

# WANG, MINKUN

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## EDUCATION

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### Virginia Tech

Ph.D student in Electrical Engineering

Department of Electrical & Computer Engineering

Member of [Computational Bioinformatics & Bio-imaging Lab](#)

*Aug. 2012 - Present*

*GPA: 3.89/4.00*

### University of Science and Technology of China

B.S. in Electrical Engineering

Department of Electronic Engineering & Information Science

Member of [Image Processing Lab](#)

*Aug. 2008 - Jun. 2012*

*GPA: 3.85/4.30*

## RESEARCH

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- **Machine Learning:** Topic Models, Bayesian Inference, Sparse Representation
- **Bioinformatics:** LC-MS Data Preprocessing, Multi-omic Data Integration
- **Signal Processing:** Image Processing, Pattern Recognition
- **Others:** Proteomics, Glycomics, Metabolomics, Cancer Biomarker Discovery

## EXPERIENCE

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### [iCarbonX Co., Ltd.](#)

*Internship, R & D Manager*

*Brain Group, Department of Bioinformatics and Artificial Intelligence*

- Statistical machine learning methods development for multi-omic data analysis
- Chatbot design for personalized and accurate health service

*Jun. 2016 - Present*

*Shenzhen, China*

### [Ressom Lab](#)

*Research Assistant*

- Algorithm and tool development for LC-MS data preprocessing
- Glycomic, Proteomic, and Glycoproteomic based liver cancer biomarker discovery
- Probabilistic generative modeling on purification of heterogeneous data

*Sep. 2012 - Present*

*Washington, DC*

### Virginia Tech

*Teaching Assistant*

- Optimization Techniques. ECE-5454. Spring 2016, Department of Electrical and Computer Engineering, Virginia Tech.

*Jan. 2016 - May. 2016*

*Falls Church, VA*

### Georgetown University

*Teaching Assistant*

- Bioinformatics in LC-MS based Proteomics and Glycomics. BIST-532-01.Fall2015: Bioinformatics for Omics Data, Department of Biostatistics.

*Aug. 2015 - Dec. 2015*

*Washington, DC*

- SAR image quality assessment
- SAR image processing, target recognition, and classification based on dictionary learning
- Department of Electronic Engineering & Information Science, USTC

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**TECHNICAL STRENGTH**

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- **Programming Languages:** Python, Matlab, Java, C, R
- **Web Design:** HTML, CSS, Photoshop
- **Bioinformatic Tools:** MaxQuant, Skyline
- **Languages:** Mandarin, English

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**PUBLICATION**

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**Conference & Journal**

- [1] **Wang M**, Di Poto C, Ferrarini A, Yu G, Resson HW (2016). Metabolomic data deconvolution using probabilistic purification models. Oral Presentation in the Proceedings of the 2016 IEEE International Conference on Bioinformatics and Biomedicine (BIBM), Shenzhen, China, December 15-18, 2016. (Awarded **the Best Student Paper**, 1/361)
- [2] **Wang M**, Tsai TH, Di Poto C, Ferrarini A, Yu G, Resson HW (2016). Topic model-based mass spectrometric data analysis in cancer biomarker discovery studies. *BMC Genomics*. 17(Suppl 4):545.
- [3] Di Poto C, Ferrarini A, Zhao Y, Varghese RS, Tu C, Zuo Y, **Wang M**, Nezami Ranjbar MR, Luo Y, Zhang C, Desai CS, Shetty K, Tadesse MG, Resson HW (2016). Metabolomic characterization of hepatocellular carcinoma in patients with liver cirrhosis for biomarker discovery. *Cancer Epidemiology, Biomarkers & Prevention*. DOI: 10.1158/1055-9965.EPI-16-0366.
- [4] Resson HW, Di Poto C, Ferrarini A, Hu Y, Nezami Ranjbar MR, Song E, Varghese RS, **Wang M**, Zhou S, Zhu R, Zuo Y, Tadesse MG, Mechref Y (2016). Multi-omic approaches for characterization of hepatocellular carcinoma. Oral Presentation in the Proceedings of the 38th Annual International Conference of the IEEE Engineering in Medicine and Biology Society, Orlando, Florida, August 16-20, 2016.
- [5] **Wang M**, Yu G, Resson HW (2016). Integrative analysis of proteomic, glycomic, and metabolomic data for biomarker discovery. *IEEE Journal of Biomedical and Health Informatics*. 20(5), 1225-1231. PMID: 27249841
- [6] **Wang M**, Tsai TH, Yu G, Resson HW (2015). Purification of LC/GC-MS based biomolecular expression profiles using a topic model. Oral Presentation in the Proceedings of the 2015 IEEE International Conference on Bioinformatics and Biomedicine (BIBM), Washington D.C., USA, November 9-12, 2015. (Student Travel Award, 9%)
- [7] **Wang M**, Yu G, Resson HW (2015). Integrative analysis of LC-MS based glycomic and proteomic data. Oral Presentation in the Proceedings of the 37th Annual International Conference of the IEEE Engineering in Medicine and Biology Society, Milano, Italy, August 25-29, 2015.
- [8] Tsai TH\*, Song E\*, Zhu R\*, Di Poto C\*, **Wang M\***, Luo Y, Varghese RS, Tadesse MG, Ziada DH, Desai CS, Shetty K, Mechref Y, Resson HW (2015). LC-MS/MS based serum proteomics for identification of candidate biomarkers for hepatocellular carcinoma. *Proteomics*. 15(13), 2369-2381. PMID: 25778709. (\* First authors )

- [9] Tsai TH, **Wang M**, Di Poto C, Hu Y, Zhou S, Zhao Y, Varghese RS, Luo Y, Tadesse MG, Ziada DH, Desai CS, Shetty K, Mechref Y, Ressom HW (2014). LC-MS profiling of N-Glycans derived from human serum samples for biomarker discovery in hepatocellular carcinoma. *J Proteome Res.* PMID: 25077556.
- [10] **Wang M**, Yu G, Mechref Y, Ressom HW (2013). GPA: an algorithm for LC/MS based glycan profile annotation. *Proceedings of the 2013 IEEE International Conference on Bioinformatics and Biomedicine Workshop (BIBMW)*, Shanghai, China, December 2013, pp. 16-22.
- [11] Wang B, Zhang Y, Zhang R, Gu J, **Wang M** (2013) A target recognition method in SAR images based on dynamic dictionary learning. *Opto-Electronic Engineering.*40(6).

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### Book Chapter

- [1] Tsai TH, **Wang M**, Ressom HW (2015). Preprocessing and Analysis of LC-MS-Based Proteomic Data. *Statistical Analysis in Proteomics (Methods in Molecular Biology)* 2016, 1362:63-76. PMID: 26519169.

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### Selected Poster

- [1] **Wang, M**, Tsai TH, Di Poto C, Ferrarini A, Yu G, Ressom HW. (2015) Topic model based purification of LC/GC-MS data acquired from heterogeneous samples in proteomic and metabolomic studies. Presented at CSH-ASIA/AACR Joint Meeting: Big Data, Computation, and Systems Biology in Cancer. December 2-5, 2015. Suzhou, China. (Awarded **the 1<sup>st</sup> Prize of CSHA fellowship**)
- [2] **Wang M**, Di Poto C, Song E, Zhu R, Mechref Y, Ressom HW. (2015) Analysis of N-linked Glycopeptides Derived from Human Liver Tissues by LC-MS/MS. Presented at the 63rd ASMS Conference on Mass Spectrometry. May 31- June 4, 2015. St. Louis, MO.
- [3] **Wang M**, Tsai TH, Hu Y, Zhou S, Mechref Y, Ressom HW. (2014) An Integrated Pipeline for Analysis of LC-MS Based Glycomics Data. Presented at the 62nd ASMS Conference on Mass Spectrometry. June 15-19, 2014. Baltimore, MD.
- [4] Tsai TH, **Wang M**, Di Poto C, Hu Y, Zhou S, Zhao Y, Varghese RS, Luo Y, Tadesse MG, Ziada DH, Desai CS, Shetty K, Mechref Y, Ressom HW. LC-MS Profiling of N-Glycans Derived from Human Serum for HCC Biomarker Discovery. Presented at the Early Detection Research Network (EDRN), 2014.
- [5] Tsai TH, **Wang M**, Di Poto C, Zhao Y, Hu Y, Zhou S, Mechref Y, Ressom HW. (2013) LC-MS Based Detection and Quantification of N-glycans in Human Serum Samples. Presented at the 61st ASMS Conference on Mass Spectrometry. June 9 - 13, 2013, Minneapolis, MN.
- [6] Ressom HW, **Wang M**, Zhao Y, Tsai TH, Di Poto C, Hu Y, Zhou S, Tadesse MG, Ziada DH, Shetty K, Mechref Y. (2013) LC-MS Profiling of N-Glycans Derived from Human Serum Samples for Biomarker Discovery in Hepatocellular Carcinoma. Presented at the American Association for the Study of Liver Diseases (AASLD), 2013.