Adib Miraki Feriz

Wellcome Sanger Institute
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SUMMARY

With about 4 years of experience in computational biology, I specialize in single cell data analysis and bioinformatics area. My passion lies in utilizing AI and machine learning techniques to further the fields of tumor immunotherapy and neuroscience. I have collaborated with several pioneer institutes such as Helmholtz Zentrum Munich, Sanger Institute, and University of Calgary, merging biological and computational aspects of different diseases to gain a deeper understanding of them. My goal is to continue to combine my expertise in both the biological and computational fields to pave the way for new medical breakthroughs that can positively impact society.

KEY SKILLS

- Micro Array, Bulk, Single-cell RNA-seq and Spatial transcriptomics data analysis
- Single-cell data integration and multi-modal analysis using scArches
- Experienced in programming languages (Python and R)
- Data classification
- Perturbation analysis
- Primer designing
- qPCR
- ELISA
- Cell culture
- MIC/MBC
- Proficient in Microsoft word, PowerPoint, Excel, Adobe Illustrator, and PRISM

HONORS AND AWARDS

- Best Oral Presenter in the 9th International Congress of Medical Student   2022
- Best Researcher at Birjand University of Medical Sciences (BUMS)   2022
- Best Researcher at Birjand University of Medical Sciences (BUMS)   2023
- Best Researcher of Iran among undergraduate students   2023

RESEARCH EXPERIENCES

- **Wellcome Sanger Institute**   2/2023-present

Research Collaborator, Bayraktar Group and Lotfollahi Group
Working on single-cell atlases, perturbation analysis and drug discovery.

- **Sharif University of Technology**   7/2022-12/2022

Research Intern, Robust and Interpretable Machine Learning Lab (Rohban Lab)
Working on machine learning methods on single-cell data analysis in TME of prostate cancer.

- **Cellular and Molecular Research Center**   1/2021-12/2022

Research Assistant, Safarpour Lab
Working on single-cell RNA-seq data analysis in TME of various solid tumors.

TEACHING EXPERIENCES

BUMS
Cellular and Molecular Biology Course

EDUCATION

B.Sc. Medical Laboratory Sciences. BUMS, Birjand, Iran. 2019-2023 (**Average Score=17.39 of 20**)

CONFERENCE PRESENTATIONS

- 23rd Annual National Congress and the 9th International Research Congress of Medical Students "The Expression Pattern of CD8+ T cells in Primary Gastric Cancer with Liver Metastasis; From Immunotherapy to Personalized Medicine" 2022, Ardabil, Iran (**Oral**)
- 2nd International and 11th National Iranian Conference on Bioinformatics "Single-cell RNA sequencing data analysis using Explainable Artificial Intelligence identified key transcriptional factors for early COVID-19 severity prediction" 2023, Tehran, Iran (**Oral**)
- 16th International Congress of Immunology and Allergy "Investigation the role of cancer associated fibroblasts in gastric cancer patients treated with nivolumab; a single cell RNA-seq study" 2023, Tehran, Iran (**Poster**)
- 1st International Congress of Cancer Genomics "Utilizing the expression profile of myeloid cells in pancreatic cancer tumor microenvironment; Toward immunotherapy, 2023, Tehran, Iran (**Poster**)
- 23rd International Congress of Microbiology of Iran "Comparative Study of antifungal effect of different active herbal compounds, 2022, Tehran, Iran (**Poster**)

PUBLICATIONS

- **Adib Miraki Feriz**., Khosrojerdi, A., Lotfollahi, M., Shamsaki, N., GhasemiGol, M., HosseiniGol, E., Fereidouni, M., Rohban, M.H., Sebzari, A.R., Saghafi, S. and Leone, P., 2023. Single-cell RNA sequencing uncovers heterogeneous transcriptional signatures in tumor-infiltrated dendritic cells in prostate cancer. **Heliyon**.
- Derakhshani, A., Asadzadeh, Z., Baradaran, B., Safarpour, H., Rahmani, S., Leone, P., Shadbad, M.A., Hosseinkhani, N., Ghasemigol, M., Ayromlou, H. and Ahmadi, H., 2022. The expression pattern of VISTA in the PBMCs of relapsing-remitting multiple sclerosis patients: A single-cell RNA sequencing-based study. **Biomedicine & Pharmacotherapy**, 148, p.112725.
- **Adib Miraki Feriz**., Bahraini, F., Khosrojerdi, A., Azarkar, S., Sajjadi, S.M., HosseiniGol, E., Honardoost, M.A., Saghafi, S., Silvestris, N., Leone, P. and Safarpour, H., 2023. Deciphering the immune landscape of head and neck squamous cell carcinoma: A single-cell transcriptomic analysis of regulatory T cell responses to PD-1 blockade therapy. **Plos one**, *18*(12), p.e0295863.
- Erfanian, N., Nasseri, S**., Adib Miraki Feriz**., Safarpour, H. and Namaie, M.H., 2023. Characterization of Wnt signaling pathway under treatment of Lactobacillus acidophilus postbiotic in colorectal cancer using an integrated in silico and in vitro analysis. **Scientific Reports**, 13(1), p.22988.
- Sanadgol, N., **Adib Miraki Feriz**., Lisboa, S.F. and Joca, S.R., 2023. Putative role of glial cells in treatment resistance depression: An updated critical literation review and evaluation of single-nuclei transcriptomics data. **Life Sciences**, 331, p.122025.
- Erfanian, N., Heydari, A.A., **Adib Miraki Feriz**., Iañez, P., Derakhshani, A., Ghasemigol, M., Farahpour, M., Razavi, S.M., Nasseri, S., Safarpour, H. and Sahebkar, A., 2023. Deep learning applications in single-cell genomics and transcriptomics data analysis. **Biomedicine & Pharmacotherapy**, *165*, p.115077.
- Shadbad, M.A.,**Adib Miraki Feriz**, Baradaran, B. and Safarpour, H., 2024. Tumor-infiltrating CD8+ sub-populations in primary and recurrent glioblastoma: An in-silico study. **Heliyon**.
- Safarpour, H., Ranjbaran, J., Erfanian, N., Nomiri, S., Derakhshani, A., Gerarduzzi, C., **Adib Miraki Feriz**., HosseiniGol, E., Saghafi, S. and Silvestris, N., Holistic exploration of CHGA and hsa-miR-137 in colorectal cancer via multi-omic data Integration. **Heliyon**.

UNDER REVIEW PAPERS

- Targeting the Dynamic Transcriptional Landscape of Treg Subpopulations in Pancreatic Ductal Adenocarcinoma: Insights from Single-cell RNA Sequencing Analysis with a Focus on CTLA4 and TIGIT. **First Author. Immunobiology.**
- Unveiling the Impact of Microglial Cells in Alzheimer's Disease Pathogenesis: Insights from Single-Cell RNA-seq Analysis and In Vivo Validation. **Co-First Author. Molecular Neurobiology.**
- Large-scale characterization of cell niches in spatial atlases using bio-inspired graph learning. **Third Author. Nature Genetics.**

ON-GOING PROJECTS

- **scMol** (Lotfollahi Lab): Generative model for drug discovery through single-cell RNA-seq data.
- **Dis2p** (Lotfollahi Lab): Generative model for batch effect correction and counterfactual prediction.

INTERESTS AND ACTIVITIES

- Drug Discovery
- Out of Sample Prediction
- Neuroscience
- Spatial Transcriptomics
- Cancer Immunotherapy
- Computational Biology

COLLABORATIONS

- Wellcome Sanger Institute, Cambridge, UK: **Omer Ali Bayraktar**, **Mo Lotfollahi**
- University of Calgary, Calgary, Canada: **Afshin Derakhshani**
- University of North Dakota, North Dakota, US: **Mohammad GhasemiGol**
- GenEdit Company, California, US: **Reyhaneh Hooshyar**
- University of Aachen, Aachen, Germany: **Nima Sanadgol**
- Genome Institute of Singapore, Singapore: **MohammadAmin Honardoost**
- University of Bari, Bari, Italy: **Vito Racanelli**
- The University of Newcastle, Newcastle, UK: **MohammadJavad Shojaei**
- Tabriz University of Medical Sciences, Tabriz, Iran: **Behzad Baradaran, Mahdi Abdoli Shadabad**

REVIEWER

- Iranian Journal of Pharmaceuticals Sciences. 2023-Present

MEMBERSHIPS

- Head of Research Department in the Student Research Committee of BUMS. 2022-2023
- Member of Iranian Bioinformatics Society. 2022-Present

REFERENCES

- **Dr. Mo Lotfollahi**. Wellcome Sanger Institute, Cambridge, UK (ml19@sanger.ac.uk)
- **Dr. Omer Ali Bayraktar**. Wellcome Sanger Institute, Cambridge, UK (ob5@sanger.ac.uk)
- **Dr. Carlos Talavera-Lopez.** Julius-Maximilian-Universität-Würzburg, Germany(carlos.talavera-lopez@uni-wuerzburg.de)