SHEN, XIAOTAO Ph.D.

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INFORMATION

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EDUCATION & RESEARCH EXPERIENCE

- Postdoctoral Research Fellow (Advisor: Dr. Michael Snyder)
  Apr. 2019 – present, Stanford University.
- Research Scientist (Advisor: Dr. Zheng-Jiang Zhu)
  Jan. 2019 – Mar. 2019, Chinese Academy of Sciences (CAS).
- Ph.D. Student in Metabolomics and Bioinformatics (Advisor: Dr. Zheng-Jiang Zhu)
  Aug. 2013 – Dec. 2018, Chinese Academy of Sciences (CAS).
- BSs in Biotechnology Aug. 2009 - Jun. 2013, Inner Mongolia University.

RESEARCH INTERESTS

- Mass Spectrometry Data (Proteomics & Metabolomics) Processing Algorithms and Software Development.
- Multi-omics Data Integration Methods Development.
- Precision Exposome and Multi-omics Integration for Health.
- Multi-omics Profiling for Human Pregnancy Related Disease Diagnosis and Mechanism Research.
- Aging and Neurodegenerative Diseases.
- Microbiome.
- Wearable Data and Precision Medicine.

HONORS AND 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 3th China Mass Spectrometry Analysis Conference (2017).
- Merit Student — University of Chinese Academy of Sciences (2016).
- Award for Outstanding Youth Report — The 34th China Mass Spectrometry Society Conference (2016).
- Inner Mongolia Outstanding Graduate — Inner Mongolia Autonomous Region (2013).
- National Encouragement Scholarship — Inner Mongolia University (2011).

PUBLICATIONS (FIRST/CO-FIRST AUTHOR)

- X. Shen, C. Wang, M.P. Snyder, massDatabase: Utilities for the Operation of the Public Compound and Pathway Database, ***Bioinformatics***, **Accepted**.
- **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***, **Accepted**.
- 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 and 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, H. Li, T. Zhang, J. Wang, F. Xue, and Z.-J. Zhu, Normalization and Integration of Large-Scale Metabolomics Data Using Support Vector Regression, ***Metabolomics***, 2016, 12: 89.

PUBLICATIONS

- 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.

PUBLICATIONS (SUBMITTED/IN PREPARATION)

- S. Chen, **X. Shen (Co-first author)**, L. Liang, M. P. Snyder, Longitudinal Urine Metabolic Profiling and Gestational Age Prediction in Pregnancy. **Submitted**.
- **X. Shen**, R. Kellogg, D. Hornburg, N. Bararpour, D.J. Panyard, M.P. Snyder, Multi-omics Data From Microsamples Captures Health Perturbations in A Lifestyle Context. **Submitted**.
- X. Zhou, **X. Shen (Co-first author)**, G.M. Weinstock, M.P. Snyder. Integrating Microbial Dynamics From Four Human Body Sites During Health and Diseases. **In Preparation**.
- **X. Shen**, M. Yu, C. Wang, M.P. Snyder. Extracting Alerted Metabolic Modules Across Human Aging. **In Preparation**.
- **X. Shen**, L. Liang, S. Chen, M.P. Snyder, Multi-Omics Molecular Profiling During Human Pregnancy. **In Preparation**.

ORAL PRESENTATIONS

- metID: an R Package for Automatable Compound Annotation for LC−MS-based Data. The 69th 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.

POSTERS PRESENTATION

- TidyMass An Object-oriented Reproducible Analysis Framework for LC-MS Data. The 70th 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.
- Longitudinal Urine Metabolic Profiling and Gestational Age Prediction in Pregnancy. The 17th International Conference of the Metabolomics Society, 2020, Virtual meeting.
- Metabolic Reaction Network based Metabolite Annotation in Untargeted Metabolomics. The 13th International Conference of the Metabolomics Society, June 2017, Brisbane, Austria.

TECHNICAL STRENGTH

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