Xiaotao Shen

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Stanford University

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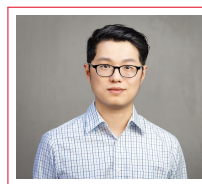+1 571 267 9283
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Research Interests

- Mass Spectrometry Data Processing Algorithms and Software Development
- Multi-omics Data Integration Methods Development
- Wearable Data and Precision Medicine
- Aging and Neurodegenerative Diseases
- Human Pregnancy-Related Disease Diagnosis and Mechanism Research
- Environmental Health

Education & Research Experiences

2019/04-Present **Postdoctoral Research Fellow**, *Stanford University*, Palo Alto, USA.

2013/09-2018/12 **Ph.D.**, *University of Chinese Academy of Sciences*, Shanghai, China.

2009/09-2013/07 **B.S.**, *Inner Mongolia University*, Hohhot, China.

Honors & Awards

2023	Young Investigator Award. The 3rd Chinese American Society For Mass Spectrometry Conference
2023	SPORR 2023 Rigor and Reproducibility Award. Stanford Program on Research Rigor and Reproducibility
2021	Winner Selected by the Event Committee. Exposome Data Challenge Event
2018	Student Travel Award for Oral Presentation. The International Metabolomics Society
2018	International Conference Travel Award. The Metabolites Journal
2017	China National Scholarship. Ministry of Education of the People's Republic of China
2017	Award for Outstanding Youth Report. The 3rd China MS Analysis Conference
2016	Merit Student. University of Chinese Academy of Sciences
2016	Award for Outstanding Youth Report. The 34th China MS Society Conference
2013	Inner Mongolia Outstanding Graduate. Inner Mongolia Autonomous Region
2011	National Encouragement Scholarship. Inner Mongolia University

Presentations

Oral Presentations

2023/09 **Nonlinear Dynamic Changes During Human Aging Revealed in Multi-omics Profiles**, *Bay Area Metabolism Meeting (BAMM) 2023*, Palo Alto, USA.

2023/08   **Multi-omics Microsampling for The Profiling of Lifestyle-Associate Changes in Health**, *The 3rd Chinese American Society for Mass Spectrometry Conference*, Virtual meeting.

2023/06   **Multi-omics Microsampling for The Profiling of Lifestyle-Associate Changes in Health**, *The 71th American Society for Mass Spectrometry Conference*, Houston, USA.

2023/04   **Remote and Flexible Microsampling Multi-omics for Precision Medicine**, *iPOP summit*, Palo Alto, USA.

2023/03   **Bioinformatics Algorithm Development for Mass Spectrometry Data and its Application to Precision Medicine. Invited presentation**, *Altos Labs*, Redwood City, USA.

2023/02   **Multi-omics Microsampling for The Profiling of Lifestyle-Associate Changes in Health**, *Invited presentation*, Wuhan, China.

2023/02   **Multi-omics Microsampling for The Profiling of Lifestyle-Associate Changes in Health**, *Stanford Postdoc Symposium*, Palo Alto, USA.

2022/11   **Bioinformatics Method Development for Mass Spectrometry and its Application to Precision Medicine**, *Stanford CVI Early Career Research Roundtable*, Palo Alto, USA.

2022/10   **Deep Learning-based Pseudo-Mass Spectrometry Imaging Analysis for Precision Medicine**, *CASMS Virtual Conference*, Virtual meeting.

2022/08   **TidyMass: An Object-oriented Reproducible Analysis Framework for LC-MS Data**, *ACS Fall 2022*, Virtual meeting.

2021/11   **metID: an R Package for Automatable Compound Annotation for LC-MS-based Data**, *The 69th American Society for Mass Spectrometry Conference*, Philadelphia, USA.

2021/04   **Decoding Links Between the Exposome and Health Outcomes by Multi-omics Analysis**, *Exposome Data Challenge Event*, Virtual meeting.

2018/06   **Metabolic Reaction Network-based Recursive Metabolite Identification for Untargeted Metabolomics**, *The 14th International Conference of the Metabolomics Society*, Seattle, USA.

2017/12   **Assessment of the Response to Neoadjuvant Chemo-Radiation in Rectal Cancer Patients based on a Metabolomics Approach**, *The 3rd China Mass Spectrometry Analysis Conference*, Xiamen, China.

2016/09 **Normalization and Integration of Large-Scale Mass Spectrometry-based Metabolomics Data Using Support Vector Regression**, *The 34th China Mass Spectrometry Society Conference*, Xining, China.

2016/06 **Normalization and Integration of Large-Scale MS-based Metabolomics Data Using Support Vector Regression**, *The 64th American Society for Mass Spectrometry Conference*, San Antonio, USA.

Poster Presentations————————————————————————

2023/09 **Nonlinear Dynamic Changes During Human Aging Revealed in Multi-omics Profiles**, *Stanford Bio-X Interdisciplinary Initiatives Seed Grants Program Symposium 2023*, Stanford, USA.

2023/05 **TidyMass: An Object-oriented Reproducible Analysis Framework for LC-MS Data**, *Stanford Data Science Conference*, Palo Alto, USA.

2022/09 **Deep Learning-based Pseudo-Mass Spectrometry Imaging Analysis for Precision Medicine**, *Stanford Genetics Retreat 2022*, Monterey, USA.

2022/09 **Deep Learning-based Pseudo-Mass Spectrometry Imaging Analysis for Precision Medicine**, *Bay Area Metabolism Meeting (BAMM) 2022*, Palo Alto, USA.

2022/06 **TidyMass An Object-oriented Reproducible Analysis Framework for LC-MS Data**, *The 70th American Society for Mass Spectrometry Conference*, Minneapolis, USA.

2022/05 **Longitudinal Interactions Between Levels of Serum Cytokine and the Microbiome from Four Body Sites**, *IMMUNOLOGY2022*, Portland, USA.

2021/09 **TidyMass: An Object-oriented Reproducible Analysis Framework for LC-MS Data**, *Stanford Genetics Retreat 2021*, Palo Alto, USA.

2020/06 **Longitudinal Urine Metabolic Profiling and Gestational Age Prediction in Pregnancy**, *The 17th International Conference of the Metabolomics Society*, Virtual meeting.

2017/06 **Metabolic Reaction Network based Metabolite Annotation in Untargeted Metabolomics**, *The 13th International Conference of the Metabolomics Society*, Brisbane, Austria.

Teaching Experiences

2022/09 LC-MS Data Processing and Analysis Using R language. Biotree Company

2022/03 R Language for Reproducible Data Analysis. SCPA

2019/08- Stanford School of Medicine Intern. Stanford University
Present

2014/09- Chinese Academy of Sciences. Mass Spectrometry Analysis
2014/12

Journal Referee

• Nature Biotechnology • Nature Communications • Briefing in Bioinformatics • Bioinformatics • GigaScience • PLOS one • Phytochemistry • Genomics, Proteomics&Bioinformatics • Communications Chemistry • Communications Biology • Frontiers Molecular Biosciences • iMeta • Proteomics

Volunteering

2023/08-Present	Member of Editorial Board. pj Women's Health
2023/02-Present	Member of Youth Editorial Board. Phenomics
2023/01-Present	Member of Youth Editorial Board. Brain-X
2022/07-Present	Member of Youth Editorial Board. iMeta
2021/07-2022/07	Co-Chair. Stanford Chinese Postdoctoral Association
2020/01-2021/12	Organizer. Stanford Chinese Postdoctoral Oral Presentation Improvement
2019/04-2022/07	Member. Stanford Chinese Postdoctoral Association

Patents

1. Snyder, M., Kellogg, R., & Shen, X. (2022). *Multi-omic sample analysis methods*. Nature Medicine.
2. Liang, L., Snyder, M., Shen, X., & Chen, S. (2021). *Methods for evaluating gestational progress and applications thereof*. Nature Medicine.
3. Shen, X., & Zhu, Z. (2019). *A method for metabolite annotation and dysregulated pathway analysis*. Nature Medicine.

Publications

First/Co-first Author Publications

1. Shen, X., Kellogg, R., Panyard, D. J., Bararpour, N., Castillo, K. E., Lee-McMullen, B., Delfarah, A., Ubellacker, J., Ahadi, S., Rosenberg-Hasson, Y., Ganz, A., Contrepois, K., Michael, B., Simms, I., Wang, C., Hornburg, D., & Snyder, M. P. (2023). Multi-omics microsampling for the profiling of lifestyle-associated changes in health. *Nature Biomedical Engineering*, 1–19. https://doi.org/10.1038/s41551-022-00999-8
2. Shen, X., Shao, W., Wang, C., Liang, L., Chen, S., Zhang, S., Rusu, M., & Snyder, M. P. (2022). Deep learning-based pseudo-mass spectrometry imaging analysis for precision medicine. *Briefings in Bioinformatics*, 23(5), bbac331. https://doi.org/10.1093/bib/bbac331
3. Shen, X., Wang, C., & Snyder, M. P. (2022). massDatabase: Utilities for the operation of the public compound and pathway database. *Bioinformatics*, 38(19), 4650–4651. https://doi.org/10.1093/bioinformatics/btac546
4. Shen, X., Yan, H., Wang, C., Gao, P., Johnson, C. H., & Snyder, M. P. (2022). TidyMass an object-oriented reproducible analysis framework for LCMS data. *Nature Communications*, 13(1), 4365. https://doi.org/10.1038/s41467-022-32155-w

5. Gao, P., Shen, X., Zhang, X., Jiang, C., Zhang, S., Zhou, X., Schüssler-Fiorenza Rose, S. M., & Snyder, M. (2022). Precision environmental health monitoring by longitudinal exposome and multi-omics profiling. *Genome Research*, *32*(6), 1199–1214. `https://doi.org/10.1101/gr.276521.121`

6. Shen, X., Wu, S., Liang, L., Chen, S., Contrepois, K., Zhu, Z.-J., & Snyder, M. (2022). metID: An R package for automatable compound annotation for LC-MS-based data. *Bioinformatics*, *38*(2), 568–569. `https://doi.org/10.1093/bioinformatics/btab583`

7. Shen, X., Wang, R., Xiong, X., Yin, Y., Cai, Y., Ma, Z., Liu, N., & Zhu, Z.-J. (2019). Metabolic reaction network-based recursive metabolite annotation for untargeted metabolomics. *Nature Communications*, *10*(1), 1516. `https://doi.org/10.1038/s41467-019-09550-x`

8. Shen, X., & Zhu, Z.-J. (2019). MetFlow: An interactive and integrated workflow for metabolomics data cleaning and differential metabolite discovery. *Bioinformatics*, *35*(16), 2870–2872. `https://doi.org/10.1093/bioinformatics/bty1066`

9. Jia, H., Shen, X., Guan, Y., Xu, M., Tu, J., Mo, M., Xie, L., Yuan, J., Zhang, Z., Cai, S., Zhu, J., & Zhu, Z. (2018). Predicting the pathological response to neoadjuvant chemoradiation using untargeted metabolomics in locally advanced rectal cancer. *Radiotherapy and Oncology*, *128*(3), 548–556. `https://doi.org/10.1016/j.radonc.2018.06.022`

10. Wang, J., Zhang, T., Shen, X., Liu, J., Zhao, D., Sun, Y., Wang, L., Liu, Y., Gong, X., Liu, Y., Zhu, Z.-J., & Xue, F. (2016). Serum metabolomics for early diagnosis of esophageal squamous cell carcinoma by UHPLC-QTOF/MS. *Metabolomics*, *12*(7), 116. `https://doi.org/10.1007/s11306-016-1050-5`

11. Shen, X., Gong, X., Cai, Y., Guo, Y., Tu, J., Li, H., Zhang, T., Wang, J., Xue, F., & Zhu, Z.-J. (2016). Normalization and integration of large-scale metabolomics data using support vector regression. *Metabolomics*, *12*(5), 89. `https://doi.org/10.1007/s11306-016-1026-5`

Collaborative Publications——————————————————————————

1. Jain, S., Pei, L., Spraggins, J. M., Angelo, M., Carson, J. P., Gehlenborg, N., Ginty, F., Gonçalves, J. P., Hagood, J. S., Hickey, J. W., Kelleher, N. L., Laurent, L. C., Lin, S., Lin, Y., Liu, H., Naba, A., Nakayasu, E. S., Qian, W.-J., Radtke, A., ... Snyder, M. P. (2023). Advances and prospects for the Human BioMolecular Atlas Program (HuBMAP). *Nature Cell Biology*, *25*(8), 1089–1100. `https://doi.org/10.1038/s41556-023-01194-w`

2. Wei, W., Riley, N. M., Lyu, X., Shen, X., Guo, J., Raun, S. H., Zhao, M., Moya-Garzon, M. D., Basu, H., Sheng-Hwa Tung, A., Li, V. L., Huang, W., Wiggenhorn, A. L., Svensson, K. J., Snyder, M. P., Bertozzi, C. R., & Long, J. Z. (2023). Organism-wide, cell-type-specific secretome mapping of exercise training in mice. *Cell Metabolism*, *35*(7), 1261–1279.e11. `https://doi.org/10.1016/j.cmet.2023.04.011`

3. Maitre, L., Guimbaud, J.-B., Warembourg, C., Güil-Oumrait, N., Petrone, P. M., Chadeau-Hyam, M., Vrijheid, M., Basagaña, X., & Gonzalez, J. R. (2022). State-of-the-art methods for exposure-health studies: Results from the exposome data challenge event. *Environment International*, *168*, 107422. `https://doi.org/10.1016/j.envint.2022.107422`

4. Zhang, S., Cooper-Knock, J., Weimer, A. K., Shi, M., Kozhaya, L., Unutmaz, D., Harvey, C., Julian, T. H., Furini, S., Frullanti, E., Fava, F., Renieri, A., Gao, P., Shen, X., Timpanaro, I. S., Kenna, K. P., Baillie, J. K., Davis, M. M., Tsao, P. S., & Snyder, M. P. (2022). Multiomic analysis reveals cell-type-specific molecular determinants of COVID-19 severity. *Cell Systems*, *13*(8), 598–614.e6. `https://doi.org/10.1016/j.cels.2022.05.007`

5. Lv, J., Wang, J., Shen, X., Liu, J., Zhao, D., Wei, M., Li, X., Fan, B., Sun, Y., Xue, F., Zhu, Z.-J., & Zhang, T. (2021). A serum metabolomics analysis reveals a panel of screening metabolic biomarkers for esophageal squamous cell carcinoma. *Clinical and Translational Medicine*, *11*(5), e419. `https://doi.org/10.1002/ctm2.419`

6. Wei, M., Zhao, L., Lv, J., Li, X., Zhou, G., Fan, B., Shen, X., Zhao, D., Xue, F., Wang, J., & Zhang, T. (2021). The mediation effect of serum metabolites on the relationship between long-term smoking exposure and esophageal squamous cell carcinoma. *BMC Cancer*, *21*(1), 415. `https://doi.org/10.1186/s12885-021-08151-6`

7. Li, X., Zhao, L., Wei, M., Lv, J., Sun, Y., Shen, X., Zhao, D., Xue, F., Zhang, T., & Wang, J. (2021). Serum metabolomics analysis for the progression of esophageal squamous cell carcinoma. *Journal of Cancer*, *12*(11), 3190. `https://doi.org/10.7150/jca.54429`

8. Liang, L., Rasmussen, M.-L. H., Piening, B., Shen, X., Chen, S., Röst, H., Snyder, J. K., Tibshirani, R., Skotte, L., Lee, N. Cy., Contrepois, K., Feenstra, B., Zackriah, H., Snyder, M., & Melbye, M. (2020). Metabolic Dynamics and Prediction of Gestational Age and Time to Delivery in Pregnant Women. *Cell*, *181*(7), 1680–1692.e15. `https://doi.org/10.1016/j.cell.2020.05.002`

9. Wang, Z., Cui, B., Zhang, F., Yang, Y., Shen, X., Li, Z., Zhao, W., Zhang, Y., Deng, K., Rong, Z., Yang, K., Yu, X., Li, K., Han, P., & Zhu, Z.-J. (2019). Development of a Correlative Strategy To Discover Colorectal Tumor Tissue Derived Metabolite Biomarkers in Plasma Using Untargeted Metabolomics. *Analytical Chemistry*, *91*(3), 2401–2408. `https://doi.org/10.1021/acs.analchem.8b05177`

10. Zhou, Z., Shen, X., Chen, X., Tu, J., Xiong, X., & Zhu, Z.-J. (2019). LipidIMMS Analyzer: Integrating multi-dimensional information to support lipid identification in ion mobilitymass spectrometry based lipidomics. *Bioinformatics*, *35*(4), 698–700. `https://doi.org/10.1093/bioinformatics/bty661`

11. Zhou, Z., Tu, J., Xiong, X., Shen, X., & Zhu, Z.-J. (2017). LipidCCS: Prediction of Collision Cross-Section Values for Lipids with High Precision To Support Ion MobilityMass Spectrometry-Based Lipidomics. *Analytical Chemistry*, *89*(17), 9559–9566. `https://doi.org/10.1021/acs.analchem.7b02625`

12. Zhou, Z., Shen, X., Tu, J., & Zhu, Z.-J. (2016). Large-Scale Prediction of Collision Cross-Section Values for Metabolites in Ion Mobility-Mass Spectrometry. *Analytical Chemistry*, *88*(22), 11084–11091. `https://doi.org/10.1021/acs.analchem.6b03091`

Submitted Publications————————————————

1. Shen, X., Wang, C., Zhou, X., Zhou, W., Hornburg, D., Wu, S., & Snyder, M. (2023). *Nonlinear dynamic changes during human aging revealed in multi-omics profiles*. Nature Medicine.

2. Shen, X., & Snyder, M. P. (2023). *Microbiomedataset: A tidyverse-style framework for organizing and processing microbiome data*. bioRxiv. `https://doi.org/10.1101/2023.09.17.558096`

3. Zhou, X., Shen, X., Johnson, J., Spakowicz, D., Agnello, M., Zhou, W., Avina, M., Honkala, A., Chleilat, F., Chen, S., Cha, K., Leopold, S., Zhu, C., Chen, L., Lyu, L., Hornburg, D., Wu, S., Zhang, X., Jiang, C., . . . Snyder, M. (2023). *Longitudinal profiling of the microbiome at four body sites reveals core stability and individualized dynamics during health and disease*. Cell.

4. Ding, D. Y., Shen, X., Snyder, M., & Tibshirani, R. (2023). *Semi-supervised Cooperative Learning for Multiomics Data Fusion*. arXiv. `https://doi.org/10.48550/arXiv.2308.01458`

5. Chen, S., Shen, X., Liang, L., Avina, M., Zackriah, H., Jelliffe-Pawlowski, L., Rand, L., & Snyder, M. (2022). *Longitudinal Urine Metabolic Profiling and Gestational Age Prediction in Pregnancy*. bioRxiv. `https://doi.org/10.1101/2022.07.10.499478`

6. Chen, S., Wang, G., Shen, X., Hornburg, D., Rego, S., Hoffman, R., Nevins, S., Cheng, X., & Snyder, M. (2021). *Integration and comparison of multi-omics profiles of NGLY1 deficiency plasma and cellular models to identify clinically relevant molecular phenotypes*. bioRxiv. `https://doi.org/10.1101/2021.05.28.446235`