Matthew J. Oldach, M.Sc.

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SUMMARY

Experienced Senior Consultant and Team Lead with expertise in software development, DevOps, and bioinformatics. Proven track record in enhancing software release delivery, leading high-performing teams, and optimizing bioinformatics solutions.

EXPERIENCE

Amaris Consulting, Toronto — *Senior Consultant & Team Lead*
April 2021 - PRESENT

- Led the enhancement of software release delivery by orchestrating seamless builds, deployments, and releases on AWS infrastructure using Infrastructure as Code (IaC) principles. Employed Amazon Web Services (AWS) to ensure efficient and scalable deployment processes, further optimizing our Continuous Integration/Continuous Deployment (CI/CD) pipeline.
- Led a team of five life science consultants, fostering a highly productive and engaged group. Held regular check-ins, empowered team members, and understood their strengths and weaknesses.
- Leveraged Python, R, and Julia scripting for bioinformatics analysis, applying DevOps practices and Data Science techniques.
- Applied deep learning and machine learning techniques in bioinformatics, using Python, to uncover insights in genomics and sequencing data.
- Ensured the team's adherence to software engineering principles, best practices, and security practices throughout the project.
- Conducted regular code reviews and mentored team members to maintain high code quality and documentation.
- Optimized performance, both in software and bioinformatics analysis, by identifying and implementing areas of improvement to cut processing time by 40%, saving $10,000 monthly.
- Demonstrated strong communication and collaboration skills within the team, working seamlessly with domain experts in genomics and bioinformatics.

Cummings School of Medicine, Calgary— *Bioinformatician*
March 2020 - March 2021

- Conducted data analysis on genomics data, including sequencing data, gene expression data, and DNA variant analysis.
- Developed Snakemake workflows to process and analyze sequencing data, saving significant computational time.
- Created Docker/Singularity containers for bioinformatics environments, improving the ease of use for researchers and reducing setup time.
- Applied statistical analysis techniques, R programming, and Python to investigate correlations and trends in genomics data.
- Utilized bioinformatics tools such as BEDTools, GATK, BWA, Bowtie, Picard, and more for genomics analysis.
- Collaborated with domain experts in genomics, molecular biology, and bioinformatics to address research questions effectively.
- Ensured data quality and integrity through thorough data cleaning and quality control.
- Utilized skills in data visualization to communicate findings to colleagues and sponsors.

SKILLS

Programming Languages: Python, R and Julia

Data Science: Machine Learning, Deep Learning, Artificial Intelligence

DevOps: Docker, CI/CD, Terraform

Cloud Computing Platforms: AWS, Azure

Bioinformatics: Genomics, DNA Sequencing, Bioinformatics Tools

Data Visualization: Data Science Tools (e.g., Jupyter, Pandas, Scikit-Learn)

High-Performance Computing: SLURM, Parallelization

Software Engineering: Software Testing Principles, Debugging, Software Architecture Design, Scalability

Data Security and Privacy: Data Privacy, Data Security

Soft Skills: Collaboration, Interpersonal Skills, Continuous Learning

Additional Skills: Shiny Development, Agile Methodology, Jenkins, Jira, Gitlab, Github

EDUCATION

University of Calgary - M.Sc. Biological Sciences 2015

Dalhousie - B.Sc. Marine Biology (Honors) 2011

Douglas Mental Health University Institute, Montreal— *Biostatistician*
August 2018 - September 2019

- Utilized statistical packages, including R and Python, to process and analyze complex datasets related to psychiatric research and genotyping.
- Developed and refined pipelines for QC and processing of genotyping and epigenetic methylation datasets, ensuring data accuracy and quality.
- Applied statistical analysis techniques to investigate and quantify trends in psychiatric research, facilitating data-driven decision-making.
- Created high-quality dynamic reports and presentations with interactive visualizations to communicate research results and findings to colleagues and sponsors, using tools like ggplot2 and plotly.
- Reduced processing and analysis time significantly by optimizing code with parallel computing, improving efficiency and saving valuable time.
- Worked with domain experts in psychiatry and genomics to address research questions effectively and provide statistical support for ongoing studies.
- Demonstrated strong oral and written communication skills in presenting research findings and collaborating with colleagues.
- Ensured the reproducibility and integrity of statistical analyses, implementing best practices for data ethics and data privacy in research.

PROJECTS

Shiny-filteRs — *RStudio Shiny Contest 2021*
https://matthew-j-oldach.shinyapps.io/shiny-filteRs/

- Developed a native mobile-phone app for RStudio's Shiny Contest 2021, blending technical prowess with artistic flair, showcasing proficiency in integrating R, Python, and JavaScript.
- Leveraged deep learning and machine learning techniques to empower users to craft art, demonstrating expertise in Machine Learning, Deep Learning, and Artificial Intelligence.

hinuhinu — *Open Source Project* https://matthew-j-oldach.shinyapps.io/hinuhinu/

- Developed an interactive Spatial Mapping R-Shiny application, enabling users to seamlessly display and overlay Shapefiles, GIS coordinates, and Elevation Raster data, demonstrating proficiency in Data Visualization.
- Implemented the app with considerations for scalability and cloud computing platforms, ensuring it can handle large datasets, in line with the emphasis on AWS and GCP.
- Facilitated collaborative research and data-driven decision-making through user-friendly data exploration and analysis tools.

vapoRwave — *Open Source Project* https://matthew-j-oldach.shinyapps.io/hinuhinu/

- Developer of the "VapoRwave Themes" R package, a popular open-source project with 277 stars on GitHub.
- This package provides a range of ggplot2 themes inspired by the vaporwave aesthetic which showcases my data visualization and graphic design prowess.
- Actively engaged with a vibrant open-source community, encouraging user contributions, resolving issues, and maintaining the project's robustness.
- Showcased my expertise in the R programming language, highlighting your proficiency in coding, package development, and data visualization.
- Evidenced my commitment to sharing my work and knowledge with the wider community, fostering collaboration and knowledge exchange.

PUBLICATIONS

MTHFD1 interaction with BRD4 links folate metabolism to transcriptional regulation. *Nature Genetics*, 2019

Distinguishing species using GC contents in mixed DNA or RNA sequences. *Evolutionary Bioinformatics,* 2019.

***De novo* assembly and annotation of the *Acropora gemmifera* transcriptome.** *Marine Genomics*, 2018

Transcriptome dynamics over a lunar month in a broadcast spawning *Acroporid* coral. *Molecular Ecology*, 2017