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Programming



Xin Wang

Genomics, Epigenetics & Bioinformatics

Education

- 2014 - 2017(exp) **PhD in Bioinformatics** [The University of New South Wales, Australia](#)
PhD Advisor: Dr. Joshua W. K. HO at the Victor Chang Cardiac Research Institute.
Co-Advisor: Assoc Prof. Catherine SUTER at VCCRI, Asst Prof. Chris, Koon Ho WONG at the University of Macau.
Currently working on a TF grammar learning project and a fungal chromatin analysis project.
- 2010 - 2013 **MRes in Genetics** [Wenzhou Medical University, China](#)
M.S. Advisor: Dr. Zhongsheng Sun, Principal Investigator of Beijing Institutes of Life Science, Chinese Academy of Sciences (BIOLS, CAS), Beijing, China and Director of the Institute of Genomic Medicine at Wenzhou Medical University, Wenzhou, China.
Co-Advisor: Dr. Jinyu Wu, now Principal Investigator of BIOLS, CAS.
Master Thesis: Xin Wang (2013) Methylome research of ovarian cancer cell line T29H based on RRBS. Institute of Genomic Medicine, WMU.
- 2005 - 2009 **BSc in Chemistry / Biology (Minor)** [Sun Yat-sen University, China](#)
B.S. Advisor: Dr. Shang-hong Zhang, Assoc Prof. of School of Life Sciences of SYSU and PI in the Key Laboratory of Gene Engineering of Ministry of Education, Sun Yat-sen University, Guangzhou, China.
Bachelor Thesis: Xin Wang (2009) Phylogenetic studies on subtypes of Ebola virus via Bioinformatics. School of Biosciences, SYSU.

Experience

- 07/15 - 12/15 **Exchange PhD student** [University of Macau, Macau SAR, China](#)
For the fungal chromatin analysis project.
- 07/13 - 06/14 **Bioinformatician** [Biocant\(Joint institute by Univ. of Coimbra and Univ. of Aveiro\), Portugal](#)
Working for Exome (Ion Proton) and genome data (Illumina) analysis.
- 01/11 - 12/11 **Exchange Master student** [BGI-Shenzhen, China](#)
Working for the joint project of Ovarian Cancer methylome by BGI and BIOLS, CAS.
- 08/09 - 07/10 **Bioinformatician** [Guangzhou HF Biotech \(Hua Feng\), China](#)
On HF-MOH's HPV census project by LAMP method. LAMP primer design.

Professional skills

Programming languages: R (skilled), Perl (skilled), Shell (skilled), Python (familiar), PHP (familiar).

Software Tools:

BWA, Bowtie2, Samtools, Picard, SOAP3-dp, Tophat, Cufflinks, STAR, FusionMap, GATK, EXCAVATOR, BSMAP, MethylKit, Bioconductor and lumi/DEGseq package, ANNOVAR, VCFtools, BEDtools, FastQC, Trim golare, TMAP, TVC, VirusFinder, BLAST/BLAT, Cytoscape, MACS, HOMER, SPP, hiHMM, LASER (Locating Ancestry from SEquence Reads), Illustrator CS, shareLATEX and Zotero.

Familiar with: online Reactome, DAVID, KEGG, CADD, Magia2 and Galaxy.

Skilled in building data process pipeline of resequencing, Exome, RRBS, RNA-seq miRNA.

Be comfortable working on various Linux/Unix operating systems with HPC cluster environment of SGE. Be familiar with various bioinformatics tools and genomics, epigenomics oncology databases. Be Skilled in handling data from both Illumina platform and Ion Proton platform.

Experienced in multiple algorithms such as SVM, HMM, PCA and MDS and interest in developing new algorithm.

Wet Lab experience: DNA/RNA extracting, running gel electrophoresis and HeLa cells' culture, etc. Lots hours in organic and analysis chemistry experiments (mostly on undergraduate courses).

Publications

Wang Y, Li G, Mao F, Li X, Liu Q, Chen L, Lv L, Wang X, Wu J, Dai W, Wang G, Zhao E, Tang KF, Sun ZS. (2014).

Epigenetic Inactivation of Ras-related Associated with Diabetes (RRAD) Promotes Glucose Uptake in a Human Ovarian Cancer Model

The Journal of Biological Chemistry, 289(20), 14225-14238.

Wu J, Liu Q, Wang X, Zheng J, Wang T, You M, Sun ZS, Shi Q. (2013).

mirTools 2.0 for non-coding RNA discovery, profiling, and functional annotation based on high-throughput sequencing

RNA biology, 10(7), 1087–1092.

Liu Q, Shen E, Min Q, Li X, Wang X, Li X, Sun ZS, Wu J. (2012).

Exome-assistant: a rapid and easy detection of disease-related genes and genetic variations from exome sequencing

BMC Genomics, 13, 692.

Book chapter:

Xin Wang, Helen M. McCormick, Djordje Djordjevic, Eleni Giannoulatou, Catherine M. Suter, Joshua W. K. Ho (2016).

Epigenomic analysis of chromatin organization and DNA methylation

Computational Biology and Bioinformatics: Gene Regulation, CRC Press, ISBN 9781498724975 - CAT K25752

Conferences & Posters

The 6th International Conference on Genomics (ICG-6) 2011.11.12-15 Shenzhen, China
Barcelona Conferences on Epigenetics and Cancer 2013.11.21-22 Barcelona, Spain

Poster:

ISMB/ECCB 2015

Comprehensive analysis of chromatin landscape in filamentous fungus *Aspergillus Nidulans*
Joshua W. K. Ho, Djordje Djordjevic, Xin Wang, Zhengqiang Miao, Chirag Parsania, Kaeling Tan, Koon Ho Wong

Membership:

Member of the Australian Bioinformatics and Computational Biology Society (ABACBS)

May 9th, 2016

Xin Wang