Jianying Li
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Seeking for a senior data scientist/bioinformatician position in an industrial/research environment

SUMMARY

- **Twelve-year** bioinformatics working experiences and modern data science concepts
- **Six-year** hands-on experiences in Next Generation Sequencing (**NGS**) analysis and development
- Strong in statistical modeling and statistical/computational programming in **SAS, JMP, R, Perl**, **PHP, Java, C++, Linux/Unix shell scripting, and Database programming**
- Highly productive in research and support with high impact peer review publications
- Self-motivated individual with smooth communication skills

WORKING EXPERIENCE

Kelly Government Solutions, Inc.   05/2012 to present Bioinformatics scientist

Duke University, CHGV   04/2011 to 05/2012 Bioinformatician II

UNC Chapel Hill, LCCC   10/2008 to 03/2011 Senior Bioinformatician

Lockheed Martin (NIEHS contractor)   01/2003 to 10/2008 Bioinformatic Scientist

- Selected projects involved

• Led and participated in a consortium base research on rat body-map microRNA sequencing projects. Drafted the main analytical component for a conference poster presentation and paper manuscript
• Led the bioinformatics component in a human mitochondrial deep sequencing projects
• Designed and conducted pathway analysis course for NIH internal training programs
• Led and participated in establishing in-house pipeline for RNA-seq project. I am a main developer for RNAseq QC modules and analytical workflow in SeqWare (http://sourceforge.net/apps/mediawiki/seqware/index.php?title=Main_Page). This project involves benchmarking and testing open source software package, implementing in-house statistical analysis, constructing customized database for data annotation, building LIMS and data storage database for *ad hoc* analyses. All statistical components are implemented in **R**, sequence processing and manipulation is implanted in **Perl**, and the final software/application is wrapped with **Java**

- Lead author on the Principal Variance Component Analysis (**PVCA**) procedure leveraging mixed linear model for genetic/genomic data analysis. The theory was published as a book chapter and the model was developed both in **SAS** (currently an analytical procedure "AP" in JMP Genomics software package from SAS Institute) and **R** (http://www.niehs.nih.gov/research/resources/software/pvca/index.cfm) for open source implementation.
- Developed in house scientific software in **Java**, for microarray quality control of in house RNA quality monitoring, hybridization quality assessment, data acquisition software performance evaluation
- Developed in house scientific software in **C++** implementing Fuzzy Logic algorithm for Rat acetaminophen dosing project
- Developed in house software in **R** providing analytical component in an in-house developed Oracle database Chemical Effect Biological System (CEBS)
- Performed regular microarray gene expression and proteomic data analysis with commercial software package, freeware as well as in house developed software in **Java, R**, **SAS** and **JMP**

EDUCATION
- Master of Bioinformatics, North Carolina State University, 2002
- Master of Science in Food Microbiology, North Carolina State University, 2001
- B.S. in Microbiology, Nankai University Tianjin, 1990

HARDWARE AND SOFTWARE SKILLS

- Operating systems: **Windows, Linux,** and **Unix**
- Programming languages: **Java, C++, SQL, Perl, SAS, R**, **JMP**
- Database system: MySQL, PostgreSQL
- Genetic/genomic analysis package: JMP Genomics Suite, Rosetta Resolver, GeneSpring, Bioconductor package, IPA, GoMiner
- NextGenSeq data analysis package: BWA, Samtools, Picard, GATK, SeqWare, Galaxy, FASTX-toolkit etc.

SELECTED RECENT PUBLICATIONS

Myrtle Davisa, Elaine Knighta, **Jianying Li**, Kellye K. Danielsc, James E. Doroshowa and Pierre R. Bushel Toxicogenomic Profiling of Bone Marrow from Rats treated with Topotecan in Combination with Oxaliplatin: A Proof of Concept Study to Identify a Strategy to Assess Risk of Enhanced Toxicity for Combination Therapies (**2013**) Submitting to Molecular Cancer Therapeutics

Wang, C, ..**Li J**, …Tong, W. A comprehensive study design reveals treatment- and transcript abundance–dependent concordance between RNA-seq and microarray data (**2014**) Nature Biotechnology (**in press**)

Laura R. Barkleya, Komaraiah Palleb, Michael Durandob,Tovah A. Dayc, Aditi Gurkard, Naoko Kakushoe,**Jianying Li**, Hisao Masaie, and Cyrus Vazirib c-Jun N-terminal kinase–mediated

Rad18 phosphorylation facilitates Polη recruitment to stalled replication forks **Mol. Biol. Cell (2012) vol. 23 no. 10, 1943 - 1954**

Chen H, **Li J**, Li H, Hu Y, Tevebaugh W, et al. (**2012**) Transcript Profiling Identifies Dynamic Gene Expression Patterns and an Important Role for Nrf2/Keap1 Pathway in the Developing Mouse Esophagus. PLoS ONE 7(5): e36504. doi:10.1371/journal.pone.0036504