

# Aylar Babaei

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## SUMMARY

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I'm a recent bioinformatics Master's graduate with a science background and 2+ years of lab research experience. My expertise lies in analyzing spatial transcriptomic data and benchmarking metabolomics data for software development. I aim to bridge the gaps between complex data analysis and biological insights.

## EDUCATION

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### George Washington University

*Master of Science in Bioinformatics And Molecular Medicine*

Washington, DC

Aug 2022 - May 2024

### Shiraz University

*Bachelor of Science in Chemistry*

Shiraz, Iran

Sep 2014 - May 2018

## TECHNICAL SKILLS

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**Languages:** R, Linux/bash, MySQL, Python

**Data Analysis:** Multi-omics integration, interpretation, Integrating Single Cell and Visium Spatial Gene Expression Data, statistical analysis, visualization

**Cloud Computing:** AWS, HPC, parallel computing

## EXPERIENCE

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### Graduate Research Assistant

Oct. 2023 – Present

*The George Washington University, Computational Biology Institute*

*Washington, DC*

- Led the profiling and quantification of LC-MS metabolomics data for the massSight benchmarking project, enhancing the software's analytical capabilities
- Analyzed and processed large metabolomics datasets like IHMP and IBD, resulting increase in data accuracy and efficiency for research projects
- Utilized an array of metabolomic analysis software, including Compound Discoverer and Asari, comparing their technical adaptability and proficiency
- Employed Excel for effective data organization and leveraged HPC environments for processing large-scale metabolomic datasets
- Applied statistical analysis and R programming skills for in-depth processing and benchmark development for massSight, ensuring reliable results
- Collaborated with a team of 5 researchers to design and conduct a study that resulted increase in grant funding, enabling further exploration of important research questions

### Pathology Laboratory Assistant

Mar 2023 - Jan 2024

*The George Washington University, Cancer Center*

*Washington, DC*

- Conducted 10X visium spatial transcriptomics to analyze the effects of CDKN2A/P16 deletion and Kras activation, contributing to the understanding of pathogenesis in the small intestine epithelial cells of mice
- Classified various epithelial groups for DE analysis and conducted comparative studies between mouse and human gene expressions to draw parallels and contrasts in pathogenesis, pathway enrichment analysis
- Managed a database of over 2,000 mice, ensuring data accuracy and integrity, contributing to reliable research outcomes
- Assisted with subcutaneous and IP injection, dissection, streamlined collection of 200 tissue samples and genotyping
- Supported research integrity by providing rigorous care for laboratory mice, including feeding, watering, and health monitoring, resulting in improved data accuracy and reliability

### Analytical Chemistry Research Assistant

Dec 2017 - Jul 2018

*Shiraz University*

*Shiraz, Iran*

- Assisted a comparative ELISA analysis for the discrimination of NSAID drugs using a colorimetric sensor array, enhancing detection capabilities via RGB incorporation
- Executed data analysis with ImageJ, and plotted calibration curves in Excel