Xiaotao Shen Ph.D.

Prof. Michael Snyder's Lab,

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Information

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2019/4 - present Stanford University

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 Experience Postdoctoral Research Fellow

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		(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
- > Inner Mongolia Outstanding Graduate
- > National Encouragement Scholarship

The 34th China MS Society Conference (2016) Inner Mongolia Autonomous Region (2013) Inner Mongolia University (2011)

First/Co-first Author Publications

- > **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 (Co-first author), 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 (Co-first author), 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 (Co-first author)**, 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. 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.
- 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

- > X. Shen, R. Kellogg, D. Panyard, N. Bararpour, M.P. Snyder, Multi-omic microsampling captures health perturbations in a lifestyle context. **Under review in** *Nature Biomedical Engineering*.
- X. Zhou, X. Shen (Co-first author), 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.
- > S. Chen, **X. Shen (Co-first author)**, L. Liang, M. P. Snyder, Longitudinal Urine Metabolic Profiling and Gestational Age Prediction in Pregnancy. **Submitted**.
- > S. Chen, G. Wang, X. Shen (Co-first author), 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.
- X. Shen, C. Wang, M.P. Snyder. Extracting Alerted Metabolic Modules Across Human Aging. Submitted.
- > **X. Shen**, C. Wang, M.P. Snyder. Nonlinear changes of human plasma multi-omics profiles across the lifespan. **Submitted**.
- > **X. Shen**, L. Liang, S. Chen, M.P. Snyder, Multi-Omics Molecular Profiling During Human Pregnancy. **Submitted**.

□ Oral Presentations

- > TidyMass an Object-oriented Reproducible Analysis Framework for LC-MS Data. **ACS Fall 2022**, August 2022, Virtual meeting.
- > metID: an R Package for Automatable Compound Annotation for LC-MS-based Data. **The 69**th **American Society for Mass Spectrometry Conference**, November 2021, Philadelphia, USA.

- Decoding Links Between the Exposome and Health Outcomes by Multi-omics Analysis. Exposome Data Challenge Event, April 2021, Virtual meeting.
- Metabolic Reaction Network-based Recursive Metabolite Identification for Untargeted Metabolomics. The 14th International Conference of the Metabolomics Society, June 2018, 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, December 2017, Xiamen, China.
- Normalization and Integration of Large-Scale Mass Spectrometry-based Metabolomics Data Using Support Vector Regression. The 34th China Mass Spectrometry Society Conference, September 2016, 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, June 2016, San Antonio, USA.

Poster Presentations

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

Responsibilities: Guest lecturer

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, <u>Stanford Chinese Postdoctoral Association</u>

> Member 2013/9-2014/7, Student Association of IRCBC Chinese Academy of Sciences

Journal Referee

- > Nature Communications
- > Briefing in Bioinformatics
- > Bioinformatics
- > GigaScience
- > PLOS One
- > Phytochemistry
- > Genomics, Proteomics&Bioinformatics
- > Communications Chemistry
- > Communications Biology
- > Frontiers Molecular Biosciences
- > iMeta

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 🥜