(Eric) Zhang Chen

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RESEARCH INTERESTS

Statistical methods for analysis of RNA-Seq, ChIP-Seq and other high-throughput sequencing data.

EDUCATION

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

2009-2011 M.Phil in Bioinformatics, Chinese University of Hong Kong, Hong Kong
Supervisor: Dennis Lo and Hao Sun
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
Supervisor: Jing-Dong Jackie Han
Thesis: *ChIP-Seq data analysis*

RESEARCH EXPERIENCE

2011-present Research Assistant, Department of Biostatistics, University of Pennsylvania
- Develop statistical models for high-throughput sequencing data analysis
- Collaborate with other researchers at School of Medicine at UPenn and provide statistical support for them

2009-2011 Research Assistant, Li Ka Shing Institute of Health Science, Chinese University of Hong Kong
- Develop a statistical model to correct the sequencing bias in the whole genome sequencing data with the application to trisomy 13 and 18 diagnosis.
- Provide statistis support for lab memebers in Dr.Dennis Lo's lab and other collaborators.

2007-2009 Undergraduate intern, Institute of Genetics and Developmental Biology,Chinese Academy of Sciences
- Analyze the ChIP-Seq data from collaborator Dr.Xin Wang at Chinese Academy of Sciences. The analysis includes read alignment, peak calling, motif identification, gene enrichment analysis.

PUBLICATIONS

1. Dale Lee, Robert N. Baldassano, Anthony R. Otley, Lindsey Albenberg,Anne M. Griffiths, Charlene Compher, **Eric Z Chen**, Hongzhe Li, Erin Gilroy, Lisa Nessel, Amy Grant, Christel Chehoud, Frederic D. Bushman, Gary D. Wu, James D. Lewis, Comparative Effectiveness of Nutritional and Biological Therapy in North American Children with Active Crohns Disease. Inflammatory Bowel Diseases. 2015.

2. 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.

3. 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.

4. 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.

5. 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.

6. 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.

7. **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.

8. 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.

9. Jiang Peiyong, Xiaoxi Su, **Eric Z Chen**, Kun Sun, Rossa Chiu, Dennis Lo, Hao Sun. Methy-Pipe: An integrated bioinformatics data analysis pipeline for whole genome methylome analysis. BIBMW,IEEE International Conference. 2011.

10. Leina Lu, Liang Zhou, **Eric Z Chen**, Kun Sun, Peiyong Jiang, Susie Su, Lijun Wang, Hao Sun, Huating Wang. Genome-wide identification of TF-miRNA regulatory networks in myogenesis. BIBMW,IEEE International Conference. 2011.

11. 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.

12. Teng Fei, Kai Xia, Zhongwei Li, Bing Zhou, Shanshan Zhu, Hua Chen, Jianping Zhang, **Zhang Chen**, Huasheng Xiao, Jing-Dong J. Han and Ye-Guang Chen. Genome-Wide Mapping of SMAD Target Genes Reveals the Role of BMP Signaling in Embryonic Stem Cell Fate Determination. Genome Research. 2010.

13. Jing-Dong J. Han, Yi Liu, Huiling Xue, Kai Xia, Hong Yu, Shanshan Zhu, **Zhang Chen**, Wei Zhang, Chunyu Jin, Bo Xian, Jing Li, Lei Hou, Yixing Han, Chaoqun Niu, Timothy C. Alcon. Developmental systems biology flourishing on new technologies. 2008. Journal of Genetics and Genomics.