Brian Bolt

Los Angeles, CA 90045
(707) 217-7598
brian.bolt@boltengineered.com

OBJECTIVE

To find work that will allow me to take full advantage of my passion and experience in software engineering, client solutions and development operations.

TECHNOLOGY SKILLS

Operating Systems: Linux (CentOS/Redhat, Ubuntu, Debian), Windows, Mac OS.
Programming Languages: R, Python, JavaScript, Bash/Shell, Java, VBA, PHP.
Operations Technologies: AWS, Docker, SVN, Git, Github, Bitbucket, npm, JIRA, Knime.
Web Technologies: NodeJS, Javascript, Coffeescript, Bootstrap, Gulp, Webpack, Nginx, Apache, REST, SQL, PostgreSQL, Oracle, Mysql.
Other Technologies: Postman, Webstorm, Eclipse, Atom, Rstudio, RApache, Slack, Hipchat, Wireshark, Fiddler, Sharepoint, Word VBA, Excel VBA.

ADDITIONAL INFORMATICS SKILLS

ACAS, LabSynch
Jchem, LiveDesign Seurat for SAR collaboration
Molecular Modeling: Sybyl, Dock, Pymol, Chimera
Molecular Visualization
Molecular Mechanics
Geometry minimization and transition state localization docking

EXPERIENCE

Scientific Software Engineer 2010 - 2018
John McNeil & Company, Inc., La Jolla, CA

- Deployed many instances of ACAS to customers, provided maintenance, backups, custom plug-ins, general support and custom configurations.
- Helped write and deploy a dose response curve fitting algorithm using R, that included automatic failing, curve classification and fit strategies (parameter fixing)
- Designed the R-based computational web-service infrastructure and libraries for ACAS. Served as team lead for reviewing all contributions to this library.
- Wrote code to Extract, Transform and Load (ETL) data from a vendor database to a custom designed table in a customer database for use with a second vendors software. This project included spec gathering from two different vendors, as well as specification for complex transformation rules from the customer.
- Architected and implemented Docker-based ACAS development workflow that enabled the development team to rapidly setup custom development areas for any client with that clients custom configuration and software modules. This saved about four hours of setup work each time a developer needed change projects.
- Architected and implemented the Docker-based ACAS production deployments. This saved two or more hours for each system upgrade and reduced upgrade error risks.
- Migrated compound structure and assay data from various third-party systems including Seurat, CoreLIMS and ActivityBase to ACAS. Wrote and ran the ETL code, and oversaw the validation of migrated data.

- Technical lead for the documentation and release of ACAS as GPLv3 open source software.

Informatics Support Scientist 2007-2010
Kalypsys, Inc., San Diego, CA

- Automated informatics software testing and monitoring processes by using Redstones Eggplant scripting language, which reduced the testing procedures from a three person, one week process to a three hour automated process.
- Deployed a commercial Structure Activity Relationship query and chemical display tool.
- Gathered and negotiated user requirements, worked with the vendor and in-house programmers to integrate the software with our in-house system and database, performed primary end user training, provided documentation and post training support.
- Setup and maintained advanced queries. This replaced and enhanced the workflow for reporting and sharing SAR driving assay data, companywide.
- Deployed a commercial dose response curve fitting and curation tool that replaced and enhanced the workflow for curve fitting and significantly improved the integrity of the database.
- Wrote and deployed an automated screening summary tool.
- Project allowed scientists to get a quick and thorough summary of a screening campaign for meetings and comparisons.
- Helped write and deploy a curve fitting algorithm and user interface using R and Excel. This project saved the company over 100K in licensing fees.

EDUCATION University of California, Santa Barbara, CA, *Bachelor of Science, Biochemistry*

RELEVANT COURSEWORK

Drug Design 1 & 2 Professor Kalju Kahn (kalju@chem.ucsb.edu)

To teach principles that governs the process of modern drug discovery and development. Students in the course follow a path similar to that taken by real-life drug developers by learning important elements of the drug design process in a logical order. This course is an overview of the process whereby one identifies and optimizes drugs against a validated biological target (e.g., a protein like HIV protease). The course requires that you have a solid understanding of organic chemistry, particularly physical organic chemistry.