp2* deletion in the Greater Mekong Subregion. *J Infect Dis.* 2020; 222: 1561-1569
4. Blomqvist K, Helmel M, **Wang C**, Absalon S, Labunska T, Rudlaff R, Adapa S, Jiang RHY, Steen H, Dvorin DJ. Influence of *Plasmodium falciparum* calcium-dependent protein kinase 5 (PfCDPK5) on the late schizont stage phosphoproteome. *mSphere.* 2020; 5, e00921-19
5. Yi H, Li H, Liang L, Wu Y, Zhang L, Qiu W, Jiang W, Yang F, Li Q, Yang Z, **Wang C**, Cui L, He Y. The glucose-6-phosphate dehydrogenase Mahidol variant protects against uncomplicated *Plasmodium vivax* infection and reduces disease severity in a Kachin population from northeast Myanmar. *Infect Genet Evol.* 2019; 75, e103980.
6. Li B, Liu R, **Wang C**, Ren C, Zhang S, Zhang F, Zhang J, Liu S, Wei Y, Liu W, Song B, Wu X. Impact of genetic and clinical factors on warfarin therapy in patients early after heart valve replacement surgery. *Eur J Clin Pharmacol.* 2019; 75, 1685-1693

7. Adapa SR, Taylor RA, **Wang C**, Thomson-Luque R, Johnson LR, Jiang RHY. *Plasmodium vivax* readiness to transmit: implication for malaria eradication. *BMC systems biology*. 2019; 13, 5.
8. Zhang M*, **Wang C***, Otto TD, Oberstaller J, Liao X, Adapa SR, Udenze K, Bronner IF, Casandra D, Mayho M, Brown J, Li S, Swanson J, Rayner JC, Jiang RHY, Adams JH. Uncovering the essential genes of the human malaria parasite *Plasmodium falciparum* by saturation mutagenesis. *Science*. 2018; 360, eaap7847.
9. Thomson-Luque R, **Wang C**, Ntumngia FB, Xu S, Szekeres K, Conway A, Adapa SR, Barnes SJ, Adams JH, Jiang RHY. In depth phenotypic characterization of reticulocyte maturation using mass cytometry. *Blood Cells Mol Dis*. 2018; 72, 22.
10. Brancucci NMB, Gerdt JP, **Wang C**, De Niz M, Philip N, Adapa SR, Zhang M, Hitz E, Niederwieser I, Boltryk SD, Laffitte MC, Clark MA, Grüring C, Ravel D, Blancke Soares A, Demas A, Bopp S, Rubio-Ruiz B, Conejo-Garcia A, Wirth DF, Gendaszewska-Darmach E, Duraisingh MT, Adams JH, Voss TS, Waters AP, Jiang RHY, Clardy J, Marti M. Lysophosphatidylcholine levels regulate stage differentiation in the human malaria parasite *Plasmodium falciparum*. *Cell*. 2017; 171, 1532.
11. **Wang C**, Adapa SR, Gibbons J, Sutton S, Jiang RHY. Punctuated chromatin states regulate *Plasmodium falciparum* antigenic variation at the intron and 2 kb upstream regions. *BMC Genomics*. 2016; 17, 652.
12. Thomas P, Sedillo J, Oberstaller J, Li S, Zhang M, Singh N, **Wang C**, Udenze K, Jiang RHY, Adams JH. Phenotypic screens identify parasite genetic factors associated with malarial fever response in *Plasmodium falciparum* piggyBac mutants. *mSphere*. 2016; 1, e00273.
13. Bronner IF, Otto TD, Zhang M, Udenze K, **Wang C**, Quail MA, Jiang RHY, Adams JH, Rayner JC. Quantitative Insertion-site Sequencing (QIseq) for high throughput phenotyping of transposon mutants. *Genome Res*. 2016; 26, 980.
14. Fang R*, **Wang C***, Skogerbo G, Zhang Z. Functional diversity of CTCFs is encoded in their binding motifs. *BMC Genomics*. 2015; 16, 649.
15. Li B, **Wang C**, Xi L, Wei Y, Duan G, Wu X. Qualitative and quantitative analysis of *Angelica sinensis* using near infrared spectroscopy and chemometrics. *Anal. Methods*. 2014; 6, 9691.
16. **Wang C**, Zhang MQ, Zhang Z. Computational identification of active enhancers in model organisms. *Genomics Proteomics Bioinformatics*. 2013; 11, 142.
17. **Wang C**, Xi L, Li S, Liu H, Yao X. A sequence-based computational model for the prediction of the solvent accessible surface area for alpha-helix and beta-barrel transmembrane residues. *J Comput Chem*. 2012; 33, 11.
18. **Wang C**, Li S, Xi L, Liu H, Yao X. Accurate prediction of the burial status of transmembrane residues of α -helix membrane protein by incorporating the structural and physicochemical features. *Amino Acids*. 2011; 40, 991.

19. Li S, Xi L, Li J, **Wang C**, Lei B, Shen Y, Liu H, Yao X, Li B. In silico Prediction of deleterious single amino acid polymorphisms from amino acid sequence. *J Comput Chem*. 2011; 32, 1211.
20. Liu H, Yao X, **Wang C**, Han J. In silico identification of the potential drug resistance sites over 2009 influenza A (H1N1) virus neuraminidase. *Mol Pharm*. 2010; 7, 894.
21. Li S, Xi L, **Wang C**, Li J, Lei B, Liu H, Yao X. A novel method for protein-ligand binding affinity prediction and the related descriptors exploration. *J Comput Chem*. 2009; 30, 900.

B. Abstracts and Proceedings

1. Zhang M, **Wang C**, Otto TD, Oberstaller J, Bronner JF, Li S, Udenze K, Mayho M, Huckle E, Quail MA, Rayner JC, Jiang RHY, Adams JH. Piggyback mutagenesis screening of thousands of *Plasmodium falciparum* genes reveals what a malaria parasite can't live without. *American Journal of Tropical Medicine and Hygiene*. 2017; 95: 390.
2. Zhang M, **Wang C**, Thomas P, Oberstaller J, Otto TD, Liao X, Li S, Udenze K, Adapa RS, Button-Simons K, Ferdig MT, Rayner JC, Jiang RHY, Adams JH. A large-scale genetic screen of *Plasmodium falciparum* identifies genotypy-phenotype mutations affecting tolerance to febrile temperatures. *American Journal of Tropical Medicine and Hygiene*. 2017; 97, 323.
3. Zhang M, **Wang C**, Oberstaller J, Otto TD, Adapa SR, Liao X, Swanson J, Li S, Udenze K, Rayner JC, Jiang RHY, Adams JH. Saturation-level piggyback mutagenesis screen of the *Plasmodium falciparum* genome defines gene important for invitro asexual blood stage growth. *American Journal of Tropical Medicine and Hygiene*. 2017; 97, 19.
4. Oberstaller J, Zhang M, **Wang C**, Otto TD, Liao X, Swanson J, Adapa SR, Udenze K, Bronner IF, Li S, Haines H, Rayner JC, Jiang RHY, Adams JH. Essential aspects of RNA metabolism for *P. falciparum* blood stage survival. *American Journal of Tropical Medicine and Hygiene*. 2017; 97, 625.
5. **Wang C**, Adapa SR, Sutton S, Jiang RHY. Bridging epigenetic and genetic controls in malaria antigenic variation with evolutionarily conserved noncoding elements. *American Journal of Tropical Medicine and Hygiene*. 2015; 93, 177.