

Alfred Stangl

SOFTWARE ENGINEER · BIOINFORMATICS

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Summary

Bioinformatics Software Engineer with 3+ with years experience developing NGS analytical pipelines to identify genomic variants. Lead the development of two analytical pipeline for use by pharmaceutical partners in under one year. Highly proficient in multiple compiled and interpreted languages, work flow management systems, and formal design processes.

Technical Skills

Programming Languages

Python, Perl, R, Java, C, PSQL/SQL, JavaScript, LaTeX

CyberInfrastructure

AWS, High-Throughput Computing, Unix, Ansible, Debian Package Manegment, TIGR Workflow, Makeflow, Jinja, Sungrid Engine

Software Development and Lifecycle

Git and Version Control, JIRA, Agile/Scrum, Iterative Waterfall, Confluence, Sharepoint, Smartsheets

BioInformatic Frameworks

Pandas/Numpy/Scipy, Matplotlib/Seaborn, Bioconductor, Plotly, Spotfire, RESTful API, Machine Learning, Data Mining, Excel

Genomic Technologies

Illumina HighSeq/NextSeq Platforms, Ion Torrent Sequencing, ,Protein Microarray, DNA Microarray, Transcriptomics, IHC/In-Situ Hybridization

Bioinformatics Tools

Samtools, Picard, BWA, BT2, NovoAlign, BLAST, MAFFT, PySam

Experience

Personal Genome Diagnostics

BIOINFORMATICS SOFTWARE ENGINEER, I

Baltimore, MD

Oct. 2017 - PRESENT

- TODO
- TODO
- TODO

Personal Genome Diagnostics

ASSOCIATE ENGINEER

Baltimore, MD

Feb. 2016 - Oct. 2017

- TODO
- TODO
- TODO

University of Arizona

GRADUATE INTERN – COMPARATIVE GENOMICS LAB

Tucson, Arizona

Feb. 2015 - Jan 2016

- Developed python programs to extract genomic and meta data from ENCODE and itegrate to data into genomic databases via RESTful API
- Interpreted NGS genomic data from external sources and validated results with different alignment software
- Reported errors to the lead software engineer in JIRA and documented causes found in Confluence
- Obtained results from analysis conducted and presented findings during laboratory meeting

Sanofi

BIOLOGY INTERN - DRUG DISCOVERY

Oro Valley, Arizona

May. 2016 - August 2016

- Programmed customized workflows in VBA and R for data extraction and statistical analysis
- Reported results to multiple project leaders and presented results during weekly staff meeting
- Investigated alternative protocols and documented experimentation to optimize microarray workflow
- Performed high-throughput small proteomic assays utilizing protein microarray technology

University of Arizona

GRADUATE TEACHING ASSISTANT

Tucson, Arizona

Aug. 2015 - Dec 2015

- Instructed two sections of introductory biology and facilitated class activates for upper division MCB course
- Established timelines for grading and feedback for students to efficient provide feedback on all assignments
- Tutored students during office hours and communicated biological principles in a clear manner

University of Arizona

UNDERGRADUATE LABORATORY TECHNICIAN

Tucson, Arizona

Jun. 2013 - Aug 2014

- Performed functional genomics utilizing PCR, in-situ hybridization, and IHC
- Analyzed NGS data from a transcriptome utilizing high-performance computing for assembly and BLAST
- Identified genetic variants using Phylogenetic analysis of gene clusters
- Documented all research in extreme detail and provided multiple labs with documentation of how to perform further analysis

Education

University of Arizona

PROFESSIONAL SCIENCE MASTERS IN APPLIED BIOSCIENCES

Tucson, AZ

May. 2016

- Focus: Bioinformatics, Data and Genomic Analysis, and Scientific Computing
- Thesis: Protein MicroArray Mediated Target Identification
- GPA: 4.0

University of Arizona

BACHELOR OF SCIENCE IN MOLECULAR AND CELLULAR BIOLOGY

Tucson, AZ

May. 2016

- Focus: Bioinformatics, Biochemistry, and Laboratory Research
- GPA: 3.6
- Cum Laude

Presentation

University of Arizona Graduate College Graduate Research Exhibition

PRESENTER FOR PROTEIN MICROARRAY MEDIATED IDENTIFICATION OF PHOSPHOHISTIDINE IN THE HUMAN PROTEOME

Tucson, AZ

Dec 2015

- Introduced the use, analysis, and utility of protein microarrays for novel detection of binding site in the human proteome.

Arizona Bio Expo

PRESENTER FOR <IRREGULAR PERIODICITY IN INSECT SEGMENTATION AND CRUSTACEAN TRANSCRIPTOMICS.>

Scottsdale, Arizona

Jun 2014

- Introduced the application of NGS Transcriptomics for the identification of uncharacterized genes in non-model organisms.