WILLIAM RICHARDS

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An accomplished developer with a proven track record for providing reliable technical expertise, project management, and program delivery. An innovator who excels in the challenge of accurate solutions for difficult situations in unique code reviews, regular production releases, and release testing to maintain program goals. A well-rounded and reliable leader with outstanding interpersonal and communication skills, driven to develop and advance industry leading solutions in a challenging and rewarding environment.

Core Skills and Knowledge

➢ Program and Project Management	Data Structures, Software Design	Git, Slurm, Frontend, Backend
➢ Collaboration and Coordination	Optimization and Troubleshooting	NodeJs, Linux, Bash, AWS, CloudFront
➢ Scheduling and Task Prioritization	C++11, Valgrind, CMake, Python3	Javascript ES6, HTML5, CSS3, SASS
➢ Optimization and Troubleshooting	Data Mining, Computational Biology	Webpack, Vue, Vue-CLI, d3

Experience

University of Utah – Department of Human Genetics, Salt Lake City, UT **April 2017 – Present**

Web Developer (April 2019 – Present)

➢ Responsible for developing pedigree visualization analysis tool for institutional data and genotype phenotype regression
➢ Designed, prototyped, implemented, and integrated tool into an access controlled protected environment data platform
➢ Interfaced with restful API including an access-controlled AWS backend, leveraging Vue, node.js, d3, and Ajax technologies
➢ Introduced local file support, and created demo workflow on real case data to showcase the tool's capabilities
➢ Performed code reviews and developed regular production releases and release testing for genomic analysis application
➢ Implemented new features following Agile methodologies, collaborating with analysts and clinicians to troubleshoot issues
➢ Rewrote and optimized visualization rendering programing within app to reduce rendering start time and the time to interact
➢ Evaluated, troubleshot and refactored code base to improve use of the Vue framework using Vue, node.js, webpack, and d3
➢ Developed interactive and real-time, quality control visualizations to analysis workflow for clinical diagnostic application
➢ Standardized visual components for reusability across different apps to advance corporate access and app reliability
➢ Coordinated team to integrate code into development and production environments, according to version control protocols
➢ Planned, scheduled, and aligned development strategies and resources to ensure corporate software and app goals are met

Software Developer (August 2017 – April 2019)

➢ Developed variant detection tool and refactored genetic discovery tool, including error checking and debugging memory leaks
➢ Modernized build environment with C++11 and CMake for improved stability across various internal systems' environments
➢ Developed and documented user-friendly interface with flexible command line interface, for wider adoption of the tool
➢ Led development for ALU detection tool, developed algorithm and implementation to find Denovo ALU mobile elements
➢ Deployed and integrated stand-alone ALU detection tool into the labs' variant calling pipeline to standardize processes
➢ Performed analysis on patient data through AWS HPC cluster while verifying findings that were to be used in lab publications
➢ Developed and implemented structural variant detection algorithm into the labs' variant calling pipeline
➢ Extended algorithm to include all mobile elements, translocations, inversions, and large structural insertions and deletions
➢ Performed analysis using variant tool on patient data to be used in lab publications according to requirements

Research Assistant (April 2017 – August 2017)

➢ Developed machine learning strategy to filter contaminated human tissue inside mouse patient derived, xenograft models
➢ Implemented data preprocessing, training, evaluation, and filtering work flows with TensorFlow to achieve results
➢ TensorFlow facilitated the uptake in an unfiltered FastQ file and returned it to a filtered FastQ file, using python3, TensorFlow

Intern (April 2016 – September 2016)

➢ Developed genetic data analysis tools and visualization processes for 10x genomic data sets according to institutional needs
➢ Implemented clustering algorithm to reconstruct large genomic regions from 10x barcoded short read sequences
➢ Deployed using C++ for the clustering algorithm and Python for the data analysis and visualizations of data sets

Education

Carleton College, Northfield, MN **2017**
Bachelor of Science – Computer Science

REFERENCES

References Will Be Provided Upon Request