Cheng Wang, Ph.D.

Jinan, China, chengwangsdu@outlook.com (86) 135-0641-0587

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MISSION

Explore the vast potential of small molecules and genomic signatures toward biomarker discovery and precision medicine.

RESEARCH INTEREST

Systems biology (*omics* study), metabolomics, lipidomics, computational drug discovery, machine learning, cancer/chronic disease prevention.

CURRENT POSITION

Shandong University, Shandong, China 06/2021-Present
Assistant Professor (Associate Research Scientist)

SELECTED RESEARCH PROJECTS

Enzymatic reaction link learning by variational graph autoencoders

- Developed a Variational Graph Autoencoders (VGAE) based framework to predict metabolite-protein interactions (MPI) in genome-scale heterogeneous enzymatic reaction networks across ten organisms.
- Incorporated molecular features of metabolites and proteins, as well as neighboring information in the MPI networks. The MPI-VGAE predictor achieved superior predictive performance compared to other machine learning methods.
- Applied the MPI-VGAE framework to reconstruct hundreds of metabolic pathways, functional enzymatic reaction networks, and a metabolite-metabolite interaction network, demonstrating the most robust performance across all scenarios.
- Implemented the MPI-VGAE framework to reconstruct disease-specific MPI networks based on disrupted metabolites and proteins in Alzheimer's disease and colorectal cancer, identifying numerous novel enzymatic reaction links.

Multi-omics integration for biomarker discovery in cardiovascular disease

- Performed metagenomic sequencing on fecal samples and untargeted metabolomics analysis on fecal, plasma, and urine samples from ischemic stroke patients and healthy volunteers.
- Conducted differential analysis to identify key microbiota and metabolites associated with ischemic stroke.
- Utilized Spearman's rank correlation and linear regression analyses to study the associations between microbiota and metabolites in various metabolic mixtures.

- Systematic association analysis between the gut microbiome and metabolomics revealed that fecal metabolites have the strongest association with the gut microbiome, followed by urine and plasma metabolites.

Accurate identification of lipids by combining NMR and MS

- Designed a new two-dimensional (2D) NMR metabolite database, "COLMAR Lipids," specifically curated for hydrophobic metabolites. This database currently contains 501 compounds with accurate experimental 2D 13C-1H chemical shift data measured in CDCl3.
- Applied nonuniform sampling in combination with pure shift spectroscopy to obtain 2D HSQC spectra with high spectral resolution along both 13C and 1H dimensions.
- Integrated the new 2D 13C-1H HSQC lipid database into COLMAR, enabling the unique identification of numerous lipids present in complex lipidomics mixtures, such as Caco-2 cell and lung tissue cell extracts.

Accurate and efficient determination of unknown metabolites in metabolomics by NMR-based cheminformatics approaches

- Developed the SUMMIT method for untargeted metabolite identification by combining ultrahigh-resolution Fourier transform ion cyclotron resonance mass spectrometry (FT-ICR MS) with 3D nuclear magnetic resonance (NMR).
- Extracted individual compound information from NMR spectra using a maximal clique algorithm and derived all possible metabolite candidates from FT-ICR MS data.
- Demonstrated the method's performance for untargeted analysis of both a model mixture and *E. coli* cell lysate using 2D/3D NMR experiments in combination with Fourier transform ion cyclotron resonance MS and MS/MS data.

PROFESSIONAL EXPERIENCE

Washington University in St. Louis, St. Louis, MO 06/2020-06/2021
Postdoctoral Researcher

Insight Data Science, San Francisco, CA 01/2020-05/2020
Health Data Science Fellow

The Ohio State University, Columbus, OH 05/2016-12/2019
Graduate Research Assistant

EDUCATION

The Ohio State University, Columbus, OH
Ph.D. Chemistry (Bioinformatics) 2014-2019
Advisor: Prof. Rafael Brüschweiler

Indiana University, Bloomington, IN
M.S. Data Science (Machine learning) 2017-2019
Advisor: Ying Ding

China University of Petroleum, Qingdao, China
B.S. Applied Chemistry (Cheminformatics) 2009-2013

RESEARCH FUNDING AND GRANTS

1. **PI, 300,000 RMB, National Natural Science Foundation of China** 2024-2026
   "Research on Metabolomic Pseudo-mass Spectrometry Imaging Feature Screening Method Based on Variational Self-coding Nonlinear Dimensionality Reduction" (Active)
2. **PI, 150,000 RMB, Natural Science Foundation of Shandong Province** 2023-2025
   "Research on Structural Identification of Metabolites Based on Density Functional Theory and Deep Learning" (Active)
3. **PI, 500,000 RMB, Future Young Schoar of Shandong University** 2022-2026
   "Integrative Multi-omics Analysis by Deep Learning" (Active)
4. **Co-PI, 200,000 RMB, "2030 Science and Technology Innovation - 'Brain Science and Neuromimetic Research' Major Project"** 2022-2026
   "Alzheimer's Disease and Other Dementia Clinical Cohort Study"(Active)
5. **PI, 150,000 RMB, Shandong First-Medical University** 2022-2024
   "Investigation of Gastric Biomarkers by Mass Spectrometry Imaging" (Completed)

PUBLICATIONS

Google scholar: https://scholar.google.com/citations?user=UAZhchQAAAAJ&hl=en

First/Corresponding author papers

1. Shi, Y.,+ Xu, B.,+ Wang, Z.,+ Chen, Q., Chai, J. *, & **Wang, C***. PhenoMultiOmics: An enzymatic reaction inferred multi-omics network visualization web server. *Bioinformatics*, 2024 (Accepted)
2. **Wang, C.**,+* Yuan, C.,+ Wang, Y.,+ Shi, Y., Zhang, T. and Patti, G.J.,* 2024. Prediction of Collision Cross-Section Values by Multimodal Graph Attention Network for Accurate Identification of Small Molecules. *Journal of Chemical Information and Modeling* (Cover Article).
3. **Wang, C.**, Yuan, C., Wang, Y., Chen, R., Shi, Y., Zhang, T., Xue, F., Patti, G.J.,* Wei, L.* and Hou, Q.,* 2023. MPI-VGAE: protein–metabolite enzymatic reaction link learning by variational graph autoencoders. *Briefings in Bioinformatics*, p.bbad189.
4. **Wang, C.**, Timári, I., Zhang, B., Li, D.W., Leggett, A., Amer, A.O., Bruschweiler-Li, L., Kopec, R.E. and Brüschweiler, R.,* 2020. COLMAR Lipids Web Server and Ultrahigh-Resolution Methods for Two-Dimensional Nuclear Magnetic Resonance-and Mass Spectrometry-Based Lipidomics. *Journal of proteome research*, *19*(4), pp.1674-1683.
5. **Wang, C.**, Zhang, B., Timári, I., Somogyi, Á., Li, D.W., Adcox, H.E., Gunn, J.S., Bruschweiler-Li, L. and Brüschweiler, R.,* 2019. Accurate and efficient determination of unknown metabolites in

metabolomics by NMR-based molecular motif identification. *Analytical chemistry*, *91*(24), pp.15686-15693.

6. **Wang, C.**,[+] He, L.,[+] Li, D.W.,[+] Bruschweiler-Li, L., Marshall, A.G. * and Brüschweiler, R.,* 2017. Accurate identification of unknown and known metabolic mixture components by combining 3D NMR with fourier transform ion cyclotron resonance tandem mass spectrometry. *Journal of proteome research*, *16*(10), pp.3774-3786.
7. Zhao, L.,[+] **Wang, C.**,[+] Peng, S., Zhu, X., Zhang, Z., Zhao, Y., Zhang, J., Zhao, G., Zhang, T.,* Heng, X.* and Zhang, L.,* 2022. Pivotal interplays between fecal metabolome and gut microbiome reveal functional signatures in cerebral ischemic stroke. *Journal of Translational Medicine*, *20*(1), pp.1-15.
8. Wang, B,[+] **Wang, C,**[+] and Hanks, A.,* 2024. Where Are They and How Do They Perform? Measuring Long-term Career Outcomes of Public Health Doctoral Recipients, *Journal of Public Health*, fdae031.
9. Xu B, Shi Y, Yuan C, Wang Z, Chen Q, **Wang C***, Chai J.* Integrated gene-metabolite association network analysis reveals key metabolic pathways in gastric adenocarcinoma. *Heliyon*. 2024 Sep 15;10(17).
10. Che J, Zhao Y, Gu B, Li S, Li Y, Pan K, Sun T, Han X, Lv J, Zhang S, Fan B., Li, C., **Wang,C.,** * Wang, J. * and Zhang, T., * 2023. Untargeted serum metabolomics reveals potential biomarkers and metabolic pathways associated with the progression of gastroesophageal cancer. *BMC cancer*. Dec 15;23(1):1238.
11. Chen, R., Li, X., Yang, Y., Song, X., **Wang, C.*** and Qiao, D.,* 2022. Prediction of protein-protein interaction sites in intrinsically disordered proteins. *Frontiers in Molecular Biosciences*, *9*.
12. Leggett, A.,[+] **Wang, C.**,[+] Li, D.W., Somogyi, A., Bruschweiler-Li, L. and Brüschweiler, R.,* 2019. Identification of unknown metabolomics mixture compounds by combining NMR, MS, and cheminformatics. *Methods in enzymology* (Vol. 615, pp. 407-422). Academic Press.

Co-author papers

13. Lv, J., Pan, C., Cai, Y., Han, X., **Wang, C.**, Ma, J., Pang, J., Xu, F., Wu, S., Kou, T. and Ren, F., 2024. Plasma metabolomics reveals the shared and distinct metabolic disturbances associated with cardiovascular events in coronary artery disease. *Nature Communications*, 15(1), p.5729.
14. Li, J., Lv, J., Yu, F., Zhang, Y., Wang, Y., Yan, L., Xiao, Q., Li, Q., **Wang, C.**, Wang, X. and Hou, Y., 2024. Temporal changes in plasma metabolic signatures to predict immune response of antiretroviral therapy among people living with HIV. *Journal of Medical Virology*, 96(8), p.e29798.
15. Li, S., Che, J., Gu, B., Li, Y., Han, X., Sun, T., Pan, K., Lv, J., Zhang, S., **Wang, C.** and Zhang, T., 2024. Metabolites, Healthy Lifestyle, and Polygenic Risk Score Associated with Upper Gastrointestinal Cancer: Findings from the UK Biobank Study. *Journal of Proteome Research*, 23(5), pp.1679-1688.
16. Gu, B., Zhang, S., Fan, Z., Che, J., Li, S., Li, Y., Pan, K., Lv, J., **Wang, C.**, Zhang, T. and Wang, J., 2023. Prognostic model construction and immune microenvironment analysis of esophageal cancer based on gene expression data and microRNA target genes. *Translational Cancer Research*, 12(5), p.1165.
17. Yuan, C.,* **Wang, C.**, Zhu, K., Li, S. and Miao, Z.,* 2022. Measles epidemiology and viral nucleoprotein gene evolution in Shandong Province, China. *Journal of Medical Virology*, *94*(10), pp.4926-4933.
18. Wang, Y., Stancliffe, E., Fowle-Grider, R., Wang, R., **Wang, C.,** Schwaiger-Haber, M., Shriver, L.P. and Patti, G.J.,* 2022. Saturation of the mitochondrial NADH shuttles drives aerobic glycolysis in proliferating cells. *Molecular cell*, *82*(17), pp.3270-3283.

19. Hansen, A.L., Kupče, E., Li, D.W., Bruschweiler-Li, L., **Wang, C.** and Brüschweiler, R.,* 2021. 2D NMR-based metabolomics with HSQC/TOCSY NOAH supersequences. *Analytical Chemistry*, *93*(15), pp.6112-6119.
20. Knobloch, T.J., Ryan, N.M., Bruschweiler-Li, L., **Wang, C.,** Bernier, M.C., Somogyi, A., Yan, P.S., Cooperstone, J.L., Mo, X., Brüschweiler, R.P. and Weghorst, C.M.,* 2019. Metabolic regulation of glycolysis and AMP activated protein kinase pathways during black raspberry-mediated oral cancer chemoprevention. *Metabolites*, *9*(7), p.140.
21. Timári, I., **Wang, C.,** Hansen, A.L., Costa dos Santos, G., Yoon, S.O., Bruschweiler-Li, L. and Brüschweiler, R.,* 2019. Real-time pure shift HSQC NMR for untargeted metabolomics. *Analytical chemistry*, *91*(3), pp.2304-2311.
22. Yuan, J., Zhang, B., **Wang, C.** and Brüschweiler, R.,* 2018. Carbohydrate background removal in metabolomics samples. *Analytical chemistry*, *90*(24), pp.14100-14104.
23. Hansen, A.L., Li, D., **Wang, C.** and Brüschweiler, R.,* 2017. Absolute Minimal Sampling of Homonuclear 2D NMR TOCSY Spectra for High-Throughput Applications of Complex Mixtures. *Angewandte Chemie*, *129*(28), pp.8261-8264.
24. Li, D.W., **Wang, C.** and Brüschweiler, R.,* 2017. Maximal clique method for the automated analysis of NMR TOCSY spectra of complex mixtures. *Journal of biomolecular NMR*, *68*(3), pp.195-202.

CONFERENCES AND PRESENTATIONS

1. Oral talk, 18th Annual Conference of the Metabolomics Society, Online, 06/2021
   "Protein–metabolite Enzymatic Reaction Link Learning by Graph Neural Network"
2. Oral talk, 2nd Annual MANA Conference, Seattle, WA, 09/2020
   "COLMAR Lipids Web Server and Ultrahigh-Resolution Methods for Two-Dimensional Nuclear Magnetic Resonance-and Mass Spectrometry-Based Lipidomics"
3. Oral talk, 3rd Gateway NMR Conference, Pittsburgh, PA, 11/2018
   "Accurate Identification of Known and Unknown Metabolites by Multidimensional NMR and Customized Metabolite Database"
4. Oral talk, 14th Annual Conference of the Metabolomics Society, Seattle, WA, 06/2018
   "Accurate Identification of Known and Unknown Metabolites by Multidimensional NMR and Customized Metabolite Database"
5. Oral talk, 2nd Annual Ohio Mass Spectrometry and Metabolomics Symposium, 05/2018
   "Accurate Identification of Known and Unknown Metabolites in Gallbladder Bile by Multidimensional NMR and Customized Metabolite Database"

ACADEMIC SERVICE AND TEACHING EXPERIENCE

Guest editor: *Metabolites* (IF:5.581), *Journal of Personalized Medicine* (IF:3.508)
Reviewer of journals: *Nature machine intelligence, Briefings in bioinformatics, eLife, Metabolites, Nutrients, IJMS, Applied Sciences, Journal of personalized medicine*, etc.

Shandong University, Jinan, China, 06/2021-present

- Instructor of data science course to biomedical data science major students.

- Lead courses including big data mining, data structure, machine learning.

The Ohio State University, Columbus, OH

Graduate Teaching Assistant, Physical Chemistry 08/2015-05/2016

- Instructor of recitation for physical chemistry course to chemical engineering major students.
- Taught basics of quantum mechanics, calculus, linear algebra and fundamentals of probability.

OTHER SKILLS

Language: Proficient in English, oral, writing and reading, native speaker of Chinese.

Programming Skills: Proficient in Python, Pytorch, Keras, Tensorflow, Cloud based web application deployment.

Data Analysis Skills: Data visualization, Bayesian inference, machine learning, and deep learning modeling.

HONORS AND AWARDS

Food for Health Graduate Student Fellowship, The Ohio State University 2017-2018

Graduate Student Fellowship for Data Science Program, Indiana University 2017-2019

Student Travel Award, 14th International Conference of Metabolomics Society 06/2018