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
CyberInfastructure	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　　　　　　　　　　　　　　　　　　　　　　*Baltimore, MD*

BIOINFORMATICS SOFTWARE ENGINEER, I　　　　　　　　　　　　　　　　*Oct. 2017 - PRESENT*

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Personal Genome Diagnostics　　　　　　　　　　　　　　　　　　　　　　*Baltimore, MD*

ASSOCIATE ENGINEER　　　　　　　　　　　　　　　　　　　　　　　*Feb. 2016 - Oct. 2017*

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University of Arizona　　　　　　　　　　　　　　　　　　　　　　　*Tucson, Arizona*

GRADUATE INTERN – COMPARATIVE GENOMICS LAB　　　　　　　　　　　*Feb. 2015 - Jan 2016*

- Developed python programs for data mining and integration to internal genomic databases via RESTful API
- Interpreted NGS genomic data from external sources and validated results with different alignment software
- Communicated bugs and root cause of failures to lead software developer for resolution

Sanofi　　　　　　　　　　　　　　　　　　　　　　　　　　　*Oro Valley, Arizona*

BIOLOGY INTERN - DRUG DISCOVERY　　　　　　　　　　　　　　　　*May. 2016 - August 2016*

- Introduced methods of analysis that automated analysis of protien microarray data using R, Perl, and VBS for Excel
- Analyzed results of multiple small molucule targets across multiple projects and teams
- Presented findings to project teams and communicated next steps for assay application

University of Arizona　　　　　　　　　　　　　　　　　　　　　　　*Tucson, Arizona*

GRADUATE TEACHING ASSISTANT　　　　　　　　　　　　　　　　　　*Aug. 2015 - Dec 2015*

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University of Arizona　　　　　　　　　　　　　　　　　　　　　　　*Tucson, Arizona*

UNDERGRADUATE LABORATORY TECHNICIAN　　　　　　　　　　　　　　*Jun. 2013 - Aug 2014*

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Education

University of Arizona   *Tucson, AZ*

PROFESSIONAL SCIENCE MASTERS IN APPLIED BIOSCIENCES   *May. 2016*

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

University of Arizona   *Tucson, AZ*

BACHELOR OF SCIENCE IN MOLECULAR AND CELLULAR BIOLOGY   *May. 2016*

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

Presentation

University of Arizona Graduate College Graduate Reseach Exhibition   *Tucson, AZ*

PRESENTER FOR PROTEIN MICROARRAY MEDIATED IDENTIFICATION OF PHOSPHOHISTIDINE IN THE HUMAN PROTEOME   *Dec 2015*

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

Arizona Bio Expo   *Scottsdale, Arizona*

PRESENTER FOR <IRREGULAR PERIODICITY IN INSECT SEGMENTATION AND CRUSTACEAN TRANSCRIPTOMICS.>   *Jun 2014*

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