

William Richards

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Education

Carleton College - Computer Science Major - 2013-2017

Coursework: Data Structures • Computer Organization and Architecture • Software Design • Programming Language Design • Computability and Complexity • Data Mining I - III • Computational Biology and Medicine • Evolutionary Computing and Artificial Life • Calculus I-III • Linear Algebra • Algorithms • Math of Computer Science • Visualization for Data Science

Skills

C++, Valgrind, CMake, Python, Javascript (ES6), HTML, CSS, Vue, d3, NodeJs, Linux, AWS, Git

Technical Experience

Research Assistant

University of Utah Department of Human Genetics (summer 2016)

- Developed genetic data analysis tools for 10x Genomic data
 - Used clustering to recover long-range information from barcoded short sequencing reads. (c++)

University of Utah Department of Human Genetics - Research Assistant (summer 2017)

- Implemented neural network to filter contaminating human tissue inside mouse patient derived xenograft models (Python)

Software Developer

University of Utah Department of Human Genetics - (August 2017 - March 2019)

- Refactored lab-developed genetic discovery tool, added error checking, debugged memory leaks, developed flexible command line interface, modernized build environment with CMake (c++)
- Wrote tool to find denovo ALU mobile elements, performed analysis on patient data on AWS HPC cluster and verified findings (c++)
- Developed tool to find more denovo mobile elements, translocations, inversions, and large structural insertions/deletions, Performed analysis with this tool and verified results (c++)

Web Developer

University of Utah Department of Human Genetics (April 2019 - Present)

- Author of pedigree visualization tool with genotype/phenotype regression visualizations
 - Worked with sensitive patient health information, HIPAA compliant, support user upload and integrated with access controlled protected environment data platform (Vue, node.js, d3)
- Developed data quality control visualizations for clinical diagnostic application
 - Worked closely with team members to integrate code into development and production environments, followed version control protocols (Vue, node.js, d3)
- Implemented features and performance improvements for genomic analysis application
 - Performed code reviews, responsible for regular production releases and release testing
 - Worked closely with analysts and clinicians to receive and implement feedback
 - Optimized visualization rendering, reducing time to start render and time to interact

Additional Activities

- Presented poster for web QC tool at Cold Spring Harbor biology of genomes 2018
- Kaggle Data Mining Challenge – “What’s Cooking?”- Top 500 finisher with over team 1500 entries

Portfolio available at: williamrichards2017.github.io