Yi Xianfu

Personal Information

Name:	Yi Xianfu	Gender:	Male
Nationality:	Han	Birthday:	2^{nd} June,1986

Educational Background

2007.09 – Present **Ph.D.**, Molecular Genetics Laboratory, Institute of Health Sciences (IHS), Shanghai Institutes for Biological Sciences (SIBS), Chinese Academy of Sciences (CAS) & Shanghai Jiao Tong University School of Medicine (SJTUSM); State Key Laboratory of Medical Genomics, Ruijin Hospital, SJTUSM.

2003.09 – 2007.06 **B.S.**, School of Life Sciences, Shandong University. Major in Biological Sciences, rank first in my major (GPA: 90.65/100, 1/96), recommended for Graduate University of CAS exempt from admission examination.

2011.12 **Workshop on RNA analysis**, Organized by Beijing Genomics Institute (BGI)-Shenzhen. Be trained with transcriptome sequencing, differential gene expression analysis and gene functional annotation.

2010.11 **Training course on frontiers of bioinformation technology**, Organized by BGI-Shenzhen & School of Life Sciences and Technology of Shanghai Jiao Tong University. Understand the next-generation sequencing (NGS) technologies and acquire the skills to analyse NGS data.

2009.06 **Bioinformatics course**, Graduate Summer School of "Dragon Star". Master basic bioinformatics (sequence alignment, phylogenetics, etc.) and primary algorithms (dynamic programming, etc.).

Research Experience

2010.01 – Present Lead the laboratory bioinformatics team, analyse and annotate the high-throughput genomic sequencing data of several diseases (congenital heart disease (CHD), lung cancer, pathological myopia (PM) in pedigrees, etc.), and identify the disease-related mutations and genes to reveal the mechanism of disease progression.

- Participate in "The Regulatory Mechanism of Epigenetic Modification in Lung Tumorigenesis" supported by the National Basic Research Program of China (973 Program, No. 2011CB510102); by comparing whole-exome sequencing data of lung adenocarcinomas and normal tissues, more than one thousand highly deleterious mutations were identified and hundreds of putative driver mutations were confirmed by resequencing [unpublished]
- Take part in "Genetic Basis of Pathological Myopia" supported by the National Natural Science Foundation of China (NSFC) (No. 81030015); by analyzing whole-exome sequencing data of samples from PM pedigrees, dozens of somatic mutations and candidate genes were identified [unpublished]

2008.02 – 2009.12 Study the factors that influence nucleosome positioning in cooperation with Prof. Cai Yudong from the CAS-MPG Partner Institute for Computational Biology (PICB). The accuracy of predicting nucleosome positioning was improved, and some transcription factors (TFs) and sequence words were found to play an interesting role in discriminating nucleosome forming and inhibiting sequences. [*PLoS ONE*, 5(9) (IF=4.41, First Author); *Protein and Peptide Letters*, 19(1) (IF=1.85, First Author)]

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2009 – 2011 Attend the 7th Asia Pacific Bioinformatics Conference (APBC 2009), the 7th International Bioinformatics Workshop (IBW 2009) and High Throughput Biology (Cold Spring Harbor Asia Conferences 2011) to track the frontiers of biology (bioinformatics, system biology, computational biology, etc.), understand some latest technologies (whole-exome sequencing, RNA-Seq, etc.) & bioinformatics methods (support vector machine, cluster analysis, etc.), and communicate with international researchers.

Personal Skills

Bioinformatics

- Proficient in NGS data analysis and high-throughput genomic analysis
- Be skilled in mining data from centers of biotechnology information (UCSC, NCBI and Ensembl); frequently use several biological databases (dbSNP, SRA, GEO, COSMIC, etc.)
- Be experienced in commonly used biological data formats (FASTA, FASTQ, BED, GFF, VCF, etc.); familiar with bioinformatics tools or softwares (Galaxy, BioMart, Genome Browser, DAVID, EMBOSS, BLAST, IGV, etc.)
- Write some guiding articles ("Genomic Coordinate Systems", "Fetch Genomic Subsequence", etc.); make several slides for training ("Learning Galaxy", "Data File Formats and Relevant Tools in NGS", etc.)

Computer

- Be experienced in using Linux operating system (Ubuntu) as routine bioinformatics working platform; founder and administrator of Linux server (CentOS), the laboratory working platform
- Be experienced in using Perl & BioPerl language for biological data processing; be skilled in using R language for statistical analysis & plotting, and Shell programming for workflow controlling
- Familiar with LaTeX / XeLaTeX and Beamer typesetting
- Write some guiding articles ("Shell Commands in Text Processing", "Two Y-axes in R Plots", etc.); write several useful Perl scripts (fetchGenomeSeq.pl, seqTools.pl, etc.); make and share several LaTeX templates ("Beamer Template Using XeLaTeX", etc.)
- Passed the National Computer Rank Examination (Grade 3) in April 2006

English

- Master specialized English in biology; be skilled in literature reading and writing
- Passed CET-6 in June 2006, scored 77/100

Awards

- First Fellowship of CAS from 2010 to 2012
- First Prize Scholarship & Outstanding Student Award of Shandong University in 2006
- Second Prize Scholarship in 2005
- First Prize Scholarship & Outstanding Student Award of Shandong University in 2004
- National Scholarship in 2003

Publications

[1] **Yi Xianfu**, Cai Yudong, He Zhisong, Cui Weiren, Kong Xiangyin. (2010). Prediction of nucleosome positioning based on transcription factor binding sites. *PLoS ONE*, 5(9), 1-7. [IF=4.411]

[2] **Yi Xianfu**, He Zhisong, Chou Kuochen, Kong Xiangyin. (2012). Nucleosome positioning based on the sequence word composition. *Protein and Peptide Letters*, 19(1), 79-90. [IF=1.849]

[3] Lin Bin*, Yin Shanye*, Shu Yang*, **Yi Xianfu***, et al. Rare variations identified in *X* are associated with congenital heart disease. (* These authors contributed equally to this work.) [*In Preparation*]

[4] Yin Shanye*, Lin Bin*, **Yi Xianfu**, Deng Wenjun, et al. Identification of lung adenocarcinoma driver mutations by pooled exome sequencing and network reconstruction. (* These authors contributed equally to this work.) [*In Preparation*]

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[5] Zhang Zhenguo, Zhou Li, Hu Landian, Zhu Yufei, Xu Heng, Liu Yang, Chen Xianfeng, **Yi Xianfu**, Kong Xiangyin, & Laurence D. Hurst. (2010). Nonsense-mediated decay targets have multiple sequence-related features that can inhibit translation. *Molecular Systems Biology*, 6(442), 1-9. [IF=9.667]

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