Tianlei Xu

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EDUCATION

2012-2018   Ph.D. in Computer Science & Informatics, Emory University, Atlanta, GA.
                Advisor: Zhaohui Steve Qin, Hao Wu

2009-2012   M.Eng. in Bioinformatics, Tongji University, China

2005-2009   B.Eng. in Bioinformatics, Tongji University, China (GPA: 4.69/5)

TEACHING

2015 Spring   *Instructor*: CS170 – Intro to Computer Science I (Java)

2014 Fall   *Instructor*: CS170 – Intro to Computer Science I (Java)

PUBLICATION

Unpublished

1. **Xu T,** Jin P, Qin Z. *loci2path: Exploiting the co-localization of trait-associated SNPs and eQTLs to identify potential biological mechanisms underlying complex diseases.* (submitted to Genome Research, packaged accepted in bioconductor)

2. Qiu T, Yang Y, Qiu J, Huang Y, **Xu T**, Xiao H, Wu D, Zhang Q, Zhou C, Zhang X, Tang K, Xu J, Cao Z. *CE-BLAST makes it possible to compute antigenic similarity for newly emerging* (**accepted** in **Nature Communication**)

3. ENCODE-DREAM Community. *Methods for predicting in vivo transcription factor binding sites across cell types and tissues by integrating DNA sequence, RNA expression and chromatin accessibility data.* (submission to Cell in progress)

4. **Xu T,** Qin Z, Wu H. *Genomic feature prediction from high-throughput data.* (manuscript in progress)

5. Liu H, **Xu T**(co-first), Jin P, Wang X. *Altered 5-hydroxymethylcytosine landscape in primary gastric adenocarcinoma.* (manuscript in progress)

6. Gollavilli PN, Romans K, Pawar A, Engelke CG, Dommeti VL, Krishnamurthy PM, Nallasivam A, Apel IA, **Xu T**, Qin ZS, Feng FY, and Asangani IA. *BET bromodomain dependency in EWS/ETS driven Ewing Sarcoma.* (submission in progress)

Method

1. Sun X, Pittard WS, **Xu T**, Chen L, Zwick ME, Jiang X, Wang F & Qin ZS (2017) *Omicseq: a web-based search engine for exploring omics datasets*, **Nucleic Acids Research**.

2. Wu H, **Xu T**, Feng H, Chen L, Li B, Yao B, Qin Z, Jin P & Conneely KN (2015) *Detection of differentially methylated regions from whole-genome bisulfite sequencing data without replicates*, **Nucleic Acids Res.**, p. gkv715-. doi: 10.1093/nar/gkv715.

3. **Xu T**, Li B, Zhao M, Szulwach KE, Street RC, Lin L, Yao B, Zhang F, Jin P, Wu H & Qin ZS (2015) *Base-resolution methylation patterns accurately predict transcription*

factor bindings in vivo., **Nucleic acids research**, pp. 1–10. doi: 10.1093/nar/gkv151.

4. **Xu T**, Zhu R, Liu Q & Cao Z (2012) *Quantitatively integrating molecular structure and bioactivity profile evidence into drug-target relationship analysis*, **BMC Bioinformatics**, 13(1), p. 75. doi: 10.1186/1471-2105-13-75.

5. Sun J, Wu D, **Xu T**, Wang X, Xu X, Tao L, Li YX & Cao ZW (2009) *SEPPA: A computational server for spatial epitope prediction of protein antigens*, **Nucleic Acids Research**, 37(SUPPL. 2).

Collaboration works

1. Weng Y, Wang X, An R, Cassin J, Vissers C, Liu YY, Liu YJ, **Xu T**, Wang X, Wong SZ, Joseph J, Dore L, Dong Q, Zheng W, Jin P, Wu H, Shen B, Zhuang X, He C, Liu K, Song H, Ming G. (2017) *Epitranscriptomic m6A Regulation of Axon Regeneration in the Adult Mammalian Nervous System.* **Neoron**, Volume 97, Issue 2, p313–325.e6

2. Rao A, Zhang W, **Xu T**, Wynn GM, Wu H, Setchell KD, Karpen S, Dawson P. (2017) *Early Anti-steatotic Actions of an Ileal Apical Sodium-dependent Bile Acid Transporter Inhibitor in High Fat Diet Fed Mice.* **Hepatology,** 66, 1049A-1050A.

3. Li L, Zang L, Zhang F, Chen J, Shen H, Shu L, Liang F, Feng C, Chen D, Tao H, **Xu T**, Li Z, Kang Y, Wu H, Tang L, Zhang P, Jin P, Shu Q & Li X (2017) *Fat mass and obesity-associated (FTO) protein regulates adult neurogenesis*, **Human Molecular Genetics**, 26(13), pp. 2398–2411. doi: 10.1093/hmg/ddx128.

4. Oh Y, Zhang F, Wang Y, Lee EM, Choi IY, Lim H, Mirakhori F, Li R, Huang L, **Xu T**, Wu H, Li C, Qin C-F, Wen Z, Wu Q-F, Tang H, Xu Z, Jin P, Song H, *et al.* (2017) *Zika virus directly infects peripheral neurons and induces cell death*, **Nature Neuroscience**. Available at: http://dx.doi.org/10.1038/nn.4612.

5. Rao A, Kosters A, Mells JE, Zhang W, Setchell KDR, Amanso AM, Wynn GM, **Xu** T, Keller BT, Yin H, Banton S, Jones DP, Wu H, Dawson PA & Karpen SJ (2016) *Inhibition of ileal bile acid uptake protects against nonalcoholic fatty liver disease in high-fat diet–fed mice*, **Science Translational Medicine**, 8(357), p. 357ra122 LP-357ra122. doi: 10.1126/scitranslmed.aaf4823.

6. Zhang F, Hammack C, Ogden SC, Cheng Y, Lee EM, Wen Z, Qian X, Nguyen HN, Li Y, Yao B, Xu M, **Xu T**, Chen L, Wang Z, Feng H, Huang WK, Yoon KJ, Shan C, Huang L, *et al.* (2016) *Molecular signatures associated with ZIKV exposure in human cortical neural progenitors*, **Nucleic Acids Research**, 44(18), pp. 8610–8620. doi: 10.1093/nar/gkw765.

7. Sun J, **Xu T**, Wang S, Li G, Wu D & Cao Z (2011) *Does difference exist between epitope and non-epitope residues? Analysis of the physicochemical and structural properties on conformational epitopes from B-cell protein antigens*, in **Immunome Research**.

8. Wu D, Sun J, **Xu T**, Wang S, Li G, Li Y & Cao Z (2010) *Stacking and energetic contribution of aromatic islands at the binding interface of antibody proteins*, in **Immunome Research**.

9. Wu D, **Xu TL**, Sun J, Dai JX, Ding GH, He Y, Zhou ZF, Xiong H, Dong H, Jin WR,

Bian C, Jin L, Wang HY, Wang XN, Yang Z, Zhong Y, Wang H, Che XY, Huang Z, *et al.* (2009) *Structure modeling and spatial epitope analysis for HA protein of the novel H1N1 influenza virus*, **Chinese Science Bulletin**, 54(13), pp. 2171–2173. doi: 10.1007/s11434-009-0429-3.

SKILLS

Programming	Proficient in: R, Bioconductor, Perl
	Familiar with: Matlab, Python, C/C++, PHP, C#, Java
Statistical Modeling	Regression (Linear, multivariate, GLM, GAM, Bayes, mixture effect, etc.), Hypothesis testing (for enrichment: ANOVA, fisher, hypergeom, etc; for differential: Non-para, Wald, permutation-based, etc.), Inference (EM, HMM, Gibbs sampler, MOM), etc.
Machine Learning	Predictive model (GBM, RF, NN, SVM, etc.), feature selection/dimension reduction (PCA, t-SNE, etc.), ensemble learning, regularization, etc.
Bio-Data analysis	Common NGS analysis tools.
Other	Linux/Shell, VIM, LaTeX, Rmarkdown/knitR, Shiny

RESEARCH PROJECTS

- **Deep Learning algorithms for epigenetics:** Develop Deep learning model to extract DNA sequence features, omics-profiles and intrinsic interactions.
- **Machine learning approaches for epigenetics:** Review recent development in applications of machine learning methods for epigenome-wide prediction between regulatory factors.
- **Functional enrichment analysis for non-coding variants:** Exploit eQTLs as resources for functional annotation of non-coding variants.
- **Statistical modeling for epigenetics:** Computational model to predict TF binding with methylation profile; Differential methylation detection method with no replicate.
- **Omics information hub design**: Design relational schema and optimize for large-scale genome data query. Mining epigenetic regulation relationships.
- **High-throughput NGS data analysis**. Collaboration work for NGS data processing and analysis, includes:
  - Enrichment/clustering/marker detection with NGS data (RNA-seq, ChIP-seq, DNase-seq, Bisulfite-seq, MeDIP-seq, RRBS, MicroArray, m6A-seq)
  - Differential Expression/function enrichment for transcriptome data
  - Single-cell RNA-seq data
  - Tissue-origin deconvolution (cfDNA methylation, transcripts as markers)
  - Motif enrichment/de-novo discovery

Before 2012 in Tongji University, China. Adviser: Cao Zhiwei.

- **Multi-view Similarity Fusion:** Developing multi-view clustering method.
- **Structural Comparison algorithm:** Structural comparison for B-cell epitope.
- **Web Server:** Building PHP server and JMOL module of SEPPA.

<u>INVITED TALK</u>
2015 Base-resolution methylation patterns accurately predict transcription factor bindings in vivo ICSA/Graybill Joint Conference**.** Fort Collins, Colorado

<u>CONFERENCE</u>
2017 The 67th Annual Meeting of The American Society of Human Genetics, October 20, 2017, Orlando, Florida. Poster: Xu T**,** Qin Z. *Exploiting the co-localization of trait-associated SNPs and eQTLs to identify potential biological mechanisms underlying complex diseases.* (Program #1383F. Reviewer's Choice award, top 10%).
2016 The Ninth Annual RECOMB/ISCB Conference on Regulatory & Systems Genomics, with DREAM Challenges. November 6 - 9, 2016. Phoenix, AZ (Top performance team; 2th of US, 7th of 61 teams and 200+ individual participants)
2015 Big Data Challenges in Life Sciences. University of Georgia. Athens, Georgia

<u>AWARDS and HONORS</u>
2017 ASHG 2017 Reviewers' Choice Abstract (top 10%)
2016 Leading participant in ENCODE-DREAM in vivo Transcription Factor Binding Site Prediction Challenge. (Leaderboard Rank: 7th among 61 teams and 200+ participants)
2015 Team leader of 2nd team in Atlanta Big Data Analytics Team Challenge 2016.
2009 Excellent Graduation Thesis& Shanghai Outstanding graduates (Top 1 department award)
2007 National Scholarship (Top 1 department award)
2006 Suntory International Group Scholarship (Top 40 Bio/Chem students in Shanghai)

<u>REVIEW SERVICES</u>
- Nucleic Acids Research, Oxford University Press