ANDREW WAGNER

LinkedIn: Andrew Wagner • Website: wagnera73.github.io

SUMMARY

MS Computer Science student with a BS in Biomedical Engineering and over six years of research experience at the intersection of bioinformatics, software development, and machine learning. Published first-author and co-author papers in top journals including *Nature Communications* and *Science Advances*. Seeking roles that leverage expertise in data analysis, machine learning, and multi-omics integration to drive translational or computational biology research.

EDUCATION

MS	University of Cincinnati, Computer Science (GPA: 3.7)	Dec 2025
BS	University of Cincinnati, Biomedical Engineering (GPA: 3.8)	May 2020
	Graduated Magna Cum Laude	

SKILLS

Programming Languages: Python, SQL, R, MATLAB, C++, bash, shell
Machine Learning: PyTorch, Tensor-Flow, Scikit-Learn, HuggingFace
Web Development: HTML, CSS, JavaScript, FastAPI, Jinja2, ShinyCell
Bioinformatics: Seurat, Signac, Bedtools, SAMtools, Homer, MACS, Galaxy, IPA, PartekFlow
Data Visualization: Cytoscape, Matplotlib, Plotly, ggplot2, pheatmap, IGV
Version Control/Environments: Git, Anaconda, Docker
Soft Skills: Project management, Multi-disciplinary team coordination, Public speaking, Requirement gathering

RESEARCH EXPERIENCE

University of Cincinnati (UC) Simulation Center, Cincinnati, OH
Research Assistant (*through UC in conjunction with Procter & Gamble)*   **Aug 2024 – Dec 2025**
Improved consumer analysis productivity by developing app to automate mandatory data pre-processing.

- Developed Python-based pipeline and webapp to automate noise correction, event detection, product analysis, and report generation on time-series data gathered from IoT-connected devices.
- Developed FastAPI-based UI to run algorithm and report device summary metrics.
- Collaborated with project leads to determine algorithm and UI requirements.
- Remotely assisted five global research teams in North America, Europe, and Japan to roll out the pipeline.

Cincinnati Children's Hospital Medical Center (CCHMC), Cincinnati, OH   **Jan 2016 – Present**
Data Analyst   May 2020 – Present
Led analysis of epigenetic regulation in LAM using single-nucleus ATAC-seq, single – cell RNA-seq, and bulk RNA-seq; applied Seurat, Python, and R to integrate and analyze multi-modal patient data; maintained a public cell atlas and published one first-author paper in a peer-reviewed journal.

- Investigated transcriptomic and epigenomic differences between control and disease state in LAM using multiple single-cell modalities to identify potential drivers of disease.
- Performed front-end and back-end developer duties by updating & maintaining a publicly available database of next-generation sequencing data as a part of the LungMAP intiative.
- Performed RNA-seq analysis and data visualization for other lab groups within CCHMC.

Capstone Student (*for Senior Engineering Project towards BS)*   Aug 2019 – May 2020
Developed method for utilizing integrated next-generation sequencing modalities to study regulatory networks inherent to cells.

- Compared networks from LAM cells with the goal of identifying functional clusters of interactions between transcription factors and target genes unique to this disease state.

Research Co-op Student (*towards BS)*   Jan 2019 – Aug 2019
Renovated open-source database using HTML, CSS, and JavaScript.

- Performed statistical analysis of single-cell transcriptomic data using MATLAB, Python, and R.

- Back end developing experience using SQL and ORACLE.

Research Student   Jan 2016 – May 2016

Selected for a mentored research opportunity through the University of Cincinnati Honors Program's Biomedical Research and Mentorship program.

- Performed PCR reactions, cell transfections, RNA synthesis, DNA transformation, fluorescent microscopy, cell culture, and agarose and acrylamide gel electrophoresis.

PUBLICATIONS

Alharbi, S., **Wagner, A.**, Merkle, S., Pastura, P., McDaniel, C. G., Fox, D., Xu, Y., & Le Cras, T. D. (2026). MEK Inhibition Reduces Vascular Malformations and Gene Dysregulation in NRASQ61R Human Endothelial Cells. Pediatric Blood Cancer, e70002. https://doi.org/10.1002/1545-5017.70002

Wagner, A., Anjum, U., & Zhan, J. Multimodal Entity Alignment via Siamese Network and Structural Attention. In Proceedings of the 2025 IEEE International Conference on Systems, Man, and Cybernetics (SMC), Vienna, Austria, Oct 5–8, 2025. [Oral presentation]

Chen, K., Zhao, S., Guo, M., Reza, H., **Wagner, A.**, Cakar, A. C., Jiang, C., Zhang, E., Green, J., Martin, E., Wikenheiser-Brokamp, K., Perl, A. K., Sinner, D., Yu, J., & Xu, Y. (2025). Decoding Lymphangioleiomyomatosis (LAM) Niche Environment via Integrative Analysis of Single Cell Multiomics and Spatial Transcriptomics. bioRxiv.

Olatoke, T., Zhang, E. Y., **Wagner, A.**, He, Q., Li, S., Astreinidis, A., McCormack, F. X., Xu, Y., & Yu, J. J. (2024). STAT1 Promotes PD-L1 Activation and Tumor Growth in Lymphangioleiomyomatosis. bioRxiv. https://doi.org/10.1101/2024.12.11.627871

Guo, M., Morley, M. P., Jiang, C., Wu, Y., Li, G., Du, Y., Zhao, S., **Wagner, A.**, Cakar, A. C., Kouril, M., Jin, K., Gaddis, N., Kitzmiller, J. A., Stewart, K., Basil, M. C., Lin, S. M., Ying, Y., Babu, A., Wikenheiser-Brokamp, K. A., Mun, K. S., Naren, A. P., Clair, G., Adkins, J. N., Pryhuber, G. S., Misra, R. S., Aronow, B. J., Tickle, T. L., Salomonis, N., Sun, X., Morrisey, E. E., Whitsett, J. A., Consortium, N. L., & Xu, Y. (2023). Guided Construction of Single Cell Reference for Human and Mouse Lung. Nat Commun, 14(1), 4566. https://doi.org/10.1038/s41467-023-40173-5

Olatoke, T., **Wagner, A.**, Astrinidis, A., Zhang, E. Y., Guo, M., Zhang, A. G., Mattam, U., Kopras, E. J., Gupta, N., Smith, E. P., Karbowniczek, M., Markiewski, M. M., Wikenheiser-Brokamp, K. A., Whitsett, J. A., McCormack, F. X., Xu, Y., & Yu, J. J. (2023). Single-Cell Multiomic Analysis Identifies a HOX-PBX Gene Network Regulating the Survival of Lymphangioleiomyomatosis Cells. Sci Adv, 9(19), eadf8549. https://doi.org/10.1126/sciadv.adf8549

Du, Y., Guo, M., Wu, Y., **Wagner, A.**, Perl, A. K., Wikenheiser-Brokamp, K., Yu, J., Gupta, N., Kopras, E., Krymskaya, V., Obraztsova, K., Tang, Y., Kwiatkowski, D., Henske, E. P., McCormack, F., & Xu, Y. (2023). Lymphangioleiomyomatosis (LAM) Cell Atlas. Thorax, 78(1), 85-87. https://doi.org/10.1136/thoraxjnl-2022-218772

Bridges, J. P., Sudha, P., Lipps, D., **Wagner, A.**, Guo, M., Du, Y., Brown, K., Filuta, A., Kitzmiller, J., Stockman, C., Chen, X., Weirauch, M. T., Jobe, A. H., Whitsett, J. A., & Xu, Y. (2020). Glucocorticoid Regulates Mesenchymal Cell Differentiation Required for Perinatal Lung Morphogenesis and Function. Am J Physiol Lung Cell Mol Physiol, 319(2), L239-L255. https://doi.org/10.1152/ajplung.00459.2019

HONORS AND AWARDS

Godown Family Fellowship (Full tuition and stipend towards MS)	2022-2025
Cincinnatus Excellence Scholarship (Full tuition and room towards BS)	2015-2020
Dean's List	2015-2020
UC University Honors Program	2015-2020