Sedat Demiriz

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Professional Summary

Bioinformatics Programmer with 3 years of experience. Specialty areas include application of reproducible software development methods to solving research problems, identifying associations in genotyping and NGS data from general and disease population cohorts

Experience

Computational Biologist - *Sequence Bio Inc.*   *Jul '21 – Nov '23*
- Lead the development of GWAS and ROH analysis pipelines with a focus on scalability and reproducibility
- Identified disease associations by analyzing data from company's Newfoundland population cohort
- Implemented algorithms to extract insights from founder population by combining company and public datasets

Research Programmer - *BC Genome Sciences Center*   *Nov '20 – Mar '21*
- Performed quality control of incoming clinical oncopanel wet lab data by NGS data quality metrics
- Streamlined existing quality control and visualization scripts and configured for reusability
- Assisted graduate students with applying computational approaches to research questions

Biosensor R&D Co-op Programmer - *CiBER Lab, SFU*   *May – Sep '18*
- Automated sensor response data processing and generation of easily digestible visualizations
- Performed collection of datafrom hundreds of sensor instances during development
- Presented and implemented metrics for determining sensor instance success based on response pattern

Genetics Co-op Student - *Istanbul University Genetics Institute*   *May – Aug '16*
- Carried out clinical PCR, DNA and RNA isolation and sample quality control procedures
- Worked routinely in cell culture laboratory to grow five varieties of tumnor cell populations for lab use
- Lead nad supported four other co-op students during their first month with the lab

Skills

- Software development experience in Python, R, and Bash using good software development practices: version control, unit testing, documentation
- Writing robust data transformation and analysis scripts and producing easy-to-understand charts and plots to visualize underlying patterns in genomics data
- Development of scalable workflows on Linux, leveraging HPC and Cloud resources for processing large NGS datasets using industry standard bioinformatics tools
- Identifying phenotype-genotype associations in clinical data from general population cohorts
- Extracting data from SQL relational databases and unstructured public data sources to derive insights

Education

BSc Joint Major Mol. Biology and Biochem. & Comp. Sci. - *Simon Fraser University*   *'15 – '20*
- Computing Science: Data Science, Machine Learning, Databases, Algorithms
- Molecular Biology: Bioinformatics, Human Genomics, Applied Wet Labs
- Statistics: Exploratory Data Analysis, Experimental Design and Analysis

Publications

- Gilbert, E., Zurel, H., MacMillan, M. E., Demiriz, S., Mirhendi, S., Merrigan, M., O'Reilly, S., Molloy, A. M., Brody, L. C., Bodmer, W., and et al. (2023). The Newfoundland and Labrador Mosaic founder population descends from an Irish and British diaspora from 300 years ago. *Nature Communications Biology*

- Zurel, H., Bhérer, C., Batten, R., MacMillan, M. E., Demiriz, S., Mirhendi, S., Gilbert, E., Cavalleri, G. L., Leach, R. A., Scott, R. E. M., and et al. (2022). Characterization of the Y chromosome in Newfoundland and Labrador: Evidence of a founder effect. *bioRxiv*