

Xiaotao Shen, Ph.D.

Postdoctoral Research Fellow, [Prof. Michael Snyder's Lab](#), Department of Genetics, Stanford University

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🔬 Research Interests

- > Mass Spectrometry Data Processing Algorithms and Software Development.
- > Multi-omics Data Integration Methods Development.
- > Precision Exposome and Multi-omics Integration for Healthcare.
- > Multi-omics Profiling for Human Pregnancy Related Disease Diagnosis and Mechanism Research.
- > Aging and Neurodegenerative Diseases.
- > Microbiome Data Processing.
- > Wearable Data and Precision Medicine.

🎓 Education & Research Experiences

- > **Postdoctoral Research Fellow** 2019/4–present, **Stanford University**
(Advisor: [Prof. Michael Snyder](#))
- > **Research Scientist** 2019/1–2019/3, **Chinese Academy of Sciences**
(Advisor: [Prof. Zheng-Jiang Zhu](#))
- > **Ph.D.** 2013/8–2018/12, **Chinese Academy of Sciences**
(Advisor: [Prof. Zheng-Jiang Zhu](#))
- > **B.S.** 2009/9–2013/6, **Inner Mongolia University**

🏆 Honors & Awards

- > Winner Selected by the Event Committee **Exposome Data Challenge Event (2021)**
- > Student Travel Award for Oral Presentation **The International Metabolomics Society (2018)**
- > International Conference Travel Award **The Metabolites Journal (2018)**
- > 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 (2017)**
- > Merit Student **University of Chinese Academy of Sciences (2016)**
- > Award for Outstanding Youth Report **The 34th China MS Society Conference (2016)**
- > Inner Mongolia Outstanding Graduate **Inner Mongolia Autonomous Region (2013)**
- > National Encouragement Scholarship **Inner Mongolia University (2011)**

📄 First/Co-first Author Publications

+: Co-first Author. *: Co-Corresponding Author

- > [X. Shen⁺⁺](#), C. Wang⁺, M.P. Snyder*, massDatabase: Utilities for the Operation of the Public Compound and Pathway Database, *Bioinformatics*, 2022, btac546. [🔗](#)
- > [X. Shen⁺](#), W. Shao⁺, C. Wang⁺, L. Liang, S. Chen, S. Zhang, M. Rusu*, M.P. Snyder*, Deep Learning-based Pseudo-Mass Spectrometry Imaging Analysis for Precision Medicine, *Briefing in Bioinformatics*, 2022, bbac331. [🔗](#)
- > [X. Shen⁺](#), H. Yan⁺, C. Wang⁺, P. Gao, C.H. Johnson*, M.P. Snyder*, TidyMass an Object-oriented Reproducible Analysis Framework for LC-MS Data, *Nature Communications*, 2022, 4365. [🔗](#)
- > P. Gao⁺, [X. Shen⁺](#), X. Zhang, C. Jiang, M. P. Snyder*, Precision Environmental Health Monitoring by Longitudinal Exposome and Multi-omics Profiling, *Genome Research*, 2022, 32, 1199-1214. [🔗](#)
- > [X. Shen⁺](#), S. Wu⁺, L. Liang, S. Chen, K. Contrepois, Z.-J. Zhu* and M.J. Snyder*, metID: an R Package for Automatable Compound Annotation for LC-MS-based Data, *Bioinformatics*, 2021, 1, 1-2. [🔗](#)

- > **X. Shen**, R. Wang, X. Xiong, Y. Yin, Y. Cai, J. Ma, N. Liu, Z.-J. Zhu*, Large-scale Metabolite Identification for Untargeted Metabolomics Using Metabolic Reaction Network, *Nature Communications*, 2019, 10:1516. [↗](#)
- > **X. Shen** and Z.-J. Zhu*, MetFlow: An Interactive and Integrated Workflow For Metabolomics Data Cleaning and Differential Metabolite Discovery, *Bioinformatics*, 2019, 35, 16. [↗](#)
- > H. Jia⁺, **X. Shen**⁺, Y. Guan, M. Xu, M. Mo, J. Zhu* and Z.-J. Zhu*, Assessment of The Response to Neoadjuvant Chemo-Radiation in Rectal Cancer Patients based on A Metabolomics Approach, *Radiotherapy and Oncology*, 2018, 128, 548-556. [↗](#)
- > J. Wang⁺, T. Zhang⁺, **X. Shen**⁺, J. Liu, D. Zhao, Y. Sun, L. Wang, Y. Liu, X. Gong, Y. Liu, Z.-J. Zhu*, F. Xue*, Serum Metabolomics for Early Diagnosis of Esophageal Squamous Cell Carcinoma by UHPLC-QTOF/MS, *Metabolomics*, 2016, 12: 116. [↗](#)
- > **X. Shen**, X. Gong, Y. Cai, Y. Guo, J. Tu, T. Zhang, J. Wang, F. Xue, Z.-J. Zhu*, Normalization and Integration of Large-Scale Metabolomics Data Using Support Vector Regression, *Metabolomics*, 2016, 12: 89. [↗](#)

■ Collaborative Publications

- > M. Wei, L. Zhao, J. Lv, X. Li, G. Zhou, B. Fan, **X. Shen**, D. Zhao, F. Xue, J. Wang, T. Zhang, The Mediation Effect of Serum Metabolites On The Relationship Between Long-Term Smoking Exposure and Esophageal Squamous Cell Carcinoma, *BMC cancer*, 21, 415. [↗](#)
- > J. Lv, J. Wang, **X. Shen**, J. Liu, D. Zhao, X. Li, B. Fan, Y. Sun, F. Xue, Z.-J. Zhu, T. Zhang, A Serum Metabolomics Analysis Reveals A Panel of Screening Metabolic Biomarkers for Esophageal Squamous Cell Carcinoma, *Clinical and Translational Medicine*, 2021, 11, 5. [↗](#)
- > X. Li, L. Zhao, M. Wei, J. Lv, Y. Sun, **X. Shen**, D. Zhao, F. Xue, T. Zhang, J. Wang, Serum Metabolomics Analysis for The Progression of Esophageal Squamous Cell Carcinoma, *Journal of Cancer*, 2021, 12, 3190–3197. [↗](#)
- > L. Liang, M. Rasmussen, B. Piening, **X. Shen**, S. Chen, H. Rost, J. Snyder, R. Tibshirani, L. Skotte, N. Lee, K. Contrepois, B. Feenstra, H. Zackariah, M.J. Snyder, M. Melbye, Metabolic Dynamics and Prediction of Gestational Age and Time to Delivery in Pregnant Women, *Cell*, 2020, 181, 7, 1680-1692. [↗](#)
- > Z. Wang, B. Cui, F. Zhang, Y. Yang, **X. Shen**, Z. Li, W. Zhao, Y. Zhang, K. Deng, Z. Rong, K. Yang, X. Yu, K. Li, P. Han, and Z.-J. Zhu, Development of A Correlative Strategy to Discover Colorectal Tumor Tissue Derived Metabolite Biomarkers in Plasma Using Untargeted Metabolomics, *Analytical Chemistry*, 2019, 91, 3, 2401-2408. [↗](#)
- > Z. Zhou, **X. Shen**, X. Chen, J. Tu, X. Xiong, and Z.-J. Zhu, LipidIMMS Analyzer: Integrating Multi-dimensional Information to Support Lipid Identification in Ion Mobility–Mass Spectrometry based Lipidomics, *Bioinformatics*, 2018, 35, 4, 698-700. [↗](#)
- > Z. Zhou, J. Tu, X. Xiong, **X. Shen**, and Z.-J. Zhu, LipidCCS: Prediction of Collision Cross-Section Values for Lipids with High Precision to Support Ion Mobility-Mass Spectrometry based Lipidomics, *Analytical Chemistry*, 2017, 89, 9559–9566. [↗](#)
- > Z. Zhou, **X. Shen**, J. Tu, and Z.-J. Zhu, Large-Scale Prediction of Collision Cross-Section Values for Metabolites in Ion Mobility-Mass Spectrometry, *Analytical Chemistry*, 2016, 88, 11084-11091. [↗](#)

■ Submitted Publications

Co-first Author. *: Co-Corresponding Author

- > **X. Shen**⁺, R. Kellogg⁺, D. Panyard⁺, N. Bararpour⁺, M.P. Snyder*, Multi-omic microsampling captures health perturbations in a lifestyle context. **Under revision in Nature Biomedical Engineering.**
- > X. Zhou⁺, **X. Shen**⁺, G.M. Weinstock, M.P. Snyder*. Longitudinal profiling of the microbiome at four body sites reveals core stability and individualized dynamics during health and disease. **Submitted to Nature.**
- > S. Chen⁺, **X. Shen**⁺, L. Liang⁺, M. P. Snyder*, Longitudinal Urine Metabolic Profiling and Gestational Age Prediction in Pregnancy. **Submitted to Science Translational Medicine.** [↗](#)

- > S. Chen⁺, G. Wang⁺, **X. Shen⁺**, D. Hornburg, S. Rego, R. Hoffman, S. Nevins, X. Cheng, M.P. Snyder*, Integration and Comparison of Multi-omics Profiles of NGLY1 Deficiency Plasma and Cellular Models to Identify Clinically Relevant Molecular Phenotypes. Submitted to *Clinical and Translational Medicine*. [↗](#)

Oral Presentations

- > Deep Learning-based Pseudo-Mass Spectrometry Imaging Analysis for Precision Medicine. **CASMS Virtual Conference, 2022/10**, Virtual meeting.
- > TidyMass: an Object-oriented Reproducible Analysis Framework for LC-MS Data. **ACS Fall 2022, 2022/8**, Virtual meeting.
- > metID: an R Package for Automatable Compound Annotation for LC-MS-based Data. **The 69th American Society for Mass Spectrometry Conference, 2021/11**, Philadelphia, USA.
- > Decoding Links Between the Exposome and Health Outcomes by Multi-omics Analysis. **Exposome Data Challenge Event, 2021/4**, Virtual meeting.
- > Metabolic Reaction Network-based Recursive Metabolite Identification for Untargeted Metabolomics. **The 14th International Conference of the Metabolomics Society, 2018/6**, Seattle, USA.
- > Assessment of the Response to Neoadjuvant Chemo-Radiation in Rectal Cancer Patients based on a Metabolomics Approach. **The 3rd China Mass Spectrometry Analysis Conference, 2017/12**, Xiamen, China. [↗](#)
- > Normalization and Integration of Large-Scale Mass Spectrometry-based Metabolomics Data Using Support Vector Regression. **The 34th China Mass Spectrometry Society Conference, 2016/9**, Xining, China.
- > Normalization and Integration of Large-Scale Mass Spectrometry-based Metabolomics Data Using Support Vector Regression. **The 64th American Society for Mass Spectrometry Conference, 2016/6**, San Antonio, USA. [↗](#)

Poster Presentations

- > Deep Learning-based Pseudo-Mass Spectrometry Imaging Analysis for Precision Medicine. **Stanford Genetics Retreat 2022, 2022/9**, Monterey, USA.
- > Deep Learning-based Pseudo-Mass Spectrometry Imaging Analysis for Precision Medicine. **Bay Area Metabolism Meeting (BAMM) 2022, 2022/9**, Palo Alto, USA.
- > TidyMass An Object-oriented Reproducible Analysis Framework for LC-MS Data. **The 70th American Society for Mass Spectrometry Conference, 2022/6**, Minneapolis, USA.
- > Longitudinal Interactions Between Levels of Serum Cytokine and the Microbiome from Four Body Sites. **IMMUNOLOGY2022, 2022/5**, Portland, USA.
- > TidyMass An Object-oriented Reproducible Analysis Framework for LC-MS Data. **Stanford Genetics Retreat 2021, 2021/9**, Palo Alto, USA.
- > Longitudinal Urine Metabolic Profiling and Gestational Age Prediction in Pregnancy. **The 17th International Conference of the Metabolomics Society, 2020/6**, Virtual meeting.
- > Metabolic Reaction Network based Metabolite Annotation in Untargeted Metabolomics. **The 13th International Conference of the Metabolomics Society, 2017/6**, Brisbane, Austria.

Teaching Experience

- > **LC-MS Data Processing and Analysis Using R language** 2022/9, Biotree Company
Responsibilities: Lecture
- > **R Language for Reproducible Data Analysis** 2020/4, SCPA
Responsibilities: Lecture
- > **Stanford School of Medicine Intern** 2019/8–Present, Stanford University
Responsibilities: Mentor
- > **Mass Spectrometry Analysis** 2014/9–2014/12, Chinese Academy of Sciences









Volunteering

- > **Co-chair** 2021/7–2022/8, [Stanford Chinese Postdoctoral Association](#)
- > **Organizer** 2020/2–2021/12, [Stanford Chinese Postdoctoral Oral Presentation Improvement](#)
- > **Member** 2019/7–2021/7, [Stanford Chinese Postdoctoral Association](#)
- > **Member** 2013/9–2014/7, [Student Association of IRCBC, Chinese Academy of Sciences](#)

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*

Technical Strength

-  Languages: Mandarin (Very fluent), English (Fluent).
-  Programming Languages: R , Python , HTML.
-  Bioinformatic Tools: RNA-seq, Proteomics.
-  Other Skills: Markdown, Photoshop, Illustrator, Linux, GitHub , Shiny 

References

- > **[Professor Michael Snyder](#)**
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- > **[Professor Zheng-Jiang Zhu](#)**
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- > **[Professor Caroline Johnson](#)**
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