

Jinling Liu, PhD, MS

Assistant Professor
Department of Epidemiology, University of Florida
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EDUCATION

Aug. 2019 M.S. in Biomedical Informatics, University of Pittsburgh, Pittsburgh, PA
Dec. 2014 Ph.D. in Biology, The Pennsylvania State University, State College, PA
Jul. 2008 B.S. in Biotechnology, East China Normal University, Shanghai, China

APPOINTMENTS

09/2023 - Present Assistant Professor (tenure track), Department of Epidemiology, University of Florida (UF)
01/2020 - 08/2023 Assistant Professor (tenure track), Department of Engineering Management and Systems Engineering, joint appointment with Biological Sciences, Missouri University Science and Technology (Missouri S&T)
09/2017 - 12/2019 National Library of Medicine Postdoctoral Fellow, Department of Biomedical Informatics, University of Pittsburgh (PITT)
02/2015 - 08/ 2017 Senior Research Specialist, UPMC Hillman Cancer Center, PITT

RESEARCH SPECIALIZATION

Biomedical Informatics | Multi-omics Analytics | Statistical Modeling | Machine Learning | Causal Inference | Cloud Computing | Statistical Genetics and Epidemiology | Personalized Medicine | Systems Biology and Engineering | Data Analytics and Decision Making

1. One of Dr. Liu's research interests lies in modeling the rapidly-accumulating big data in biology and medicine for precision medicine. Her unique expertise in both biology and informatics not only allows her to identify interesting biomedical problems to model, but also helps build a better model with molecular-level biological understanding of the complex data. **One main theme of her research is to infer from the multi-omics data the activation states of signaling pathways and utilize such information in precision medicine.** She is committed to advancing precision medicine and improving health equity through her work.

Examples of ongoing projects under this research direction:

- **Causal discovery of novel genomic variants for diseases using an instance-specific machine learning framework**
 - Supported by [the NHLBI BioData Catalyst Fellowship award](#)
- **A novel framework for estimating personalized genomic variants of hypertension for precision medicine**
 - Supported by [the NHLBI K01 award](#)
- **Investigation and deployment of novel Bayesian inference algorithms in the cloud-computing platform of CAVATICA to identify genomic causes of congenital heart defects from Kids First and INCLUDE datasets**

- Supported by the NHLBI R03 award
 - Supported by [the NIH INCLUDE Program](#) for Cloud Credit
 - Supported by the Center for Biomedical Research at Missouri S&T
- **Multi-omics data analysis to reveal causal signaling networks underlying diseases**
2. Dr. Liu is also interested in collaborating with investigators from various disciplines who need help with data analytics and decision making. Her expertise in statistical analysis and machine learning techniques can help identify the pattern in the data for extracting useful knowledge or helping with prediction.

Examples of ongoing collaborations:

- **Machine learning-assisted material design**
 - Supported by the Intelligent Systems Center at Missouri S&T
 - [A feasibility study of machine learning-assisted alloy design using wrought aluminum alloys as an example](#)
 - [An adaptive physics-based feature engineering approach for machine learning-assisted alloy discovery](#)
- **Machine learning-assisted sensor design**
 - [Real-time detection and analysis of foodborne pathogens via machine learning based fiber-optic Raman sensor](#)

EXTERNAL FUNDING

2023 - 2025	Investigation and deployment of novel Bayesian inference algorithms in CAVATICA for identifying genomic variants underlying congenital heart defects in Down syndrome individuals, R03 Award, National Heart, Lung and Blood Institute (NHLBI), National Institutes of Health (NIH), \$308,928, PI
2022 - 2027	A novel framework for estimating personalized genomic variants of hypertension for precision medicine, Career Development (K01) Award, NHLBI/NIH, \$721,025, PI
2022	Investigating personalized genomic variants of congenital heart defects on the cloud-computing platform of Cavatica, NIH INCLUDE Cloud Credit Program, NIH, \$6,000, PI
2021	Apply and evaluate an instance-specific causal machine learning framework for identifying the causative genomic variants of cardiovascular diseases, NHLBI Cloud Credit Program, NHLBI/NIH, \$8,422 of STRIDES credits, PI
2021	Analyzing the INCLUDE dataset on the cloud-computing platform of Cavatica, NIH INCLUDE Cloud Credit Program, NIH, \$1,000, PI

2020 – 2021 Apply and evaluate an instance-specific causal machine learning framework for identifying the causative genomic variants of cardiovascular diseases, BioData Catalyst Fellowship Award, NHLBI/NIH, \$69,733, PI

INTERNAL FUNDING

2021 – 2022 Develop and apply a novel instance-specific causal inference tool for identifying causal genomic variants of pediatric conditions, Center for Biomedical Research (CBR), Missouri University of Science and Technology, \$15,000, PI

2021 – 2022 Lightweight Alloy Design by Machine Learning, Intelligent Systems Center (ISC), Missouri University of Science and Technology, \$9,648, PI

2021 Apply and evaluate an instance-specific causal machine learning framework for identifying the causative genomic variants of cardiovascular diseases, Intelligent Systems Center (ISC), Missouri University of Science and Technology, \$6,697, PI

PUBLICATIONS

1. Rahman M.A., Cai C, Bo N, McNamara D, Ding Y, Cooper G.F., Lu X, **Liu J***. An individualized Bayesian method for estimating genomic variants of hypertension. **BMC Genomics**. 2023. 23 (Suppl 5), 863 (2022). doi: 10.1186/s12864-023-09757-9
2. Rahman M.A., **Liu J***. A genome-wide association study coupled with machine learning models to identify influential demographic and genomic factors underlying Parkinson's disease. **Frontiers in Genetics**. 2023. 14:1230579. doi: 10.3389/fgene.2023.1230579
3. Jamalipour Soofi Y., Gu Y, **Liu J***. A novel adaptive physics-based feature engineering approach for machine learning-assisted alloy discovery. **Computational Materials Science**. 2023. Volume 226, 112248, ISSN 0927-0256. doi: 10.1016/j.commatsci.2023.112248.
4. Zhang B, Rahman MA, **Liu J**, Huang J, Yang Q. Real-time detection and analysis of food-borne pathogens via machine learning based fiber-optic Raman sensor. **Measurement**. 2023. Volume 217, 113121, ISSN 0263-2241. doi: 10.1016/j.measurement.2023.113121.
5. Jamalipour Soofi Y., Rahman M. A., Gu Y., **Liu J***. A feasibility study of machine learning-assisted alloy design using wrought aluminum alloys as an example. **Computational Materials Science**. 2022, volume 215, 111783, ISSN 0927-0256. doi: 10.1016/j.commatsci.2022.111783.
6. Liu Z, Cai C, Ma X, **Liu J**, Chen L, Lui V, Cooper G.F., Lu X. A novel Bayesian framework infers driver activation states and reveals pathway-oriented molecular subtypes in head and neck cancer. **Cancers**. 2022, 14, 4825. doi: 10.3390/cancers14194825.
7. Cai M, Yue M, Chen T, **Liu J**, Forno E, Lu X, Billiar T, Celedon J, McKennan C, Chen W, Wang J. Robust and accurate estimation of cellular fraction from tissue omics data via ensemble deconvolution. **Bioinformatics**. 2022. Epub 20220419. doi: 10.1093/bioinformatics/btac279. PubMed PMID: 35438146.
8. **Liu J**, Ma X, Cooper GF, Lu X. Explicit representation of protein activity states significantly improves causal discovery of protein phosphorylation networks. **BMC Bioinformatics**. 2020;21(Suppl 13):379. Epub 2020/09/18. doi: 10.1186/s12859-020-03676-2. PubMed PMID: 32938361; PMCID: PMC7496209.
9. Jin Q, **Liu, J.** and Lu, X. Deep Contextualized Biomedical Abbreviation Expansion. **Proceedings of ACL BioNLP**, 2019.

10. Matte-Martone C, **Liu J**, Zhou M, Chikina M, Green DR, Harty JT, Shlomchik WD. Differential requirements for myeloid leukemia IFN-gamma conditioning determine graft-versus-leukemia resistance and sensitivity. **J Clin Invest**. 2017;127(7):2765-76. Epub 2017/06/13. doi: 10.1172/JCI85736. PubMed PMID: 28604385; PMCID: PMC5490746.
11. **Liu J**, Zeng H, Liu A. The loss of Hh responsiveness by a non-ciliary Gli2 variant. **Development**. 2015;142(9):1651-60. Epub 2015/04/03. doi: 10.1242/dev.119669. PubMed PMID: 25834022.
12. **Liu J**, Liu A. Immunohistochemistry and RNA in situ hybridization in mouse brain development. **Methods Mol Biol**. 2014; 1082:269-83. Epub 2013/09/21. doi: 10.1007/978-1-62703-655-9_18. PubMed PMID: 24048940.
13. **Liu J**, Heydeck W, Zeng H, Liu A. Dual function of suppressor of fused in Hh pathway activation and mouse spinal cord patterning. **Dev Biol**. 2012; 362(2):141-53. Epub 2011/12/21. doi: 10.1016/j.ydbio.2011.11.022. PubMed PMID: 22182519.

MANUSCRIPTS

1. Jamalipour Soofi Y, Rahman M.A., **Liu J***. The application of an individualized Bayesian method to Parkinson's disease in identifying novel genomic variants. 2023. **In Preparation**.
2. Rahman M.A., Cooper G.F., Lu X, **Liu J***. A novel tree-based approach for identifying cancer drivers and their interactions – in conjunction or disjunction? 2023. **In Preparation**.
3. Rahman M.A., Cooper G.F., Lu X, **Liu J***. Individualized Bayesian methods identified novel genomic variants for congenital heart defects from a relatively small cohort. 2023. **In Preparation**.

(* indicates corresponding author while ‘_’ indicates my PhD students)

SELECTED PRESENTATIONS

1. Rahman M.A., Cai C, Bo N, McNamara D, Ding Y, Cooper G.F., Lu X, **Liu J**. (Nov 2023) An individualized Bayesian inference framework for precision medicine. **Poster presentation** at the annual meeting of American Society of Human Genetics, Washington, DC.
2. Rahman M.A., Cai C, Bo N, McNamara D, Ding Y, Cooper G.F., Lu X, **Liu J**. (April 2023) An individualized Bayesian inference framework for detecting genomic variants and their interactions for complex diseases. **Invited talk** by Center for Data Science, Emory University, Virtual.
3. Rahman M.A., Cai C, Bo N, McNamara D, Ding Y, Cooper G.F., Lu X, **Liu J**. (March 2023) An individualized Bayesian inference framework for detecting genomic variants and their interactions for complex diseases. **Invited talk** by Department of Epidemiology, University of Florida, Virtual.
4. Rahman M.A., Cai C, Bo N, McNamara D, Ding Y, Cooper G.F., Lu X, **Liu J**. (Nov 2022) A complementary approach to GWAS in identifying genomic variants of complex traits. **Invited talk** by the Department of Biomedical Informatics, University of Pittsburgh, Virtual.
5. Rahman M.A., Cai C, McNamara D, Ding Y, Cooper G.F., Lu X, **Liu J**. (Oct 2022) An individualized Bayesian method for precision medicine. **Poster presentation** at the CHARGE meeting, Seattle, WA.
6. Jamalipour Soofi Y, Rahman M.A., Gu Y, **Liu J**. (Oct 2022) A feasibility study of machine learning-assisted alloy design using wrought aluminum alloys as an example. **Selected talk** at Materials Science & Technology Technical Meeting and Exhibition (MS&T), Pittsburgh, PA

7. Rahman M.A., Cai C, McNamara D, Ding Y, Cooper G.F., Lu X, **Liu J.** (Apr 2022) An individualized Bayesian method for estimating genomic variants of hypertension. **Selected talk** at 20th Asia Pacific Bioinformatics Conference, Virtual.
8. **Rahman M.A.**, Cai C, Bo N, McNamara D, Ding Y, Cooper G.F., Lu X, **Liu J.** (Oct 2021) A method for estimating personalized causal genomic variants of disease. **Poster presentation** at the annual conference of American Society of Human Genetics (ASGH), Virtual.
9. **Liu J.**, Rahman M.A.. (Oct 2021) Apply and evaluate an instance-specific causal machine learning framework for identifying the causative genomic variants of cardiovascular diseases. **Invited talk**, “Advances in Health Informatics” session at the annual conference of the Institute for Operations Research and the Management Sciences (INFOMRS), Virtual.
10. **Liu, J.**, Ma, X. and Lu, X. (2020) Explicit representation of protein activity states significantly improves causal discovery of protein phosphorylation networks. **Selected talk** at 18th Asia Pacific Bioinformatics Conference, Seoul, South Korea
11. **Liu, J.**, Ma, X. and Lu, X. (2019) Explicit representation of protein activity states significantly improves causal discovery of protein phosphorylation networks. **Selected talk** at NLM informatics training conference, Indianapolis, IN
12. **Liu, J.**, Ma, X. and Lu, X. (2019) Explicit representation of protein activity states significantly improves causal discovery of protein phosphorylation networks. **Talk** at Biomedical Informatic Lecture Series, University of Pittsburgh
13. **Liu, J.**, Zeng, H. and Liu, A. (2014) Ciliary localization of Gli2 is critical for its activation by hedgehog signaling. **Poster presentation** at Keystone Symposia on Developmental Pathways and Cancer, Banff, Canada
14. **Liu, J.**, Heydeck, W., Zeng, H. and Liu, A. (2013) Dual Function of Suppressor of Fused in Shh Pathway Activation and Mouse Spinal Cord Patterning. **Talk** in the CMIND research talk series, The Pennsylvania State University
15. **Liu, J.**, Heydeck, W., Zeng, H. and Liu, A. (2012) Dual Function of Suppressor of Fused in Shh Pathway Activation and Mouse Spinal Cord Patterning. **Talk** in the "Development Biology" group, The Pennsylvania State University
16. **Liu, J.**, Heydeck, W., Zeng, H. and Liu, A. (2012) Dual Function of Suppressor of Fused in Shh Pathway Activation and Mouse Spinal Cord Patterning. **Poster presentation** in Mid-Atlantic SDB Meeting, State College, PA
17. **Liu, J.**, Heydeck, W., Zeng, H. and Liu, A. (2011) Dual Function of Suppressor of Fused in Shh Pathway Activation and Mouse Spinal Cord Patterning. **Selected talk** in Mid-Atlantic SDB Meeting, Philadelphia, PA

RESEARCH ADVISING

Ph.D. Advisor

- Fall 2020 – Present: Md Asad Rahman, “Causal Discovery of Individual-specific Genomic Variants of Cardiovascular Diseases”, Department of Engineering Management and Systems Engineering
- Fall 2021 – Present: Yasaman Jamalipour Soofi, “Machine learning applications for complex data systems analysis: case studies of precision medicine and alloy discovery”, Department of Engineering Management and Systems Engineering

- Fall 2022 – Summer 2023: Prithbey Raj Dey, “Develop and apply an individualized framework for understanding the personalized genomic factors regulating blood lipid phenotypes”, Kummer I&E Doctoral Fellow, Department of Engineering Management and Systems Engineering
- Fall 2023 – Present: Jin Ren, TBD, Department of Engineering Management and Systems Engineering

Ph.D. Committee Member

- Spring 2021 - Fall 2021: Sima Azizi, “Multimodal Neuroscience Data Modeling and Inference”, Advisor: Donald Wunsch, Department of Electrical and Computer Engineering
- Spring 2021 – Present: Prince Titus Codjoe, “Using Machine Learning and Price Momentum for Stock Trend Prediction”, Advisor: David Enke, Department of Engineering Management and Systems Engineering
- Fall 2021 – Present: Oluwadamilare Akinpelu Omole, “A hybrid computational intelligence, data processing, and complex systems model for describing the bitcoin / cryptocurrency market”, Advisor: David Enke, Department of Engineering Management and Systems Engineering
- Spring 2022 – Present: Harishankar V Subramanian, “A theoretical and empirical analysis on explainable AI and transparent AI methods to improve performance of human-AI teams”, Advisor: Casey Canfield, Department of Engineering Management and Systems Engineering
- Spring 2022 – Present: Ankit Agarwal, “Interactions Between Available Choices and Preferences for Infrastructure Technology Adoption”, Advisor: Casey Canfield, Department of Engineering Management and Systems Engineering
- Fall 2022 – Present: Alex Price, “Modeling large-scale healthcare interventions within an existing healthcare infrastructure”, Advisor: Casey Canfield, Department of Engineering Management and Systems Engineering

M.S. Committee Member

- Fall 2021- Present: Hailey Swain, “Effects of Disease States on Mesenchymal Stem Cells”, Advisor: Julie Semon, Department of Biological Sciences
- Fall 2022: Aishwarya Sriram, Non-thesis student, Department of Biological Sciences

TEACHING

Missouri University of Science and Technology (Lecturer)

- EMGT 5412: Operations Management Science (Spring 2021 – Spring 2022)
- BIO SCI 4393: Immunology (Fall 2020 – Fall 2022)
- EMGT 3310: Operations and Production Management (Spring 2020)

The Pennsylvania State University (Teaching Assistant)

- BIOL 240W: Function and Development of Organisms (Spring 2010-2014)

SERVICE AND ENGAGEMENT

EXTERNAL

- Member in NHLBI BioData Catalyst Consortium (2020 – present)
- Journal Reviewer
 - PLOS Computational Biology

- Human Molecular Genetics
- Frontiers in Molecular Neuroscience
- American Journal of Translational Research
- Journal of Neurology, Neurosurgery and Psychiatry
- Professional Societies
 - American Society of Human Genetics (ASHG)
 - Institute for Operations Research and the Management Sciences (INFORMS)

INTERNAL

- University of Florida Centers
 - Center for Genetic Epidemiology and Bioinformatics (GeneBio)
- Missouri S&T Research Centers
 - Center for Biomedical Research (CBR)
 - Intelligent Systems Center (ISC)
 - High Performance Computing Center (HPCC)
- New Faculty Search Committee for Department of Biological Sciences, Missouri University of Science and Technology (07/2021 – 04/2022)
- New Faculty Search Committee for Department of Engineering Management and Systems Engineering, Missouri University of Science and Technology (10/2022 – present)

PROFESSIONAL DEVELOPMENT

July 23 – August 5, 2023 U.S. Ten-Day seminar on the Epidemiology and Prevention of Cardiovascular Diseases and Stroke
Tahoe City, California

HONORS AND AWARDS

2020 – 2021	BioData Catalyst Fellowship, National Heart, Lung and Blood Institute, NIH
2017 – 2019	National Library of Medicine Postdoctoral Fellowship, Department of Biomedical Informatics, University of Pittsburgh
2009	Braddock Scholarship, the Eberly College of Science, The Pennsylvania State University
2007	Second Class Scholarship, East China Normal University
2006	Third Class Scholarship, East China Normal University