(Eric) Zhang Chen

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Research Interests

Bioinformatics, statistical methods for analysis of RNA-Seq, ChIP-Seq and other high-throughput sequencing data with application to microbiome, non-coding RNA and prenatal dignoisis.

Education

2011-2016 Ph.D student in Genomics and Computational Biology, University of Pennsylvania, USA
Thesis Topic: *Statistical methods for microbiome data anlaysis*

2009-2011 M.Phil in Bioinformatics, Chinese University of Hong Kong, Hong Kong
Thesis: *Development of bioinformatics algorithms for trisomy 13 and 18 detection by next generation sequencing of maternal plasma DNA*

2004-2008 BS in Biology, University of Science and Technology of China, China
Thesis: *ChIP-Seq data analysis*

Research Experience

2011-present Research Assistant
　　Department of Biostatistics, University of Pennsylvania
2009-2011 Research Assistant
　　Li Ka Shing Institute of Health Science, Chinese University of Hong Kong
2007-2009 Undergraduate intern
　　Institute of Genetics and Developmental Biology, Chinese Academy of Sciences

Paper Revivew Experience

Reviwed five manuscripts for BioData Mining, Transactions on Computational Biology and Bioinformatics, Biometrics.

Publications

1. Jaewook Oh, Iryna F Sanders, **Eric Z Chen**, Hongzhe Li, John W Tobias, et al. Genome Wide Nucleosome Mapping for HSV-1 Shows Nucleosomes Are Deposited at Preferred Positions During Lytic Infection. Plos One. 2015.

2. Gary D Wu, Charlene Compher, **Eric Z Chen**, Sarah A Smith, Rachana D Shah, Kyle Bittinger, Christel Chehoud, et al. Comparative metabolomics in vegans and omnivores reveal constraints on diet-dependent gut microbiota metabolite production. Gut. 2014.

3. Chenhuan Xu, Xiaowen Lu, **Eric Z Chen**, Zhiying He, Borjigin Uyunbilig, Guangpeng Li, Yue Ma, et al. Genome-Wide Roles of Foxa2 in Directing Liver Specification. Journal of Molecular Cell Biology. 2012.

4. Leina Lu, Liang Zhou, **Eric Z Chen**, Kun Sun, Peiyong Jiang, Lijun Wang, Xiaoxi Su, Hao Sun, and Huating Wang. A Novel YY1-miR-1 Regulatory Circuit in Skeletal Myogenesis Revealed by Genome-Wide Prediction of YY1-miRNA Network. PloS One. 2012.

5. Yama W L Zheng, K C Allen Chan, Hao Sun, Peiyong Jiang, Xiaoxi Su, **Eric Z Chen**, Fiona M F Lun, et al. Nonhematopoietically Derived DNA Is Shorter Than

Hematopoietically Derived DNA in Plasma: a Transplantation Model. Clinical Chemistry. 2012.

6. **Eric Z Chen**, Rossa W K Chiu, Hao Sun, Ranjit Akolekar, K C Allen Chan, Tak Y Leung, Peiyong Jiang, et al. Noninvasive Prenatal Diagnosis of Fetal Trisomy 18 and Trisomy 13 by Maternal Plasma DNA Sequencing. PloS One. 2011.

7. Daan van Abel, Dennis R Hlzel, Shushant Jain, Fiona M F Lun, Yama W L Zheng, **Eric Z Chen**, Hao Sun, et al. SFRS7-Mediated Splicing of Tau Exon 10 Is Directly Regulated by STOX1A in Glial Cells. PloS One. 2011.

8. Y M Dennis Lo, K C Allen Chan, Hao Sun, **Eric Z Chen**, Peiyong Jiang, Fiona M F Lun, Yama W Zheng, et al. Maternal Plasma DNA Sequencing Reveals the Genome-Wide Genetic and Mutational Profile of the Fetus. Science Translational Medicine. 2010.

9. Teng Fei, Kai Xia, Zhongwei Li, Bing Zhou, Shanshan Zhu, Hua Chen, Jianping Zhang, **Zhang Chen**, et al. Genome-Wide Mapping of SMAD Target Genes Reveals the Role of BMP Signaling in Embryonic Stem Cell Fate Determination. Genome Research. 2010.