Murto Hilali

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SUMMARY OF QUALIFICATIONS

- 5+ years of experience in biological data analysis & collaborative workflow development (Python, R, WDL, Bash, Git).
- Expertise with HPC clusters and containerization methods from OICR & LatchBio (Docker, SLURM, Cromwell).
- Proficiency with large -omics databases and tools for literature review (RCSB PDB, UniProtKB, NCBI, ClinVar, IntAct).
- Skilled in 3D-protein modeling & structural biology from interactomics study at SickKids (PyMol, ChimeraX, AlphaFold).
- Strong understanding of core machine learning skills, including exploratory analysis, visualization, & feature engineering.
- Influential communication (interpersonal, written, presentation) skills.

EXPERIENCE

Bioinformatics Researcher | The Hospital for Sick Children | Toronto, ON   01/2023–12/2023

- Implemented a machine learning algorithm (XGBoost) to classify and predict structural impacts of de novo missense variants on protein interactions with a micro-average Area Under Curve of 0.91.
- Leveraged biocomputational best practices and tools (exploratory data analysis, Jupyter notebooks, GPU parallelization, hyperparameter tuning, SHAP values) to find 2 potential protein mechanisms involved in Autism Spectrum Disorder.
- Pioneered a novel approach to predict disease mechanisms of de novo mutations in Cerebral Palsy by mastering AlphaFold2-Multimer and structural biology fundamentals, generating interaction data on 25+ proteins and leading to upwards of 500+ new research paths per data point.
- Contributed to a paper published in Nature Genetics, collaborating with 10+ researchers and 3 organizational stakeholders, including Holland Bloorview Kids Rehabilitation Hospital.
- Presented project insights to 45+ researchers and executives at the Scherer Lab in The Center for Applied Genomics.
- Achieved authorship credits on a scientific abstract presented at the International Cerebral Palsy Genomics Consortium.
- Developed DAMIA, a pipeline and open-source library of command-line tools, streamlining Disease-Associated Missense Interactome Analysis for the scientific research and therapeutics community.
- Created high-impact visuals for a faculty candidate research presentation, visualizing and presenting complex data in an understandable and actionable way.

Bioinformatics Workflow Developer | OICR | Toronto, ON   01/2022–04/2022

- Accelerated workflow execution time by 50% via parallelization techniques.
- Developed several workflows from scratch in a high-performance computing (HPC) cluster environment.
- Collaborated via GitHub, Bitbucket, Jira, and Confluence to enhance four existing pipelines in OICR's codebase.
- Constructed regression tests for all pipelines via Jenkins that accounted for speed and stochastic elements in data.
- Spearheaded the creation of an internal visualization tool for novel pipelines to increase documentation efficiency, generating diagrams used in internal wikis and READMEs.
- Explored FASTQ, BAM, and BED files through command-line tools like Samtools, Picard, and GATK.

Biocomputing Developer | LatchBio | Remote   05/2022–08/2022

- Developed and implemented multiple cloud-based pipelines using LatchBio's Python SDK, including functions from MMSeqs2.
- Integrated diverse testing methodologies to contribute to the feedback process of SDK development and iteration.
- Launched and generated live-stream content around collaborative bioinformatics development.

SKILLS

- *Scientific:* Protein-Protein Interactions, Immunology, Structural Bioinformatics, WGS/WES Data, Biostatistics
- *Development:* Distributed Model Training, Large Dataset Management, Parallelized Hyperparameter Tuning, Workflow Development, Regression Testing, Agile Development, Agile Research, Machine Learning, Deep Learning, Statistics
- *Software:* Microsoft Office (Word, PowerPoint, Excel), Python, R, Jira, Confluence, BitBucket, WDL, Bash, Git, SLURM, NumPy, SciPy, BioPython Seaborn, Scikit-Learn, PyTorch, TensorFlow, XGBoost, AlphaFold

EDUCATION

University of Waterloo, Waterloo, ON

Honour's Bachelor of Science (BSc) in Biotechnology/Economics

Relevant Courses: Mathematical Modeling of Molecular Systems, Methods in Bioinformatics, Biostatistics & Experimental Design, Advanced Cell Biology

Expected Graduation: 04/2025