SAI ZHANG

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RESEARCH INTERESTS

Computational Biology, Machine Learning, Genomics, Genetics, Precision Medicine

RESEARCH EXPERIENCE

Stanford University School of Medicine, Stanford, CA

- Instructor, Department of Genetics   Sept. 2021 – Present

- Postdoctoral Scholar, Department of Genetics   Sept. 2017 – Aug. 2021
    - Machine learning-based genome analysis for disease prediction and gene discovery for complex diseases
    - Advisor: Michael P. Snyder

- Visiting Student, Department of Genetics   Dec. 2016 – Feb. 2017
    - Genome analysis for autism spectrum disorder and abdominal aortic aneurysm
    - Advisor: Michael P. Snyder

Palo Alto Veterans Institute for Research, Palo Alto, CA

- Research Associate (without compensation)   Dec. 2019 – Present
    - Integrative analysis of genetics and electronic medical records for cardiovascular diseases
    - Advisor: Philip S. Tsao

Tsinghua University (THU), Beijing, China

- Research Assistant, Institute for Interdisciplinary Information Sciences (IIIS) Sep. 2013 – Jun. 2017
    - Deep learning applications in computational genomics
    - Advisor: Jianyang Zeng

- Research Assistant, Department of Computer Science and Technology   Sep. 2010 – Jul. 2013
    - Measurement and analysis of online social networks
    - Advisor: Ke Xu

EDUCATION

Tsinghua University, Beijing, China

- Ph.D. in Computer Science and Technology   Sep. 2013 – Jun. 2017
    - Thesis: *Deep Learning in Computational Genomics*
    - Advisor: Jianyang Zeng

- M.E. in Computer Technology   Sep. 2010 – Jul. 2013
    - Thesis: *Measurement, Analysis and Modeling of Information Propagation in Online Social Networks*
    - Advisor: Ke Xu

Nanjing University of Science and Technology (NJUST), Nanjing, China

- B.E. in Computer Science and Technology   Sep. 2006 – Jun. 2010

PUBLICATIONS   (*: equal contribution)

1. T.H. Julian, S. Boddy, M. Islam, J. Kurz, K.J. Whittaker, T. Moll, C. Harvey, **S. Zhang**, M.P. Snyder, C. McDermott, J. Cooper-Knock, P.J. Shaw. A review of Mendelian randomization in amyotrophic lateral sclerosis. *Brain*, awab420, 2021.

2. T. Moll, J.N.G. Marshall, N. Soni, **S. Zhang**, J. Cooper-Knock, P.J. Shaw. Membrane lipid raft homeostasis is directly linked to neurodegeneration. *Essays in Biochemistry*, EBC20210026, 2021.

3. J. Cooper-Knock, C. Harvey, **S. Zhang**, T. Moll, I.S. Timpanaro, K.P. Kenna, A. Iacoangeli, J.H. Veldink. Advances in the genetic classification of amyotrophic lateral sclerosis. *Current Opinion in Neurology*, Aug 02, 2021.

4. T.H. Julian, N. Glascow, A.D.F. Barry, T. Moll, C. Harvey, Y.C. Klimentis, M. Newell, **S. Zhang**, M.P. Snyder, J. Cooper-Knock, and P.J. Shaw. Physical exercise is a risk factor for amyotrophic lateral sclerosis: Convergent evidence from mendelian randomization, transcriptomics and risk genotypes. *EBioMedicine*, 68:103397, 2021.

5. Y. Li, **S. Zhang**, M.P. Snyder, and K.J. Meador. Precision medicine in women with epilepsy: The challenge, systematic review and future direction. *Epilepsy & Behavior*, 118:107928, 2021.

6. X. He, **S. Zhang**, Y. Zhang, Z. Lei, T. Jiang, and J. Zeng. Characterizing RNA pseudouridylation by convolutional neural networks. *Genomics, Proteomics & Bioinformatics*, 2021.

7. J. Cooper-Knock, **S. Zhang**, K.P. Kenna, T. Moll, J. Franklin, S. Allen, H.G. Nezhad, N.S. Yacovzada, C. Eitan, E. Hornstein, E. Ehilak, P. Celadova, D. Bose, S.M.K. Farhan, S. Fishilevich, D. Lancet, K.E. Morrison, C. Shaw, A. Al-Chalabi, Project MinE ALS Sequencing Consortium, J.H. Veldink, J. Kirby, M.P. Snyder, and P.J. Shaw. Rare variant burden analysis within enhancers identifies *CAV1* as a new ALS risk gene. *Cell Reports*, 33(9):108456, 2020.

8. Y. Zhang, **S. Zhang**, X. He, J. Lu, and X. Gao. DeepRibSt: A multi-feature convolutional neural network for predicting ribosome stalling. *Multimedia Tools and Applications*, 1-17, 2020.

9. J. Li, X. Li, **S. Zhang**, and M.P. Snyder. Gene-environment interaction in the era of precision medicine. *Cell*, 177(1):38-44, 2019.

10. H. Hu, A. Xiao, **S. Zhang**, Y. Li, X. Shi, T. Jiang, L. Zhanng, L. Zhang, and J. Zeng. DeepHINT: Understanding HIV-1 integration via deep learning with attention. *Bioinformatics*, 35(10):1660-1667, 2019.

11. J. Li*, C. Pan*, **S. Zhang***, J.M. Spin, A. Deng, L.L.K. Leung, R.L. Dalman, P.S. Tsao, and M.P. Snyder. Decoding the genomics of abdominal aortic aneurysm. *Cell*, 174(6):1361-1372, 2018.

12. G. Zhu, W. Deng, H. Hu, R. Ma, **S. Zhang**, J. Yang, J. Peng, T. Kaplan, and J. Zeng. Reconstructing spatial organizations of chromosomes through manifold learning. *Nucleic Acids Research*, 46(8):e50, 2018.

13. **S. Zhang**, H. Hu, J. Zhou, X. He, T. Jiang, and J. Zeng. Analysis of ribosome stalling and translation elongation dynamics by deep learning. *Cell Systems*, 5(3):212-220, 2017. An early version appeared in *Proceedings of the 21th Annual International Conference on Research in Computational Molecular Biology (RECOMB 2017)*; Hong Kong, China; May 3-7, 2017.

14. **S. Zhang**, H. Hu, T. Jiang, L. Zhang, and J. Zeng. TITER: Predicting translation initiation sites by deep learning. *Bioinformatics*, 33(14):i234-i242, 2017. Also appeared in *Proceedings of the 25th Conference on Intelligent Systems for Molecular Biology/16th European Conference on Computational Biology (ISMB/ECCB 2017)*; Prague, Czech Republic; Jul. 21-25, 2017.

15. **S. Zhang**, M. Liang, Z. Zhou, C. Zhang, N. Chen, T. Chen, and J. Zeng. Elastic restricted Boltzmann machines for cancer data analysis. *Quantitative Biology*, 5(2):159-172, 2017. (Cover Article)

16. S. Li, F. Dong, Y. Wu, **S. Zhang**, C. Zhang, X. Liu, T. Jiang, and J. Zeng. A deep boosting based approach for capturing the sequence binding preferences of RNA-binding proteins from high-throughput CLIP-seq data. *Nucleic Acids Research*, 45(14):e129, 2017.

17. **S. Zhang**, J. Zhou, H. Hu, H. Gong, L. Chen, C. Cheng, and J. Zeng. A deep learning framework for modeling structural features of RNA-binding protein targets. *Nucleic Acids Research*, 44(4):e32, 2016.

18. H. Gong, **S. Zhang**, J. Wang, H. Gong, and J. Zeng. Constructing structure ensembles of intrinsically disordered proteins from chemical shift data. *Journal of Computational Biology*, 23(5):300-310, 2016. An early version appeared in *Proceedings of the 19th Annual International Conference on Research in Computational Molecular Biology (RECOMB 2015)*; Warsaw, Poland; Apr. 12-15, 2015.

19. K. Xu, **S. Zhang**, H. Chen, and H. Li. Measurement and analysis of online social networks. *Chinese Journal of Computers*, 37(1):165-188, 2014. (in Chinese)

MANUSCRIPTS & PREPRINTS

(*: equal contribution)

1. **S. Zhang**, J. Cooper-Knock, A.K. Weimer, M. Shi, L. Kozhaya, D. Unutmaz, C. Harvey, T.H. Julian, S. Furini, E. Frullanti, F. Fava, A. Renieri, P. Gao, X. Shen, I.S. Timpanaro, K.P. Kenna, J.K. Baillie, M.M. Davis, P.S. Tsao, and M.P. Snyder. Multiomic analysis reveals cell-type-specific molecular mechanisms of COVID-19 severity. *Science Translational Medicine*, under review.

2. **S. Zhang**, J. Cooper-Knock, A.K. Weimer, C. Harvey, T.H. Julian, C. Wang, J. Li, S. Furini, E. Frullanti, F. Fava, A. Renieri, C. Pan, J. Song, P. Billing-Ross, P. Gao, X. Shen, I.S. Timpanaro, K.P. Kenna, VA Million Veteran Program, GEN-COVID Network, M.M. Davis, P.S. Tsao, and M.P. Snyder. Common and rare variant analyses combined with single-cell multiomics reveal cell-type-specific molecular mechanisms of COVID-19 severity. *medRxiv*, doi: 10.1101/2021.06.15.21258703, 2021.

3. **S. Zhang**, J. Cooper-Knock, A.K. Weimer, M. Shi, T. Moll, C. Harvey, H.G. Nezhad, J. Franklin, C.D.S. Souza, C. Wang, J. Li, C. Eitan, E. Hornstein, K.P. Kenna, Project MinE Sequencing Consortium, J. Veldink, L. Ferraiuolo, P.J. Shaw, and M.P. Snyder. Genome-wide identification of the genetic basis of amyotrophic lateral sclerosis. *bioRxiv*, doi: 10.1101/2020.11.14.382606, 2020. *Neuron*, under revision.

4. Y. Wang, X. Zhang, C. Lam, H. Guo, C. Wang, **S. Zhang**, J. Wu, M.P. Snyder, and J. Li. Systems analysis identifies a molecular network in congenital heart diseases. *Circulation*, under review.

5. **S. Zhang**, K. Xu, X. Chen, and X. Liu. Characterizing information spreading in online social networks. *arXiv*:1404.5562 [cs.SI], 2014.

TEACHING EXPERIENCE	(*: graduate course)

Teaching Assistant

- Tsinghua University

– Advanced Applications of Machine Learning	Fall 2016
– Calculus A II	Spring 2016
– Hot Topics in Computational Biology*	Fall 2015
– Calculus A II	Spring 2015
– Hot Topics in Computational Biology*	Fall 2014
– Calculus A II	Spring 2014
– Linear Algebra I	Fall 2013

MENTORING
EXPERIENCE

- Omar Nour Niagne (PhD Student, Stanford Genetics)   Jul. 2021 - Present

- Saahil Jain (MS Student, Stanford CS)   Sept. 2020 - Feb. 2021

POSTERS   (*: equal contribution)

1. **S. Zhang**, J. Cooper-Knock, A.K. Weimer, M. Shi, T. Moll, C. Harvey, H.G. Nezhad, J. Franklin, C.D.S. Souza, C. Wang, J. Li, C. Eitan, E. Hornstein, K.P. Kenna, Project MinE Sequencing Consortium, J. Veldink, L. Ferraiuolo, P.J. Shaw, and M.P. Snyder. Genome-wide identification of the genetic basis of amyotrophic lateral sclerosis. *CSHL Meeting: Neurodegenerative Diseases-Biology & Therapeutics* (Virtual); Dec. 2-4, 2020.

2. J. Li*, C. Pan*, **S. Zhang***, J.M. Spin, A. Deng, L.L.K. Leung, R.L. Dalman, P.S. Tsao, and M.P. Snyder. A novel approach for decoding the genomics of a complex disease: Abdominal aortic aneurysm. *16th CEGS Annual Grantee Meeting*; Chicago, IL; Nov. 19-20, 2018.

3. **S. Zhang**, H. Hu, T. Jiang, L. Zhang, and J. Zeng. TITER: Predicting translation initiation sites by deep learning. *ISMB/ECCB 2017*; Prague, Czech Republic; Jul. 21-25, 2017.

4. **S. Zhang**, H. Hu, J. Zhou, X. He, T. Jiang, and J. Zeng. ROSE: A deep learning based framework for predicting ribosome stalling. *ISMB/ECCB 2017*; Prague, Czech Republic; Jul. 21-25, 2017.

5. **S. Zhang**, H. Hu, J. Zhou, X. He, T. Jiang, and J. Zeng. ROSE: A deep learning based framework for predicting ribosome stalling. *IIIS Research Festival 2016*, THU; Dec. 16, 2016.

6. **S. Zhang**, J. Zhou, H. Hu, H. Gong, L. Chen, C. Cheng, and J. Zeng. Deep learning for modeling structural features of RNA-binding protein targets. *IIIS Research Festival 2015*, THU; Dec. 24, 2015.

PRESENTATIONS

- Stanford SystemX Alliance 2021 Fall Conference (invited talk, virtual)   Nov. 10, 2021
- Stanford CEGS GGR Meeting (invited talk, virtual)   Jul. 26, 2021
- Fred Hutchinson Cancer Research Center (invited talk, virtual)   May 24, 2021
- Department of Computer Science and Technology, Tsinghua University (invited talk, virtual)   Feb. 23, 2021
- Illumina AI Lab (invited talk, virtual)   Feb. 9, 2021
- Regeneron Genetics Center (invited talk, virtual)   Jan. 11, 2021

- Institute of Modern Biology, Nanjing University (invited talk, virtual) Nov. 17, 2020
- 16th CEGS Annual Grantee Meeting (rapid poster talk), Chicago, IL   Nov. 19-20, 2018
- ISMB/ECCB 2017, Prague, Czech Republic   Jul. 21-25, 2017
- CSHA/AACR Joint Meeting: Big Data, Computation and Systems Biology in Cancer, Suzhou, China   Dec. 2-5, 2015
- 2012 CCF National Conference on Service Computing (NCSC 2012), Xi'an, China Aug. 16-18, 2012

PATENTS & PATENT APPLICATIONS

1. J. Li, **S. Zhang**, M.P. Snyder, C. Pan, and P.S. Tsao. Processes for genetic and clinical data evaluation and classification of complex human traits. US Patent Application 16/961,120, May 2021.

2. **S. Zhang**, J. Li, and M.P. Snyder. Systems and methods for predicting genetic diseases. US Patent Application 16/248,314, Jul. 2019.

ACADEMIC SERVICE

Invited editor

- Frontiers in Genetics

Reviewer

- Conferences
  - NIPS Workshop on Machine Learning in Computational Biology (MLCB) (2014); International Conference on Intelligent Computing (ICIC) (2018); RECOMB (2018, 2019, 2020, 2021, 2022); ISMB (2020, joint with ECCB in 2019 & 2021); ACM-BCB (2019)

- Journals
  - Nature Machine Intelligence; Bioinformatics; PLOS Computational Biology; IEEE/ACM Transactions on Computational Biology and Bioinformatics; Briefings in Bioinformatics; Genomics, Proteomics & Bioinformatics; Scientific Reports; IEEE Journal of Biomedical and Health Informatics; IEEE Transactions on Network Science and Engineering; Journal of Bioinformatics and Computational Biology; Quantitative Biology

- Grants
  - Motor Neurone Disease Association

AWARDS & HONORS

- Outstanding Graduate, IIIS   2017
- Travel Fellowship Award, ISMB/ECCB 2017   2017
- Travel Fellowship Award, RECOMB 2017   2017
- Tsinghua - Baidu Rising Star Scholarship, THU   2015
- Outstanding Master's Thesis Award, THU   2013
- Outstanding Student Scholarship, NJUST   2007, 2008, 2009
- Admitted to the Special Pilot Class, NJUST   2007

REFERENCES

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