Jianying Li

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OBJECTIVE

Seek a computational biologist position in an industrial research environment

QUALIFICATION

- **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**, **Java,** and **C++, Linux/Unix shell scripting**
- Self-motivated individual with smooth communication skills

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

WORKING EXPERIENCE

Duke University, Center for Human Genome Variation

04/2011 to present   Bioinformatician II

- Major duties

  - Oversee a team of CHGV Bioinformaticians that focuses on new software development as well as development and maintenance of specific areas of the analysis pipeline
  - Lead the computational development for CHGV's next-generation sequencing (NGS) pipeline
  - Develop and implement innovative computational approaches for the analysis of large sequence datasets from NGS technologies
  - Collaborate and consult with CHGV researchers to analyze problems and recommend solutions to meet the computational needs for a wide range of biological research

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). 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.

• Participated in recently funded (by NIH) **The Caner Genome Atlas (TCGA)** project, mainly relying on next generation sequence platform (plus genotyping and other high throughput method) to detect new mutation in cancer cell, find new transcripts, and study novel cancer mechanistic system. My main responsibility is statistical analysis and model on high-throughput NGS data.

• Collaborated and led the bioinformatics component on a project "to determine the DNA replication system for caner 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 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)
• 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 analysis with commercial software package, freeware as well as in house developed software in **Java, R**, **SAS** and **JMP**

■ Selected research projects involved

- Developed statistic prediction models in the FDA MAQC consortium for standardized procedure for prediction phenotypic outcome using the transcriptome biomarkers, and currently involving in cross-platform and cross-tissue prediction research
- Participated in scientific director's CpG project, implementing genome searching algorithms to search for domains in human and mouse genome
- Participated in the collaborated research for statistic modeling in Toxicogenomics Research Consortium cross platform and cross laboratory gene expression

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

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

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