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I am a data scientist and software developer in bioinformatics, working in a computational biology lab at the University of Utah.

EXPERIENCE

University of Utah, Dept of Human Genetics

Senior Software Developer
2014 – Present

Developed real-time genomic visualizations for the web, including QC app that shows various metrics on a VCF (variant control format) file <http://vcf.iobio.io> and an application for performing real-time variant discovery <http://gene.iobio.io>. This app streams data to services which annotate variants with functional impact, protein prediction, allele frequency, and regulatory elements.

Currently working on a deep learning model to predict cancer drug response from tumor somatic mutations, copy number variations, and gene expression.

University of California Berkeley

TA
2020 – Present

Advise graduate students taking Data Visualization and Communications course through the Masters of Data Science (MIDS) program. Hold regular office hours to guide students creating D3 and Altair data visualizations.

Huntsman Cancer Institute

Senior Software Developer
2004 - 2014

Co-developer of BioMiner, a tool that queries ChIP Seq, RNA Seq, Bisulfite Seq, and Variant analysis based on region and gene-based criteria. Results provide information about analysis and samples with links to visualize data tracks in IGV genome browser.

Principle developer of GNomEx, a LIMs and Analysis Project repository for high throughput sequencing facilities. Software tracks genomic experiments from ordering through results delivery and downstream analysis. Responsibilities include leading team of 4 developers and working closely with core facility managers and bioinformatics analysts to provide technical solutions that keep pace with fast-changing, ever expanding needs.

Utah Genome Project, Cimarron Software

Software Developer

1994 - 2004

Developed a framework for laboratory management. Developed general purpose Ad hoc reporting application that allows the end-user to enter search criteria and generate queries with intuitive user interface which hides the complexity of the underlying relational database.

EDUCATION

Master of Information and Data Science – UC Berkeley

GPA – 3.96

Jack Larson Data for Good Fellowship – Spring 2021

Hal R. Varian MIDS Capstone Award – Summer 2021

Bachelor of Science – DeVry University

GPA – 4.0, Student of the Year 1985, Presidential Honor Society, Epsilon Delta Pi

PUBLICATIONS

Di Sera, T., Velinder, M., Ward A, Qiao Y, Georges S, Miller C, Pitman A, Richards W, Ekawade A, Viskochil D, Carey J, Pace L, Bale J, Clardy S, Andrews A, Botto L & Marth G, "Gene.iobio: an interactive web tool for versatile, clinically-driven variant interrogation and prioritization" Nature Scientific Reports 2020 Nov 6:2020.11.05.20224865

Ostrander BEP, Butterfield RJ, Pedersen BS, Farrell AJ, Layer RM, Ward A, Miller C, DiSera T, Filloux FM, Candee MS, Newcomb T, Bonkowsky JL, Marth GT, Quinlan AR. "Whole-genome analysis for effective clinical diagnosis and gene discovery in early infantile epileptic encephalopathy." NPJ Genome Med. 2018; 3: 22.

Ward, Alistair, Mary A. Karren, Tonya Di Sera, Chase Miller, Matt Velinder, Yi Qiao, Francis M. Filloux, et al. 2017. "Rapid Clinical Diagnostic Variant Investigation of Genomic Patient Sequencing Data with iobio Web Tools." Journal of Clinical and Translational Science 1 (6): 381–86.

Layer, Ryan M., Brent S. Pedersen, Tonya DiSera, Gabor T. Marth, Jason Gertz, and Aaron R. Quinlan. 2018. "GIGGLE: A Search Engine for Large-Scale Integrated Genome Analysis." Nature Methods 15 (2): 123–26.

Miller C, Yi Qiao, Tonya DiSera, Brian D'Astous, and Gabor T. Marth. 2014. "Bam.iobio: A Web-Based, Real-Time, Sequence Alignment File Inspector." Nature Methods 11 (12): 1189.

Nix DA, Di Sera TL, Dalley BK, Milash BA, Cundick RM, Quinn KS, Courdy SJ: Next generation tools for genomic data generation, distribution, and visualization. BMC Bioinformatics 2010, 11:455