Christopher Rosenthal

Seattle, Washington   crosenth@gmail.com

Experience

Bioinformatics Software Engineer   **2012 - Present**
University of Washington Department of Laboratory Medicine, Seattle, Washington
I develop bioinformatics pipelines for molecular microbiology analysis. My work has resulted in several publications. I also help mentor new bioinformatics engineers and promote common software development practices to manage growing project demands and workflows.

Full Stack Software Engineer   **2009 - 2012**
The Seattle Times Company, Seattle, Washington
I developed and maintained digital content management systems. My role required the flexibility to develop new software while supporting minimally documented legacy systems. I had the pleasure of working alongside Pulitzer prize winning journalists, photographers and videographers.

Graduate Student   **2007 - 2009**
Indiana University School of Informatics and Computing, Bloomington, Indiana
Thesis Project: Coral Reef Ecosystem Gene Ontologies

Software Development Engineer   **2005 - 2007**
Regenstrief Institute, Indianapolis, Indiana
At Regenstrief I developed Java software applications to help doctors, pharmacists and physicians prescribe medicine and manage patient records.

Software Development Engineer   **2003 - 2005**
Indiana University Department of Chemistry, Bloomington, Indiana
At Chemistry I developed a content management system for digital classroom homework assignments. The system was built from scratch using Perl and Javascript without the availability of today's web based software stack technologies.

Education

Indiana University, Bloomington, Indiana
  M.S., Bioinformatics, 2009
  B.S., Computer Science with Honors, 2005
  Biology Minor

Skills

Portfolio: https://github.com/crosenth
Software Languages: Python, Java, Perl, Lisp, SQL and more
Python Libraries: Pandas, Numpy, Scipy, Biopython, Scons
Databases: Postgres, SQLite, MySQL, HSQL, Oracle, MS SQL Server
Productivity: Linux, Vim, Git, tmux, Bash, Docker, cloud computing, AWS and more

Publications

[1] *Improved species level clinical identification of Enterobacteriaceae through broad range dnaJ PCR and sequencing*, American Society for Microbiology

[2] *Clinical Next Generation Sequencing Outperforms Standard Microbiological Culture for Characterizing Polymicrobial Samples*, Clinical Chemistry

[3] *Performance Comparison of Illumina and Ion Torrent Next-Generation Sequencing Platforms for 16S rRNA-Based Bacterial Community Profiling*, Applied Environmental Microbiology

[4] *Molecular Diagnosis of Actinomadura madurae Infection by 16S rRNA Deep Sequencing*, Journal of Clinical Microbiology

[5] *Rapid 16S rRNA Next-Generation Sequencing of Polymicrobial Clinical Samples for Diagnosis of Complex Bacterial Infections*, PLoS One