

Yixiao Gong

New York University Langone Medical Center - Department of Pathology - Aifantis Lab

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KEY QUALIFICATIONS

- Routinely working on pipeline design and development for different Next-Gen Sequencing data analysis including WGS, RNA-Seq, ChIP-Seq, Hi-C, etc.
 - Provide service, collaboration and advice on bioinformatics analysis for different research groups.
 - High Performance Computing (HPC) environment experience for big data processing.
 - Programming skills: Proficient in BASH, TCSH, CSH, Perl, R, JAVA, MySQL, PostgreSQL and HTML/JavaScript. Familiar with C/C++, VBA, PHP, Python.
 - Develop and administrate local LINUX and other cloud computing resources including AWS, google genomics, Basespace, etc.
 - Bioinformatics tools skills: BWA, Bowtie2, TopHat2, STAR, Cufflinks, GATK, CASAVA, PiCard, Velvet, Samtools, Bioconductor, DESeq, DiffBind, bedtools, GenomicTools,, ggplot2, IGV, UCSC Genome Browser, etc.
 - Comprehensive knowledge and hands on experience of genomic databases, including TCGA, SRA, GEO, HGMD, ExAC, EVS, 1000 Genome, ClinVar, UniProt, Ensembl, UCSC, ENCODE, Alamut Visual.
 - Statistical skills: SAS (Macro, GRAPH, SQL)/R Programming, categorical analysis, regression analysis, survival analysis, logistic regression and other machine learning approaches.
 - In-depth understanding of human genetics and molecular mechanisms of cancers
 - Good leadership, teamwork and communication skill, experience in working with and supporting Ph.D/MD scientists. Be able to work independently, mature and resourceful.
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EXPERIENCE

- ***Senior Bioinformatician, New York University Langone Medical Center*** Mar 2014 – Present
 - Develop and operate the pipelines for next generation sequencing based cancer molecular diagnostics and stem cell biology, including DNA-Seq (somatic and germline SNVs, indels, structural variants, de novo assembly), RNA-Seq (differential expression, alternative splicing, gene fusions), and ChIP-Seq (peak calling, differential binding) data.
 - Develop and operate lncRNA discovery pipeline for different projects in diverse cancer research and molecular biology labs. Integrative analyses of lncRNA and histone markers, Hi-C interactions, micro-RNA, transcription factors, SNPs, CNVs, etc.
 - Conduct comprehensive analysis for variety of data type in TCGA data in different cancers and integrate with in-house generated data to discover cancer related abnormalities
 - Develop and maintain a database of sequence mutations from all disease sequencing projects as well to develop pipelines to integrate and automate procedures and produce analytical reports.

Yixiao Gong – Senior Bioinformatician

- Perform other types bioinformatics supports for research group.

 - **Bioinformatics Analyst, Center for Prostate Disease Research,** Jan 2011 – Mar 2014
 - Design pipeline and perform analysis in Prostate Next-Generation Sequencing project. Tasks include QC, data processing, mapping, SNVs / InDels / SVs / CNVs calling, annotation, filtration, RNA-Seq differential analysis, DNA-RNA-Protein results cross validation using existing datasets (1000 Genome, TCGA) and databases (GO, KEGG, UniGene, dbSNP).
 - Develop and maintain a bioinformatics analysis server which is running in-house Galaxy platform, to support CPDR bioinformatics analysis. Develop wrappers to add applications to Galaxy. This server is also used to analyze raw sequencing data coming out of Illumina sequencing machine from USUHS research lab.
 - Design, develop, publish and maintain multi-center clinical prostate cancer database to support translational and bioinformatics analysis. System functions include clinical data collection, data query, statistical analysis, bio-specimen inventory management, microarray data analysis system. System has being used in 6 military hospitals.
 - Perform microarray, antibody array, RNA-Seq and other bioinformatics analysis for translational research group.

 - **Researcher, Georgetown University,** Jan, 2010 – Jan 2011
MicroRNA Target Prediction Project,
 - Use Perl to manipulate the data from different database and software, extract features from variety of data types.
 - Use R to extract the features for Machine Learning procedure.
 - Use Machine Learning algorism (Weka) to predict the potential microRNA targets.

 - **Researcher, Georgetown University,** Aug, 2009 – Dec, 2009
LCMS Result Analysis and Optimizing Project,
 - Analyze 2-D image, optimize analyzed results using statistical method. Tool: Matlab

 - **Initiator and Group Leader, Soochow University,** Oct.2007 - Feb.2009
Prediction and Analysis of Gene Cluster,
 - Initial the research project, involving budget control, team management and plan implementation.
 - Project involves database management, data mining and machine learning.

 - **Marketing Investigator, Inside Sales, Jinghua Network Company, China,** July 2008 – Sep, 2008
 - Investigate market change, analyze weekly sales report, present analysis results
 - Communicated with suppliers and customers, and provide operating strategies.
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Yixiao Gong – Senior Bioinformatician

EDUCATION

- **Georgetown University**, Washington, DC, Aug, 2009 – Dec, 2010
Master of Science in Biostatistics, Bioinformatics Track
GPA:3.67. Department of Biostatistics, Bioinformatics and Biomathematics. Medical Center
 - **Soochow University**, China Sep, 2005 - Jun, 2009
Bachelor of Science in Bioinformatics
GPA:3.67 Department of Basic Medical Science and Biology, Medical School
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ACTIVITIES AND LEADERSHIP

Soochow University:

- Best Students Scholarship, 2008; Specific Scholarship, 2006
 - Class President, 2005,2006,2007,2008 Best Class President Award, 2005, 2006, 2007, 2008
 - Vice President, School Student Union, 2005, 2006
President, School Ziqin Ge Drama Club, 2005, 2006 Excellence Award, English Drama Competition
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SELECTED PUBLICATIONS

- Mullenders J, Aranda-Orgilles B, Lhoumaud P, Keller M, Pae J, Wang K, Kayembe C, Rocha PP, Raviram R, **Gong Y**, Premrsirut PK, Tsirigos A, Bonneau R, Skok JA, Cimmino L, Hoehn D, Aifantis I. “*Cohesin loss alters adult hematopoietic stem cell homeostasis, leading to myeloproliferative neoplasms.*” **J Exp Med.** 2015 Oct 19;212(11):1833-50.
- Pitt LA, Tikhonova AN, Hu H, Trimarchi T, King B, **Gong Y**, Sanchez-Martin M, Tsirigos A, Littman DR, Ferrando AA, Morrison SJ, Fooksman DR, Aifantis I, Schwab SR. “*CXCL12-Producing Vascular Endothelial Niches Control Acute T Cell Leukemia Maintenance.*” **Cancer Cell.** 2015 Jun 8;27(6):755-68.