WEB: HTTP://JASONNEROTHIN.COM

JASON NEROTHIN

PROFILE

Highly-productive independent developer. Scientific computing and machine learning.

SKILLS

LANGUAGES

Java - Scala - Python - SQL - C# - HTML - Javascript - Ruby - C/C++ - PHP - PERL - R - DRL - XML - Pig Latin

ENVIRONMENTS

J2EE - GigaSpaces - grid computing - LAMP - EC2 - Google App Engine - .Net - HFS -

PROCESSES

Agile - Waterfall - Cowboy

DATABASES

Postgres - Oracle - SQL Server - mySQL - Derby - MongoDB - Cassandra - HFS

FRAMEWORKS/LIBRARIES

AJAX - GWT - Rails - jQuery - script.aculo.us - prototype - Spring - guice - gin - SOAP - WebServices - Struts - OpenJPA - Hibernate - Grails

ETC

Unix (Solaris) - Linux - Mac - Windows - svn - git - github - cvs - MS TFS - sed - g/awk - grep - find ... etc - IntelliJ IDEA - Eclipse - Visual Studio - Swing - lucene - vi - emacs - maven - ant - junit - testNG - scalatest - drools - hudson - BioPERL - BLAST

EXPERIENCE

INDEPENDENT GIGASPACES CONTRACTOR

MILWAUKEE WI 2013

Upgraded GigaSpaces middleware as part of a large scale e-commerce migration. Provided code, configuration and QA support to multiple teams for two applications and two platforms, that were upgraded side-by-side in three data centers. Developed a customized asynchronous write behind in memory data grid to database mirror, customized for customers' runtime requirements.

SENIOR DEVELOPER/INDEPENDENT CONTRACTOR, PHARMACY ONESOURCE MIDDLETON WI 2010-2013

Developed an XML to DRL transpiler that takes legacy SQL-driven business rule metadata and submits it to a massively-parallel rule engine. Produced functionality for message processing system responsible for processing messages from hospital data feeds. \$10M+ decrease in ongoing operating costs. Agile process. SQL Server, Drools, GigaSpaces (grid) architecture.

SOFTWARE ENGINEER, ROCHE-NIMBLEGEN INC MADISON, WI 2008-2010

Delivered core functionality for DIVA, a desktop application for analysis of DNA micro-array results. Wrote a binary data engine capable of IO sufficient to power statistical analyses in R for both 32- and 64-bit platforms. Waterfall process. Derby, Linux, Java/Swing, R.

PROGRAMMER ANALYST IV/DBA, UCLA-DOE INSTITUTE OF GENOMICS & PROTEOMICS

LOS ANGELES CA 2005-2007

Published. Provided application and database administration for the Prolinks and DIP scientific databases. Developed a AJAX application that enabled curation of protein-protein interaction data in the MIF format. Cowboy (no) process. Linux, postgres, C, python, Java, PHP, PERL.

RESEARCH INVESTIGATOR, DEPT OF PHARMACY ANN ARBOR MI 2004-2005

Published. Wrote web application to provide access to the BindingMOAD binding database. Cowboy (no) process. EJB 2.1, Struts, XML/XSL, mySQL.

EDUCATION

MS MOLECULAR & CELLULAR BIOLOGY

AUGUST 2003 - EASTERN MICHIGAN UNIVERSITY - YPSILANTI MI

BS COMPUTER SCIENCE (MATHEMATICS MINOR)

JUNE 2005 - EASTERN MICHIGAN UNIVERSITY - YPSILANTI MI

BA CHEMISTRY

JUNE 1997 - ST. OLAF COLLEGE - NORTHFIELD MN

PUBLICATIONS

Nucleic Acids Res. 2007 Nov 30; 18055497 "Binding MOAD, a high-quality protein ligand database."

BMC Biol. 2007 Oct 9; 5 (1):44 17925023 "Broadening the Horizon - Level 2.5 of the HUPO-PSI Format for Molecular Interactions."

Proteomics. 2007 Sep 24;7 (S1):28-34 17893861 "Submit Your Interaction Data the IMEx Way: a Step by Step Guide to Trouble-free Deposition."

Proteomics. 2006 Aug 8;6 (16):4439-4443 16897683 "Proteomics and Beyond A report on the 3(rd) Annual Spring Workshop of the HUPO-PSI 21-23 April 2006, San Francisco, CA, USA."