

Jianying Li

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Seeking a challenging bioinformatics developer position in industry research environment

SUMMARY

- **Ten-year** bioinformatics working/research experiences with focus on genome informatics, microarray and next generation sequencing
- **Three-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**
- Self-motivated individual with smooth communication skills

WORKING EXPERIENCE

Duke University, Center for Human Genome Variation

04/2011 to present Bioinformatician II

■ Selected recent projects involved

- Led and participated in upgrading in-house variant calling pipeline for **whole genome** and **exome** projects. In the project, we evaluated main third party software include BWA, Samtools, GATK, etc. and optimized the processes for the best performance. Eventually, deployed it for regular process.
- Constructed an in-house MySQL database keeping track of the variant calling project progress, including three major components (GWAS experiment, Illumina sequencing and variant calling).
- Developed a sequencing QC platform for real time comparison to traditional GWAS experiment, this involves direct process sequencing .bam file, curating Illumina “topstrand” output from GWAS, consulting current dbSNP databases and performing two parts of concordance check.

UNC Chapel Hill, Lineberger Comprehensive Cancer Center

10/2008 to 03/2011 Senior Bioinformatician

■ Selected recent projects involved

- 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).

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- Lead author on the Principal Variance Component Analysis (**PVCA**) procedure leveraging mixed linear model for genetic/genomic data analysis.
- Participated in recently funded (by NIH) **The Cancer Genome Atlas (TCGA)** project, mainly relying on next generation sequence technology in cancer research.
- Collaborated and led the bioinformatics component on a project “to determine the DNA replication system for cancer mechanism using next generation whole genome sequencing”

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

■ Bioinformatics application and statistical methodology development

- 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 a Rat acetaminophen dosing project
- Developed in house software in **R** providing analytical component for in house developed Oracle database Chemical Effect Biological System (CEBS)
- Implemented Mixed Linear Model in **SAS** for customized Micro Array data analysis, include data quality evaluation, data normalization, and statistical modeling

■ Statistical consultation and bioinformatics support

- Provided training of application statistics using **JMP**: acted as a leading role to coordinate with IT training department to design class, construct class materials and present in a live training class
- Performed regular microarray gene expression and proteomic data using **Java, R, SAS** and **JMP**

■ Selected research projects involved

- Participated in FDA-led MAQC consortium phase II and developed statistic prediction models in the transcriptome biomarkers identification
- Participated in scientific director's CpG project in human and mouse genome
- Participated in the collaborated research for statistic modeling in Toxicogenomics Research Consortium research project

University of Hawaii/North Carolina State University, 1998-2002 Research Assistant

- Research on genes (in *Listeria monocytogenes*) responsible for surface antigen determinants involving all molecular technique, i.e. DNA/RNA manipulation, microarray experiment, and function study
- Research involving search for major genes contributing to favorable commercial properties in loblolly pine

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++, PHP, Perl, SAS, R, JMP**
- Database system: MySQL, PostgreSQL, and Oracle
- 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

Hao Chen, **Jianying Li**, Haiyan Li, Yuhui Hu, Masayuki Yamamoto, Jianwen Que, Xiaoxin Chen Dynamic changes of gene expression during the development of mouse esophageal epithelium and the role of Nrf2/Keap1 pathway (co-first author, **submitted to PloSOne**, 2011)

Hong Xu, **Jianying Li**, Jay Li, Ming-Zhu Shi and De-Yu Xie An integrative approach of transcriptomics and metabolomics demonstrates genome-wide reprogramming in metabolically programmed red tobacco plants (co-first author, **submitted to PNAS**, 2011)

J Huang, W Shi, J Zhang, J W Chou, R S Paules, K Gerrish, **J Li**, et al on the MAQC consortium, (2010) Genomic indicators in the blood predict a drug-induced liver injury response **The Pharmacogenomics Journal** (2010) 10, 267–277

Cabanski CR, Qi Y, Yin X, Bair E, Hayward MC, **Li J**, et al. (2010) SWISS MADE: Standardized Within class Sum of Squares to evaluate Methodologies And Dataset Elements **PloS ONE** 5(3): e9905

Jianying Li, Chu-TZ, Wolfinger, R, Bushel, P.R. (2009) Batch Effects and Noise in Microarray Experiments: Sources and Solutions. John Wiley & Sons, Ltd.

Song, M.O., **J. Li**, and J.H. Freedman (2009) Physiological and Toxicological Transcriptome Exposure Levels Changes in HepG2 Cells Exposed to Copper” **Physiol. Genomics**. 38: 386-401.

P. R. Bushel, A. N. Heinloth, **J. Li**, et al (2007) “Blood Gene Expression Signatures Predict Exposure Levels” **PNAS**. v.104, no. 46: 18211-18216

REFERENCES

References are available upon request