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Samantha Taffner

Highlights of Qualifications

- Accomplished full stack web developer & data scientist who pioneered the development of a laboratory electronic medical record, big data analysis pipeline, and multiple interactive data visualization applications.
- Accelerated the advancement of scientific research by continually improving my craft and implementing the latest technologies.
- Creative thinker with excellent critical thinking and problem solving skills.
- Excellent written, as well as verbal, communication skills.
- Extensive teaching experience, including time spent teaching chemistry at the college level, as well as conducting in-depth software training seminars for colleagues at the University of Rochester Medical School and Washington University Medical School.
- Solid managerial skills with 10 years of experience managing a small business, including developing software which reduced personnel time by 75%.
- Experience developing HIPAA-compliant applications.
- Excited by the thrill of learning new technologies, beginning a new project, and applying my skills to industries beyond genetics.

Technical Skills

- JavaScript: JQuery, D3.js, RequireJS, QUnit, MVC
- PHP: FPDF, MVC
- Databases: MySQL, SQLite
- HTML: HTML5, SEO
- CSS: CSS3, Bootstrap
- Python: numpy, scipy, pandas, matplotlib, parallel processing
- R: CummeRbund, DESeq
- Version Control: Git
- Graphics Editing: Inkscape, Gimp
- Operating Systems: Linux, Mac OSX, bash

Work Experience

Web Application Developer / Bioinformatics Analyst

July 2017 - Present

University of Rochester Pathology Department

Rochester, NY

Independently working on a variety of clinical and research projects including web development and command line linux programs.

Key Projects

- Revolutionized the Molecular Diagnostics laboratory, by pinpointing the need and solely developing a clinical molecular diagnostics electronic medical record system at URM, called Molecular Diagnostics Infotrack. Stepping away from a paper system, freed up staff time, resulting in a great reduction of operating costs. The web application is built using Linux, Apache, MySQL, PHP, Python, and JavaScript.
- Created a clinical microbiology pipeline, a robust, quality-controlled, modular process for diverse applications and pathogens in Python, SQLite, and JavaScript which runs on a Slurm high performance cluster.
- Initiated the development of a clinical research sample inventory and reporting system, called Microbiology Infotrack. Clinical research was accelerated via sample organization and built in graphical apps for data analysis. Built using Linux, Apache, MySQL, PHP, JavaScript, and D3.js.

Web Application Developer / Bioinformatics Analyst

Nov. 2011 - June 2017

Washington University in St. Louis

St. Louis, Missouri

Performed a variety of both front and back end development tasks on a diverse set of projects including: developing inventory management tools, designing custom visualizations in D3.js, establishing NGS Data Analysis workflows, building a human sample biorepository database, and automating everyday tasks.

Responsible for all phases of the software development life cycle of the following key projects. The elegant graphs described below can be viewed in my portfolio.

Key Projects

- Developed Turbo Storage, a browser-based database-driven inventory tracking application in the LAMP environment, for tracking biological samples in freezers. Turbo Storage was developed as a desktop and mobile friendly free application to save researchers time, money, and frustration. Turbo Storage was built with an MVC architecture and a responsive layout.
- Pinpointed the need for a HIPAA compliant patient database to store patient history and symptoms for a rapidly growing biorepository. This application was developed in the LAMP environment, and included a clickable svg of a human skeleton to store patient symptoms. The skeleton was drawn in Inkscape, with the interactive features powered by D3.js. The project resulted in a manuscript being published in the widely respected medical journal, *Arthritis and Rheumatology*, which uncovered

the differences between symptoms of Rheumatoid Arthritis and Chikungunya patients.

- Created Rainbow HiC, a tool to discover the complex DNA folding structure. A manuscript is currently being written where Rainbow HiC was successfully used to discover the differences in the DNA structure between Natural Killer Cells and B-cells. Datasets are mined using python, numpy, the MapReduce algorithm, and parallel processing. The interactive genome browser is powered by JavaScript, D3.js, JQuery, and Bootstrap. The MVC architecture was custom designed using RequireJS.
- Devised Splicer, the first interactive sashimi plot software, which identifies unique RNA splicing events anywhere in the genome. Splicer allows researchers to identify a disturbance in splicing which can be the cause of disease. The data sets are mined to find unique events using python, numpy, scipy, & pandas. JavaScript, D3.js, and JQuery are used to produce the dynamic interactive graphs.
- Invented IRS, the first Single Cell RNA-Seq tracker which provides a better understanding of the function of an individual cell in the context of its microenvironment. JavaScript, D3.js, and JQuery are used to produce thousands of linked interactive dot plots. A lasso tool is implemented to select groups of dots and highlight the same dots in all of the plots.

Manager of Rheumatic Disease Core Center (RDCC)

July 2007 - May 2017

Washington University in St. Louis

St. Louis, Missouri

Responsible for project management, customer relations, customer education, strategic decision-making, database implementation, and providing scientific testing (e.g. microsatellite analysis, paternity testing, and genetic linkage analysis) for the RDCC, a NIH core center. Core centers operate as a non-profit while receiving some funding from the NIH with the purpose of centralizing research expertise.

Spearheaded the development of a small business database to automate daily core center tasks, including testing, tracking, invoicing, and reporting tools. This database drastically reduced personnel time, making it possible to increase responsibilities. Technologies included PHP with an MVC architecture, MySQL, JavaScript, JQuery, RequireJS, and Bootstrap.

Adjunct Professor

McKendree University

Aug. 2007 - Dec. 2007

Lebanon, Illinois

Taught general chemistry lab. Designed and implemented course curriculum and structure, assessed student progress and provided guidance and assistance in laboratory tasks. Coordinated with Department Chair to ensure curriculum and course material met university guidelines.

Agronomy Lab Assistant

Michigan State University

May 2006 - Mar. 2007

East Lansing, Michigan

Assisted in a research project to determine the best crop rotations and cover crops for

bioavailable phosphorus in the soil.

Teaching Assistant
Michigan State University

Aug. 2004 - Dec. 2006
East Lansing, Michigan

Taught 6 sections of general chemistry lab and 9 sections of organic chemistry lab. Responsible for pre-lab lectures and demos, grading, help room tutoring, and answering questions. Student evaluations were excellent.

Next Generation Sequencing (NGS) Data Analysis

- Data Types: Whole Genome (Illumina, Nanopore and PacBio long reads), Amplicon Targeted, Hi-C, RNA-Seq, Single Cell RNA-Seq, ChIP-Seq, Whole Exome
- Analysis Tools: SPAdes, RAST, Prokka, Unicycler, Bowtie, TopHat, Cufflinks, Samtools, BedTools

Laboratory Techniques

Microsatellite Analysis, SNP analysis, PCR, Sanger Sequencing, Genetic Linkage Analysis, Primary Cell Culture, Flow Cytometry, PBMC Isolation, Production of Monoclonal Antibodies, Thymectomy Survival Surgery, Mouse Handling, IP Injection, Tail Vein Injection

Education

Software Product Management Specialization Nov.2019-present
3 out of 6 courses complete
University of Alberta Coursera

Computation & Comparative Genomics Oct. 2014
Cold Spring Harbor Laboratory Cold Spring Harbor, NY

Master of Science in Organic Chemistry Dec. 2006
Michigan State University East Lansing, MI

Bachelor of Arts in Chemistry
Minors: Mathematics & Biology May 2004
State University of New York College of Potsdam Potsdam, NY

Publications

1. Mostafa HH, Cameron A, **Taffner SM**, Wang J, Malek A, Dumyati G, Hardy DJ, Pecora ND. Genomic Surveillance of Ceftriaxone-Resistant *Escherichia coli* in Western New York Suggests the Extended-Spectrum β -Lactamase blaCTX-M-27 Is Emerging on Distinct Plasmids in ST38. *Front Microbiol.* 2020;11:1747. Published 2020 Jul 30.
2. Mostafa HH, **Taffner SM**, Wang J, Malek A, Hardy DJ, Pecora ND. Genome Sequence of a *Facclamia hominis* Isolate from a Patient with Urosepsis. *Microbiol Resour Announc.* 2019;8(17):e00100-19. Published 2019 Apr 25.
3. Malek A, McGlynn K, **Taffner S**, Fine L, Tesini B, Wang J, Mostafa H, Petry S, Perkins A, Graman P, Hardy D, Pecora N. Next-Generation-Sequencing-Based Hospital Outbreak Investigation Yields Insight into *Klebsiella aerogenes* Population Structure and Determinants of Carbapenem Resistance and Pathogenicity. *Antimicrob Agents Chemother.* 2019 May 24.
4. Bern MD, Beckman DL, Ebihara T, **Taffner SM**, Poursine-Laurent J, White JM, Yokoyama WM. (2017) Immunoreceptor tyrosine-based inhibitory motif-dependent functions of an MHC class I-specific NK cell receptor. *PNAS.*
5. Lauron EJ, Aw Yeang HX, **Taffner SM**, Sehgal RN. (2015) De novo assembly and transcriptome analysis of *Plasmodium gallinaceum* identifies the Rh5 interacting protein (ripr), and reveals a lack of EBL and RH gene family diversification. *Malar J.* 296.
6. Miner JJ, Aw Yeang HX, Fox JM, **Taffner S**, Malkova ON, Oh ST, Kim AH, Diamond MS, Lenschow DJ, Yokoyama WM. (2015) Brief report: chikungunya viral arthritis in the United States: a mimic of seronegative rheumatoid Arthritis. *Arthritis Rheumatol.* 1214.
7. Miner J, Fox J, **Taffner S**, Kim A, Diamond M, Lenschow D, Yokoyama W. (2014) Immunological Phenotyping of a Cohort of American Travelers with Chikungunya Viral Arthritis. *Arthritis & Rheumatology* 66 (12), 3534-3535
8. Kreisel D, Gelman AE, Higashikubo R, Lin X, Vikis HG, White JM, Toth KA, Deshpande C, Carreno BM, You M, **Taffner SM**, Yokoyama WM, Bui JD, Schreiber RD, Krupnick AS. (2012) Strain-Specific Variation in Murine Natural Killer Gene Complex Contributes to Differences in Immunosurveillance for Urethane-Induced Lung Cancer. *Cancer Res.* 4311.
9. Jonsson AH, Yang L, Kim S, **Taffner SM**, Yokoyama WM. (2010) Effects of MHC class I alleles on licensing of Ly49A+ NK cells. *J Immunol* 3424.