

Xiaotao Shen, Ph.D.

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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.** 2013/9–2018/12, **Chinese Academy of Sciences**
(Advisor: [Prof. Zheng-Jiang Zhu](#))
- > **B.S.** 2009/9–2013/6, **Inner Mongolia University**

🏆 Honors & Awards

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. Contrepois, 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](https://doi.org/10.1038/s41551-022-00999-8). [🔗](#)
2. [X. Shen⁺⁺](#), C. Wang⁺, M.P. Snyder*, **massDatabase: Utilities for the Operation of the Public Compound and Pathway Database**, *Bioinformatics*, 2022, btac546. [🔗](#)
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. [🔗](#)
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. [🔗](#)

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. [↗](#)
6. 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. [↗](#)
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. [↗](#)
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. [↗](#)
9. 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. [↗](#)
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. [↗](#)
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. [↗](#)

Collaborative Publications

1. 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, **Multimic analysis reveals cell-type-specific molecular determinants of COVID-19 severity**, *Cell Systems*, 13(8):598-614, 2022. [↗](#)
2. 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. [↗](#)
3. 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. [↗](#)
4. 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. [↗](#)
5. 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. [↗](#)
6. 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. [↗](#)
7. 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. [↗](#)
8. 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. [↗](#)
9. 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. 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. Contrepolis, 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*.
2. S. Chen⁺, **X. Shen⁺**, L. Liang⁺, M. P. Snyder*, **Longitudinal Urine Metabolic Profiling and Gestational Age Prediction in Pregnancy.** Submitted to *Science Translational Medicine*. [↗](#)
3. 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. **Bioinformatics Algorithm Development for Mass Spectrometry Data and its Application to Precision Medicine**, 2023/1, Rutgers New Jersey Medical School, USA.
2. **Bioinformatics Method Development for Mass Spectrometry and its Application to Precision Medicine.** Stanford CVI Early Career Research Roundtable, 2022/11, Palo Alto, USA.
3. **Deep Learning-based Pseudo-Mass Spectrometry Imaging Analysis for Precision Medicine.** CASMS Virtual Conference, 2022/10, Virtual meeting.
4. **TidyMass: an Object-oriented Reproducible Analysis Framework for LC-MS Data.** ACS Fall 2022, 2022/8, Virtual meeting.
5. **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.
6. **Decoding Links Between the Exposome and Health Outcomes by Multi-omics Analysis.** Exposome Data Challenge Event, 2021/4, Virtual meeting.
7. **Metabolic Reaction Network-based Recursive Metabolite Identification for Untargeted Metabolomics.** The 14th International Conference of the Metabolomics Society, 2018/6, Seattle, USA.
8. **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. [↗](#)
9. **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.
10. **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. **Deep Learning-based Pseudo-Mass Spectrometry Imaging Analysis for Precision Medicine.** Stanford Genetics Retreat 2022, 2022/9, Monterey, USA.

2. Deep Learning-based Pseudo-Mass Spectrometry Imaging Analysis for Precision Medicine. Bay Area Metabolism Meeting (BAMM) 2022, 2022/9, Palo Alto, USA.
3. TidyMass An Object-oriented Reproducible Analysis Framework for LC-MS Data. The 70th American Society for Mass Spectrometry Conference, 2022/6, Minneapolis, USA.
4. Longitudinal Interactions Between Levels of Serum Cytokine and the Microbiome from Four Body Sites. IMMUNOLOGY2022, 2022/5, Portland, USA.
5. TidyMass An Object-oriented Reproducible Analysis Framework for LC-MS Data. Stanford Genetics Retreat 2021, 2021/9, Palo Alto, USA.
6. Longitudinal Urine Metabolic Profiling and Gestational Age Prediction in Pregnancy. The 17th International Conference of the Metabolomics Society, 2020/6, Virtual meeting.
7. 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 | 2023/1–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 

References

- > **Professor Michael Snyder**
Postdoctoral Advisor
Chair, Department of Genetics, Stanford University
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- > **Professor Zheng-Jiang Zhu**
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- > **Professor Caroline Johnson**
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