

# 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, App Developer, & Technical Lead, *Celligent-AI*

**08/2022 - Present**

- Initiated an automating workflow for data integration, cleaning, manipulation, and preprocessing, effectively communicating with stakeholders to understand their needs and streamline complex processes (C#, SQL, ETL ).
- Led a patent project to drive innovative research, involving design & development of a new AI Agent-based tool to help researchers to perform and interpret complex single-cell RNA-seq (scRNAseq) analysis, especially those without programming expertise.
- Integrated automated data analysis with ML and a user-friendly LLM-driven chat interaction UI, empowering experts and non-experts to integrate user feedback and generate new hypothesis based on their intuition of data through streamlining the integration and visualization 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

**09/2024 - Present**

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

#### **Research Project**

- Collaborated with diverse multidisciplinary research teams to identify therapeutically targetable tumour-immune interactions in small cell lung cancer (SCLC), contributing to impactful translational research.
- Communicated findings clearly and effectively with both technical and non-technical audiences, bridging gaps between computational and clinical teams.
- Developed machine learning models to identify predictive biomarkers in SCLC, achieving ~99% classification accuracy for epithelial cells and ~95% for immune cells, while adapting models based on ongoing feedback and validation results.
- Took the initiative in refining the analysis pipeline, ensuring reproducibility and maintainability for future team use, and contributing to the preparation of publication.

## Post-Doctoral Fellow, Data analyst

07/2024 - 03/2025

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

- Collaborated with researchers to analyze large-scale experimental genomic data (CRISPR screens), applying machine learning techniques and statistical analysis to detect biologically significant signals, with a focus on non-coding RNA regulation.
- Created an effective analysis pipeline combining R and Python frameworks to process, visualize, and analyze data, accelerating research timeline.
- Work closely with researchers to understand and translate their needs into efficient computational solutions.
- Assist in organizing a series of workshops and events.
- Prepared & delivered a series of workshops in “Machine Learning with Python” to graduate students.

## Research Assistant

01/2020 - 04/2024

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

- Demonstrated effective collaboration and mentorship; guiding undergraduate and graduate students to ensure individual and team success; 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 (including data gathering) to identify and characterize intercellular signaling networks from single-cell transcriptomics data (scRNAseq).
- 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 (including data gathering) 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.

## 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.

- 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.

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## Education

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**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**

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## Technical Skills

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### Machine Learning & AI, Data Analysis

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

### Tools & Platforms

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

### Bioinformatics Tools

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

### Leadership & Product Management

- Modularization & Scalable Architecture | Model Optimization | Documentation and Version Control (Git) | 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=mJSJoqIAAAAJ&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).

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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. 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

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## Honors, Awards, & Hobbies

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