

# Akram Vasighi

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## Professional Summary

- PhD, Computer Science with strong background in machine learning, DNN programming & AI modeling.
- AI specialist with 5+ years of experience in implementing and deploying various industrial (nationwide) and academic projects.
- Successful background in leadership in developing large-scale AI models, leading to innovative patent.
- Proficient in Python, R, PyTorch, Scikit-learn, and various data analysis & machine learning frameworks.
- Strong publication records in data analysis, computational biology & healthcare with valuable cross-functional team experience.
- Delivered courses, workshops, & presentations in top-tier conferences.
- Valued member of scientific journal reviewer community.

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## Work Experience

### AI Engineer, Product Developer, & Technical Lead, *Celligent-AI*

**08/2024 - Present**

- Initiated an automating workflow for data integration, cleaning, and preprocessing, effectively communicating with stakeholders to understand their needs and streamline complex processes (C#, SQL, ETL).
- Led a patent project involving the design & development of a new AI Agent-based tool to help researchers to perform and interpret complex single-cell RNA-seq analysis, especially those without programming expertise.
- Integrated automated data analysis with ML and LLM-driven chat interaction to solve significant scientific problems, and generate new proposals based on their intuition of data through the integration, visualization, and analysis of large and complex scRNA seq and clinical data, integrated with public datasets and custom data.
- Ensured testable, maintainable code, subprocess, and refactoring.
- Cross-functional team communication.

### Research Assistant (Volunteer)

**09/2024 – 03/2025**

*Joint work with School of Computer Science, University of Windsor & Windsor Regional Hospital*

#### **Research Project**

- Identified *therapeutically targetable tumour-immune interactions in small cell lung cancer (SCLC)*
- Processed and analyzed large-scale clinical scRNA-seq datasets, implementing quality control protocols and preprocessing techniques.
- Developed machine learning models to identify predictive biomarkers in SCLC expression, achieving ~99% classification accuracy for epithelial cells and ~95% for immune cells.
- Applied recursive feature selection to identify key therapeutic targets, demonstrating that gene expression patterns could predict treatment response with ~96% accuracy for epithelial cells.

## Post-Doctoral Fellow, Data analyst

07/2024 - 03/2025

*Joint work with School of Computer Science & Biomedical Science*

- Analyzed large-scale experimental genomic datasets (CRISPR screen), machine learning techniques and statistical analysis, aiming at detecting biologically significant signals, particularly in non-coding RNA regulation, to understand their roles.
- Created an effective analysis pipeline combining R and Python frameworks to process, visualize, and analyze data, accelerating research timeline.

## Sessional Instructor

09/2023 – 12/2023

*School of Computer Science, University of Windsor, Canada*

- Taught COMP 3670, 102 enrolment, Computer Networks, undergraduate, required course. (Fall 2023)
- Taught COMP 4770, 12 enrolment, AI for Games, undergraduate, elective course. (Winter 2023)

## Graduate Assistant

01/2020 – 04/2024

*School of Computer Science, University of Windsor, Canada*

- Provided supportive mentorship and clear, patient communication as a graduate assistant, guiding students through complex concepts, facilitating engaging discussions, and collaborating effectively with faculty to enhance student learning and academic success.
- COMP 3057 (Cyber Ethics). Undergraduate (2024)
- COMP 2077 (Problem Solving & Information on the Internet), undergraduate (2024)
- COMP 2120 (Object-oriented programming using Java). (2021, 2022, 2023)
- COMP 2540 (Data structure and algorithm), undergraduate, required course. (2020)
- COMP 8967 (Internship Project), graduate, required course. (2022)
- COMP 8547 (Advanced Computing Concepts), a graduate-required course. (2022)
- COMP 8347 (Internet Apps. distributed systems), undergraduate (2021)

## Research Assistant

01/2020 - 04/2024

*School of Computer Science, University of Windsor, Canada*

- Demonstrated effective mentorship by guiding undergraduate and graduate students, clearly communicating complex research concepts, confidently leading collaborative projects, and applying strong problem-solving and writing skills to contribute to scientific publications and reports, while consistently meeting tight conference/presentation deadlines and research milestones.

### **Research Project - SEGCECO**

- I designed and developed ML pipeline for large-scale data to identify and characterize intercellular signaling networks from single-cell transcriptomics data.
- Trained deep learning models, embedding models, optimization, fine-tuning, and benchmarking.

### **Research Project**

- I developed a data analysis pipeline for cell type annotation on COVID-19 scRNA-seq data sets of human & mouse.
- I addressed the significant challenges of high-dimensionality and sparsity.

- Results are published in Scientific Reports (Nature Portfolio), showing improved cell type identification accuracy in complex tissues compared to standard approaches.

**Teaching & Project Assistant,**

*Research group of COMP Science (RPM), University of Windsor, Canada*

- Assist in organizing a series of workshops and events.
- Prepared & delivered a series of workshops in "[Machine Learning with Python](#)" to graduate students.

**Python Teacher (Volunteer)**

**01/2022 -04/2022**

*Canadian Association for Girls in Science (CAGIS), Canada*

- As a best researcher in the Science department, I have been selected to teach Python to kids (7-12 years) using hands-on Python projects.
- I helped to brainstorm, organize, and plan STEM events for members.

**Data Analyst**

**01/2023 -04/2023**

*Academic Data Centre, Leddy Library, University of Windsor, Canada*

- Applied strong analytical thinking in integrating NLP techniques for historical text analysis, effectively collaborating with library staff and researchers to facilitate meaningful interpretation and accessibility of archival resources.
- Helped instructors and speakers with 3 workshops for Codefest.

**Help Desk,**

**05/2022 – 12/2022**

*Leddy Library, University of Windsor, Canada*

- Provided approachable, patient, and clear communication while assisting students and faculty with technology troubleshooting, facilitating productive collaboration and enhancing user confidence in library IT resources.

Education	
Ph.D. in Computer Science, University of Windsor, Canada	01/2020 – 04/2024
M.Sc. in Computer Engineering, Tehran University, Iran	09/2015 – 01/2017

Technical Skills
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**Machine Learning & AI, Data Analysis**

- Python | R | Pytorch | Pandas | NumPy | Matplotlib | Scikit-learn | Pytest | Streamlit | LLMs (GPT) | Prompt Engineering | Automation | Testing & CI/CD | RAG | AI Agents | LangChain

**Tools & Platforms**

- Docker & Containerization | Git | HPC | Bash/Shell Scripting | Data Pipeline & ETL | SQL | LaTeX

**Bioinformatics Tools**

- Scanpy | Seurat | Squidpy | DESeq2 | SAMtools | BEDTools | IGV | GSEA | Cytoscape | STAR | MaGeCK | CaseFinder | Crisprscore

**Leadership & Product Management**

- Modularization & Scalable Architecture | Model Optimization | UI/UX Flow | Cross-functional Team Collaboration

Familiar With: Java | front-end technologies (HTML | React | TypeScript | Tailwind CSS | JavaScript | Responsive Design | WordPress) | Amazon Web Service (AWS) | AWS S3 | Google Cloud Platform (GCP) | Azure ML Studio, Reinforcement Learning techniques (RLHF)

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## Selected Publications in Peer Reviewed Scientific Journals

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[publications accessible via Google scholar profile (<https://scholar.google.com/citations?user=mJSJoqlAAAAJ&hl=en>)]

1. **A. Vasighizaker**, S. Hora, R. Zeng, L. Rueda, "[SEGCECO: Subgraph Embedding of Gene expression matrix for CELL cell COmmunication prediction](#)", Briefings in Bioinformatics, (2024)
2. **Vasighizaker, A.**; Trivedi, Y. Rueda, L., "[Cell Type Annotation Model Selection: General-purpose vs Pattern-aware Feature Gene Selection in Single-cell RNA-seq Data](#)". MDPI GENES (2023)
3. **Vasighizaker, A.**, Danda, S., & Rueda, L. "[Discovering cell types using manifold learning and enhanced visualization of single-cell RNA-Seq data](#)". Scientific Reports, Nature Portfolio, (2022).
4. M. Naik, L. Rueda, **A. Vasighizaker**, "[Identification of Enriched Regions in ChIP-seq Data via a Linear-time Multi-level Thresholding Algorithm](#)", IEEE/ACM Transactions on Computational Biology and Bioinformatics, (2021).
5. **A. Vasighizaker**, A. Sharma, A. Dehzangi. "[A novel one-class classification approach to accurately predict disease-gene association in acute myeloid leukemia cancer](#)", PlosOne Journal, 14 (12), (2019).
6. **A. Vasighizaker**, S. Jalili. "[C-PUGP: A Cluster-Based Positive Unlabeled Learning Method for Disease Gene Prediction and Prioritization](#)", Journal of Computational Biology and Chemistry, (2018).

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## Selected Conference Presentations

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1. Nakul Pandya, Raymond Zeng, Biren Dave, **Akram Vasighizaker**, Swati Kulkarni, Ming Pan, Junaid Yousuf, Luis Rueda, "Identifying Therapeutically Targetable Tumor-Immune Interactions in Small Cell Lung Cancer", WE-SPARK's Health Research, Canada, 2025.
2. **A. Vasighizaker**, S. Hora, L. Rueda, "Exploring Cell-Cell Communication in Pancreas Tissue via Attributed-graph Convolutional Neural Networks on Single-cell RNA-sequencing Data", ISMB/ECCB 2023, Lyon, France
3. **A. Vasighizaker**, S. Hora, L. Rueda, "Unravelling the Complexity of Cellular Interactions using Underlying Graph Representations of Single-Cell Transcriptomics Data", GLBio 2023, Montreal, Canada
4. **A. Vasighizaker**, S. Danda, Luis Rueda, "Discovering cell types using manifold learning and enhanced visualization of single-cell RNA-Seq data", Highlight paper presentation in ECCB 2022, Barcelona.
5. **A. Vasighizaker**, S. Hora, L. Rueda, "A Novel Method to Predict Intercellular Signaling in Single-cell RNA-seq Data via Graph Convolutional Network", ISMB 2022, Madison, USA
6. **A. Vasighizaker**, S. Danda, Luis Rueda, "Discovering cell types using manifold learning and enhanced visualization of single-cell RNA-Seq data", Highlight paper presentation in ACM/BCB 2022, Chicago, IL, USA
7. S. Hora, **A. Vasighizaker**, L. Rueda, "SEGCECO: Subgraph Embedding of Gene expression matrix for CELL cell COmmunication prediction", RECOMB 2022, La Jolla, USA
8. **A. Vasighizaker**, S. Hora, Y. Trivedi, L. Rueda, "Supervised Cell Type Heterogeneity Detection in Single-cell RNA-seq Data", in IWBBIO conference (virtual) 2022.
9. **A. Vasighizaker**, S. Danda, G. Peralta Milla, Luis Rueda, "Cell Type Identification Single-cell RNA-Seq Data via Modified Locally Linear Embedding" in RECOMB conference (virtual) 2021.
10. **A. Vasighizaker**, L. Zhou, L. Rueda, "Cell Type Identification via Convolutional Neural Networks and Self-Organizing Maps on Single-Cell RNA Sequencing Data" in ACM/BCB conference (virtual) 2021.
11. **A. Vasighizaker**, L. Zhou, L. Rueda, "Prediction of Human Pancreas Cell Types via ConvNet on Two-dimensional Mapping of Single-cell RNA-seq Data" in ISMB/ECCB conference (virtual) 2021.
12. **A. Vasighizaker**, S. Hora, A. Nagarajan, Y. Trivedi and L. Rueda, "Supervised Cell Type Heterogeneity Detection in Single-cell RNA-seq Data", ICML 2021, virtual.
13. S. Danda, **A. Vasighizaker**, L. Rueda, "Unsupervised Identification of SARS-CoV-2 Target Cell Groups via Nonlinear Dimensionality Reduction on Single-cell RNA-Seq Data" in IEEE BIBM conference, Seoul, South Korea, (virtual) 2020.
14. **A. Vasighizaker**, "Disease Gene Identification and Prioritization using Machine Learning Algorithms", Conference on Computer and Information Technology, Tabriz, Iran, 2014.

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## Honors, Awards, & Hobbies

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- Mitacs Research Training Award and NSERC Scholarship.
- Member of International Society for Children with Cancer.
- Dancing, Cooking, Traveling, House Decoration, Embroidery!