Curriculum Vitae

Xiang Li Zhang, B.Eng, B.Sc

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Objective: Bioinformatics Analyst focusing on Data Analysis, Data Mining, Systems Biology

SUMMARY OF QUALIFICATIONS

- Research experience with genomic and transcriptomic sequencing data, including new analysis methods and writing publications
- Combined background in Biochemistry, Molecular biology, Computer Science and Bioinformatics
- Over 3 years bioinformatics data analysis experience in a biofuel project funded by Genome Canada at University of Manitoba

PUBLICATION

Zhang, X., Bjorklund, N. K., Alvare, G., Rydzak, T., Sparling, R., Fristensky, B. (2013) ELBOW (Improved Fold Change Test for Differential Gene Expression Analysis), R Bioconductor Package, in releasing

Tobin J. Verbeke, Vic Spicer, Oleg V. Krokhin, **Xiangli Zhang**, John J. Schellenberg, Brian Fristensky, John A. Wilkins, David B. Levin, and Richard Sparling (2013) T*hermoanaerobacter thermohydrosulfuricus* WC1 shows protein complement stability during the fermentation of key lignocellulose-derived substrates, American Society For Microbiology *In press*

Sadhana Lal, Umesh Ramachandran, **Xiangli Zhang**, Richard Sparling, and David Levin (2013) Draft genome sequence of the hydrogen and ethanol producing bacterium Clostridium intestinale strain URNW, American Society For Microbiology

Tobin J. Verbeke, **Xiangli Zhang**, Bernard Henrissat, Vic Spicer, Thomas Rydzak, Oleg V. Krokhin, Brian Fristensky, David B. Levin, Richard Sparling(2013) Genomic Evaluation of Thermoanaerobacter spp. for the Construction of Designer Co-cultures to Improve Lignocellulosic Biofuel Production, PLOS ONE

Parveen Sharma, Jilagamahzi Fu, **Xiang Li Zhang**, Brian Fristensky, Karen Davenport, Patrick Chain, Richard Sparling, and David Levin (2013) Draft Genome Sequence of Medium Chain Length Polyhydroxyalkanoates Producing Pseudomonas putida LS46, American Society For Microbiology

Sadhana Lal, Umesh Ramachandran, **Xiangli Zhang**, Riffat Munira, Richard Sparlingb, David B. Levin (2013) Draft Genome Sequence of the Cellulolytic, Mesophilic, Anaerobic Bacterium *Clostridium termitidis* Strain CT1112 (DSM 5398) American Society For Microbiology

PRESENTATION

Xiangli Zhang, Natalie Bjorklund, Thomas Rydzak, Richard Sparling, Graham Alvare, Brian Fristensky (2013, April 7-10) "An Elbow Method for Transcriptomic Data Mining with 'Omics Data", Beijing, China: 17th Annual International Conference on Research in Computational Biology (RECOMB2013) - http://bioinfo.au.tsinghua.edu.cn/recomb2013/; Research Gate.

Xiangli Zhang, Natalie K Björklund, Thomas Rydzak, Richard Sparling, Graham Alvare, Brian Fristensky (2012, November 5-6) "Transcriptomic Data Mining with Microbiology and Proteomic data for Biofuel Producing Bacteria: Clostridium thermocellum", MGCB2 Annual General Meeting, Winnipeg, Canada

Xiangli Zhang, Brian Fristensky (2011, November 7-8) "Assembly and Annotation of Genomes from Microorganisms Targeted to the Production of Biofuel and Bioproducts", MGCB2 Annual General Meeting, Winnipeg, Canada

EDUCATION

B.Sc. Bioinformatics, Simon Fraser University, Burnaby BC Canada	2007.06
B.Eng. Chemical Engineering, Tsinghua University, Beijing, China	1992.07

INDEPENDENT COURSERA COURSES

Mathematical Biostatistics Boot Camp 1 (at Coursera By Brian Caffo Johns Hopkins University) Nov 18th 2013

Network Analysis in Systems Biology (at Coursera by Avi Ma'ayan Mount Sinai) Oct. 2013

Introduction to Systems Biology (at Coursera by Ravi Iyengar Mount Sinai) July, 2013

Data Analysis (at Coursera By Jeff Leek Johns Hopkins Bloomberg School of public health) April, 2013

Machine Learning (at Coursera by Andrew Ng Stanford University) October, 2012

EXPERIENCE

UNIVERISTY OF MANITOBA, Winnipeg, MB CANADA

Bioinformatician 2010.7~present

- Worked as a bioinformatician in a multidisciplinary team on biofuel research project to characterize bacterial genome
- Analyzed next-generation sequencing data, such as processing sequence data, sequence assembly, genome annotation, genomic variant analysis, transcriptomics analysis with RNA-seq, pathway annotation, and comparative genomics for microbial genome
- Experienced with Newbler, Velvet, Samtools, Bamview, Bowtie, Tophat, Cufflinks, IMG ER etc. bioinformatic tools
- Developed analysis method for gene differential expression
- Wrote publication for the session of analysis method
- Worked in Sun UNIX system and Linux system
- Programmed with Shell, Python, Perl and R
- Designed and analyzed Agilent gene expression microarray data with R and TigrMev

PUBLIC HEALTH AGENCY OF CANADA, CANADA

Bioinformatician 2009.7~2010.05

- Worked on an information pipeline of an E. Coli project to identify group of genes associated with each seropathotype
- Programmed with Perl, Bioperl and Shell in Linux system
- Analyzed sequence data on comparative genomics with Blast, gene association with different groups of pathogenic strains and 5 reference strains with Fisher Exact test
- Developed “Genome Fisher” gene association application with grouping module and statistics test module for microarray data and genome data with EXCEL VBA
- Analyzed microarray data of 150 Campy strains and 1800 genes with Tigr MEV clustering tool and “Genome Fisher” statistics test
- Involved in paper publication for bioinformatics application
- Communicated effectively with research scientist to make application meet requirement exactly
- Familiarized with statistics tests: Fisher Exact, t-test, probability corrections
- Wrote documentation for application

DR. HONG QIN, Department of Biology, Spelman College, Atlanta

Bioinformatician (VOLUNTEER) 2009.5~2009.10

- Performed orthologous analysis of *Bacillus exosporium* genes
- Programmed with Linux, Shell, Perl, Bioperl, R, Blast, MCL (Markov Clustering Algorithm)
- Experienced with NCBI databases
- Installed and maintained Linux Fedora 11

CANADIAN GRAIN COMMISSION, WINNIPEG, MB, CANADA

Programmer Analyst 2009.1~2009.5

- Worked with a software development team
- Programmed with VB 6.0 and Microsoft SQL
- Experienced with Citrix, Team Track and PVCS
- Maintained and upgraded existing application
- Provided technical support to clients

VB.NET Programmer (Image Analysis Technician) 2007.2~2009.1

- Developed Software Application of Grain Quality Control with VB.NET
- Experienced with object oriented programming and full life cycle of software development
- Communicated with research scientists and software users
- Experienced with Scanner programming control with EZTwain
- Experienced with image analysis

PUBLIC HEALTH AGENCY OF CANADA, LETHBRIDGE, CANADA

Bioinformatics Programmer 2006.9~2007.2

- Developed Excel VBA application for analyzing microarray data
- Experienced with statistics analyses, t-test and Fisher exact test
- Communicated with research scientist