

Xiaotao Shen, Ph.D.

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

3165 Porter Drive, Palo Alto, CA 94304, USA.

✉ shenxt@stanford.edu 🏠 shenxt.info ☎ +1 571-267-9283 🌐 [Xiaotao Shen](#) 🗣 [jaspershen](#) 📄 [Xiaotao Shen](#) 🆔 [0000-0002-9608-9964](#)

🔬 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
- > Wearable Data and Precision Medicine

🎓 Education & Research Experiences

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

🏆 Honors & Awards

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| 1. SPORR 2023 Rigor and Reproducibility Awards | Stanford Program on Research Rigor and Reproducibility (2023) |
| 2. Winner Selected by the Event Committee | Exposome Data Challenge Event (2021) |
| 3. Student Travel Award for Oral Presentation | The International Metabolomics Society (2018) |
| 4. International Conference Travel Award | The Metabolites Journal (2018) |
| 5. China National Scholarship | Ministry of Education of the People's Republic of China (2017) |
| 6. Award for Outstanding Youth Report | The 3rd China MS Analysis Conference (2017) |
| 7. Merit Student | University of Chinese Academy of Sciences (2016) |
| 8. Award for Outstanding Youth Report | The 34th China MS Society Conference (2016) |
| 9. Inner Mongolia Outstanding Graduate | Inner Mongolia Autonomous Region (2013) |
| 10. National Encouragement Scholarship | Inner Mongolia University (2011) |

📄 First/Co-first Author Publications

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

1. **X. Shen⁺**, R. Kellogg⁺, D. Panyard⁺, N. Bararpour⁺, K. Castillo, B. Lee-McMullen, A. Delfarah, J. Ubellecker, S. Ahadi, Y. Rosenberg-Hasson, A. Ganz, K. Contrepolis, B. Michael, I. Simms, C. Wang, D. Hornburg, M.P. Snyder*, **Multi-omic Microsampling Captures Health Perturbations in A Lifestyle Context. *Nature Biomedical Engineering*, 2023, 10.1038/s41551-022-00999-8.** 🔗 (Citation: 4, IF: 29.2)

2. X. Shen⁺, C. Wang⁺, M.P. Snyder^{*}, **massDatabase: Utilities for the Operation of the Public Compound and Pathway Database**, *Bioinformatics*, 2022, btac546. [↗](#) (Citation: 1, IF: 6.9)
3. 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. [↗](#) (Citation: 1, IF: 14.0)
4. 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. [↗](#) (Citation: 11, IF: 17.7)
5. 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. [↗](#) (Citation: 15, IF: 9.4)
6. X. Shen⁺, S. Wu⁺, L. Liang, S. Chen, K. Contrepois, Z.-J. Zhu^{*} and M.J. Snyder^{*}, **metlD: an R Package for Automatable Compound Annotation for LC-MS-based Data**, *Bioinformatics*, 2021, **1**, 1-2. [↗](#) (Citation: 18, IF: 6.9)
7. 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. [↗](#) (Citation: 200, IF: 17.7)
8. X. Shen and Z.-J. Zhu^{*}, **MetFlow: An Interactive and Integrated Workflow For Metabolomics Data Cleaning and Differential Metabolite Discovery**, *Bioinformatics*, 2019, **35**, 16. [↗](#) (Citation: 27, IF: 6.9)
9. H. Jia⁺, X. Shen⁺, Y. Guan, M. Xu, M. Mo, J. Zhu^{*} and Z.-J. Zhu^{*}, **Predicting the pathological response to neoadjuvant chemoradiation using untargeted metabolomics in locally advanced rectal cancer**, *Radiotherapy and Oncology*, 2018, **128**, 548-556. [↗](#) (Citation: 38, IF: 6.9)
10. 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. [↗](#) (Citation: 109, IF: 4.7)
11. 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. [↗](#) (Citation: 144, IF: 4.7)

Collaborative Publications

1. S. Jain, L. Pei, J. Spraggins, M. Angelo, J. Carson, N. Gehlenborg, F. Ginty, J. Gonçalves, J. Hagood, J. Hickey, N. Kelleher, L. Laurent, S. Lin, Y. Lin, H. Liu, A. Naba, E. Nakayasu, W. Qian, A. Radtke, P. Robson, B. Stockwell, R. Plas, I. Vlachos, M. Zhou, **HuBMAP Consortium**, K. Borner, M. Snyder, **HuBMAP Consortium**, **Advances and Perspectives for the Human BioMolecular Atlas Program (HuBMAP)**, *Nature Cell Biology*, 2023.
2. W. Wei, N. Riley, X. Lyu, X. Shen, J. Guo, S. Raun, M. Zhao, M. Moya-Garzon, H. Basu, A. Tung, V. Li, W. Huang, A. Wiggenshorn, K. Svensson, M. Snyder, C. Bertozzi, J. Long, **Organism-wide, cell-type-specific secretome mapping of exercise training in mice**, *Cell Metabolism*, **35**: 1-19, 2023.
3. S. Zhang, J. Cooper-Knock, A. Weimer, M. Shi, L. Kozhaya, D. Unutmaz, C. Harvey, T. Julian, S. Furini, E. Frullanti, F. Fava, A. Renieri, P. Gao, X. Shen, I. Timpanaro, K. Kenna, J. Baillie, M. Davis, P. Tsao, M.P. Snyder, **Multiomic analysis reveals cell-type-specific molecular determinants of COVID-19 severity**, *Cell Systems*, **13**(8):598-614, 2022. [↗](#)
4. 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. [↗](#)

5. 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. [↗](#)
6. 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. [↗](#)
7. 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. Zackriah, 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. [↗](#)
8. 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. [↗](#)
9. 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. [↗](#)
10. 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. [↗](#)
11. 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

1. X. Shen⁺, C. Wang⁺, X. Zhou, W. Zhou, D. Hornburg, S. Wu, and M.P. Snyder*, **Nonlinear Dynamic Changes During Human Aging Revealed in Multi-omics Profiles**. Submitted.
2. X. Shen⁺, M.P. Snyder*, **microbiomeDataset: A tidyverse-style framework for organizing and processing microbiome data**. Under review in *Bioinformatics*.
3. X. Zhou⁺, X. Shen⁺, J. Johnson, D. Spakowicz, M. Agnello, W. Zhou, M. Avina, A. Honkala, F. Chleilat, S. Chen, K. Cha, S. Leopold, C. Zhu, L. Chen, L. Lyu, D. Hornburg, S. Wu, X. Zhang, C. Jiang, L. Jiang, L. Jiang, R. Jian, A. Brooks, M. Wang, K. Contrepois, P. Gao, S. Rose, T. Tran, H. Nguyen, A. Celli, B. Hong, E. Bautista, Y. Dorsett, P. Kavathas, Y. Zhou, E. Sodergren, 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**. Under review in *Cell*.
4. S. Chen⁺, X. Shen⁺, L. Liang⁺, M. P. Snyder*, **Longitudinal Urine Metabolic Profiling and Gestational Age Prediction in Pregnancy**. Submitted to *Science Translational Medicine*. [↗](#)
5. 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*. [↗](#)

Patents

1. M.P. Snyder, R. Kellogg, X. Shen, **Multi-omic Sample Analysis Methods**, 2022, USA.

2. L. Liang, M.P. Snyder, **X. Shen**, S. Chen, **Methods for Evaluating Gestational Progress and Applications Thereof**, 2021, USA.
3. Z-J. Zhu, **X. Shen**, **A Method for Metabolite Annotation and Dysregulated Pathway Analysis**, 2019, China.

Oral Presentations

1. **Multi-omics Microsampling for The Profiling of Lifestyle-Associate Changes in Health. The 71th American Society for Mass Spectrometry Conference**, 2023/6, Houston, USA.
2. **Remote and Flexible Microsampling Multi-omics for Precision Medicine. Invited presentation**, 2023/4, iPOP summit, Stanford University, USA.
3. **Bioinformatics Algorithm Development for Mass Spectrometry Data and its Application to Precision Medicine. Invited presentation**, 2023/3, Altos Labs, Redwood City, USA.
4. **Multi-omics Microsampling for The Profiling of Lifestyle-Associate Changes in Health. Invited presentation**, 2023/2, Huazhong University of Science and Technology, China.
5. **Multi-omics Microsampling for The Profiling of Lifestyle-Associate Changes in Health. Stanford Postdoc Symposium**, 2023/2, Stanford, USA.
6. **Bioinformatics Method Development for Mass Spectrometry and its Application to Precision Medicine. Stanford CVI Early Career Research Roundtable**, 2022/11, Stanford, USA.
7. **Deep Learning-based Pseudo-Mass Spectrometry Imaging Analysis for Precision Medicine. CASMS Virtual Conference**, 2022/10, Virtual meeting.
8. **TidyMass: an Object-oriented Reproducible Analysis Framework for LC-MS Data. ACS Fall 2022**, 2022/8, Virtual meeting.
9. **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.
10. **Decoding Links Between the Exposome and Health Outcomes by Multi-omics Analysis. Exposome Data Challenge Event**, 2021/4, Virtual meeting.
11. **Metabolic Reaction Network-based Recursive Metabolite Identification for Untargeted Metabolomics. The 14th International Conference of the Metabolomics Society**, 2018/6, Seattle, USA.
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**, 2017/12, Xiamen, China. [🔗](#)
13. **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.
14. **Normalization and Integration of Large-Scale MS-based Metabolomics Data Using Support Vector Regression. The 64th American Society for Mass Spectrometry Conference**, 2016/6, San Antonio, USA. [🔗](#)

Poster Presentations

1. **TidyMass An Object-oriented Reproducible Analysis Framework for LC-MS Data. Stanford Data Science Conference**, 2023/5, Stanford University, USA.

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

Teaching Experience

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| > 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 Responsibilities: Guest lecturer |

Volunteering









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| > Member of Youth Editorial Board | 2023/2–present, Phenomics |
| > Member of Youth Editorial Board | 2023/1–present, Brain-X |
| > Member of Youth Editorial Board | 2022/7–present, iMeta |
| > 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, Bash.
-  **Bioinformatic Tools:** RNA-seq, Proteomics.
-  **Other Skills:** Markdown, Photoshop, Illustrator, Linux, GitHub , Shiny 

Referrers

- > **Professor Michael Snyder**
Postdoctoral Advisor
Chair, Department of Genetics, **Stanford University**
Phone number: +1 (650) 723-4668
Email: mpsnyder@stanford.edu
- > **Professor Zheng-Jiang Zhu**
Ph.D. Advisor
Director of Metabolomics Research Center, The Interdisciplinary Research Center on Biology and Chemistry, **Chinese Academy of Sciences**
Phone number: +86 21-68582296
Email: jiangzhu@sioc.ac.cn
- > **Professor Caroline Johnson**
Collaborator
Yale School of Public Health
Phone number: +1 (203) 785-2882
Email: caroline.johnson@yale.edu