Han Sun, PhD

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EXPERIENCE

Research Scientist/Senior Computational Biologist **2020 –**

Department of Pediatrics, School of Medicine, Stanford University, **Prof. Anna Gloyn**

Postdoc **2015 – 2019**

Department of Genetics, School of Medicine, Stanford University, **Prof. Lars Steinmetz**

EDUCATION

PhD, Bioinformatics **2009 – 2014**

University of Chinese Academy of Sciences, **Prof. Yixue Li** and **Prof. Lu Xie**

Bachelor, Software Engineering **2004 – 2008**

East China Normal University

SKILLS

- Python, R, C/C++, FastHTML, high performance computing, and cloud computing
- **Multiomics for identifying causal genes/variants and understanding disease mechanisms**: Genomics (WGS, WES, Array), Transcriptomics (RNA-Seq, scRNA-Seq), Proteomics (MS/MS), Epigenomics (ATAC-Seq, ChIP-Seq, WGBS), Linkage analysis, QTL mapping, and GWAS
- **Artificial intelligence for target identification and drug discovery**: Machine Learning (scikit-learn, cross validation, overfitting, linear model, generalized linear model, Support Vector Machine, Random Forrest…) and Deep Learning (PyTorch/Tensorflow, pre-train and fine-tuning, transfer learning, CNN, RNN, ResNet, Transformer, GPT, Agentic AI…)
- Bioinformatics (blast, bwa, STAR, GATK, seurat, scanpy, docker/singularity, nextflow/snakemake workflow) and Biostatistics (hypothesis testing, confidence interval, power calculation, and Bayesian inference)

PACKAGES AND CERTIFICATIONS

- **Python packages I have developed: gap, spredle, deepSec, hla6, and dustle.**
- Machine Learning Specialization, Andrew Ng, 2022, Stanford University
- Deep Learning Specialization, Andrew Ng, 2022, DeepLearning.AI
- Fundamentals of Deep Learning, 2022, NVDIA

PROJECTS

Mutliomics integration to study disease mechanisms of cancers, cardiomyopathy, and diabetes

- Identified disease-causing somatic/germline mutations, gene fusions, and splicing events (potential drug targets) from whole genome/exome/RNA sequencing data.

- Analyzed bulk and single cell RNA-Seq/ATAC-Seq, ChIP-Seq/Cut-And-Run, and MS/MS data in dozens of projects to characterize disease-associated genes and pathways.

- Led collaborations with wet-lab colleagues to validate findings using CRISPR/Cas9 editing, iPS and mouse models, RT-PCR, Sanger sequencing, qPCR, and phenotyping assays.

Developed deep learning models to predict functional elements from DNA sequences

- Reproduced the SpliceAI model (CNN with RestNet) in PyTorch, replicating the original TensorFlow implementation.

- Evaluated the performance of Transformer (GPT) and Hyena architectures by substituting the SpliceAI component to predict splice sites and usage (spredle).

- Applied deep learning models to predict Selenocysteine (the 21st amino acid) incorporation sites (deepSec).

Implemented machine learning models to predict genetic ancestry and HLA types from genotyping/WGS data

- Developed a random forest model — chosen based on cross-validation metrics across multiple models — to accurately infer genetic ancestry from genotyping data (gap).

- Benchmarked the performance of various algorithms, including Hidden Markov Model-based SNP2HLA, machine learning-based HIBAG, CNN-based DEEP*HLA, and Transformer-based HLARIMNT, against HLA typing results (hla6).

PATENTS

- Methods of Treatment, Genetic Screening, and Disease Models for Heart Conditions Associated with RBM20 Deficiency. Francesca Briganti, Lars M. Steinmetz, **Han Sun**, and Wu Wei. WO 2020/092171.

PUBLICATIONS

1. **Han Sun**, Huiying Yan, Kathryn Bieging-Rolett, Michelle Nguyen, William F. Mueller, Zhuanfen Cheng, Hong Zeng, Laura Attardi, Wu Wei, and Lars M. Steinmetz et al. “CDKN1A-RAB44 transcript fusion and oncogene activation in cancers.”, bioRxiv, **co-first author**.

2. Francesca Briganti, **Han Sun**, Wu Wei, Jingyan Wu, Chenchen Zhu, Martin Liss, Ioannis Karakikes et al. “iPSC Modeling of RBM20-Deficient DCM Identifies Upregulation of RBM20 as a Therapeutic Strategy.” Cell Reports 32, no. 10 (2020): 108117, **co-first author**.

3. **Han Sun**, Seth A Sharp, Nicole A J Krentz, Anna Gloyn et al., “Deep learning prediction of selenocystine element and its application in diabetes”, in preparation, **co-first author**.

4. Russ-Silsby, James, Yunkyeong Lee, Varsha Rajesh, **Han Sun**, Mahsa Amoli, Nasser Ali Mirhosseini, Tushar Godbole, Matthew B. Johnson et al. “Complete Loss of PAX4 causes Transient Neonatal Diabetes in Humans.” Molecular Metabolism (2025): 102201.

5. de Winter, Twan JJ, Miha Sovrovic, Esmee Dekker, Natascha de Graaf, **Han Sun**, James D. Johnson, Anna L. Gloyn, Francoise Carlotti, Eelco JP de Koning, and Anna Alemany. “Cell type-specific eQTL detection from single-cell RNA-seq reveals post-transcriptional regulatory mechanisms in human islets.” bioRxiv (2025): 2025-01.

6. Evans-Molina, Carmella, Yasminye D. Pettway, Diane C. Saunders, Seth A. Sharp, Thomas SR Bate, **Han Sun**, Heather Durai et al. “Heterogeneous endocrine cell composition defines human islet functional phenotypes.” bioRxiv (2024): 2024-11.

7. Kolic, Jelena, WenQing Grace Sun, Haoning Howard Cen, Jessica D. Ewald, Jason C. Rogalski, Shugo Sasaki, **Han Sun**, et al. “Proteomic predictors of individualized nutrient-specific insulin secretion in health and disease.” Cell

Metabolism 36, no. 7 (2024): 1619-1633.

8. Ewald, Jessica D., Yao Lu, Cara E. Ellis, Jessica Worton, Jelena Kolic, **Han Sun**, Shugo Sasaki, Dahai Zhang et al. "HumanIslets. com: Improving accessibility, integration, and usability of human research islet data." Cell Metabolism (2024).

9. Rottner, Antje K., Yingying Ye, Elena Navarro-Guerrero, Varsha Rajesh, Alina Pollner, **Han Sun**, Romina J. Bevacqua, Jing Yang et al. "A genome-wide CRISPR screen identifies CALCOCO2 as a regulator of beta cell function influencing type 2 diabetes risk." Nature Genetics 55, no. 1 (2023): 54-65.

10. Lau, Hwee Hui, Nicole AJ Krentz, Fernando Abaitua, Marta Perez-Alcantara, **Han Sun**, Jun-Wei Chan, Jila Ajeian, Soumita Ghosh et al. "PAX4 loss of function increases diabetes risk by altering human pancreatic endocrine cell development." Nature Communications 14, no. 1 (2023): 6119.

11. Mattis, Katia K., Nicole AJ Krentz, Christoph Metzendorf, Fernando Abaitua, Aliya F. Spigelman, **Han Sun**, Jennifer M. Ikle et al. "Loss of RREB1 in pancreatic beta cells reduces cellular insulin content and affects endocrine cell gene expression." Diabetologia 66, no. 4 (2023): 674-694.

12. Cortez, Briana N., Hui Pan, Samuel Hinthorn, **Han Sun**, Nicola Neretti, Anna L. Gloyn, and Cristina Aguayo-Mazzucato. "Heterogeneity of increased biological age in type 2 diabetes correlates with differential tissue DNA methylation, biological variables, and pharmacological treatments." GeroScience (2023): 1-21.

13. Torres, Jason M., **Han Sun**, Vibe Nylander, Damien J. Downes, Martijn van de Bunt, Mark I. McCarthy, Jim R. Hughes, and Anna L. Gloyn. "Inferring causal genes at type 2 diabetes GWAS loci through chromosome interactions in islet cells." Wellcome Open Research 8 (2023).

14. Alghamdi, Tamadher A., Nicole AJ Krentz, Nancy Smith, Aliya F. Spigelman, Varsha Rajesh, Alokkumar Jha, **Han Sun**, Mourad Ferdaoussi et al. "Zmiz1 is required for mature β-cell function and mass expansion upon high fat feeding." Molecular Metabolism 66 (2022): 101621.

15. Chenchen Zhu, Jingyan Wu, **Han Sun**, Francesca Briganti, Benjamin Meder, Wu Wei, and Lars M. Steinmetz. "Single-molecule, full-length transcript isoform sequencing reveals disease-associated RNA isoforms in cardiomyocytes." Nature Communications 12, no. 1 (2021): 1-9.

16. Benedikt Rauscher, William F Mueller, Sandra Clauder-Münster, Petra Jakob, M Saiful Islam, **Han Sun**, Sonja Ghidelli-Disse, Markus Boesche, Marcus Bantscheff, Hannah Pflaumer, Paul Collier, Bettina Haase, Songjie Chen, Rene Hoffman, Guangwen Wang, Vladimir Benes, Gerard Drewes, Michael Snyder, Lars M Steinmetz. "Patient-derived gene and protein expression signatures of NGLY1 deficiency", Journal of Biochemistry, 2021

17. Semih Calamak, Menekse Ermis, **Han Sun**, Saiful Islam, Michael Sikora, Michelle Nguyen, Vasif Hasirci, Lars M. Steinmetz, and Utkan Demirci. "A Circulating Bioreactor Reprograms Cancer Cells Toward a More Mesenchymal Niche." Advanced Biosystems 4, no. 2 (2020): 1900139, **co-first author**.

18. Jay W Schneider, Saji Oommen, Muhammad Y Qureshi, Sean C Goetsch, Rhianna S Sundsbak, Wei Guo, Mingming Sun, **Han Sun**, Dennis A Webster, Alex W Coutts, Francesca Briganti, Wu Wei, Lars Steinmetz, Daniel F Carlson, and Timothy J. Nelson et al. "Dysregulated ribonucleoprotein granules promote cardiomyopathy in RBM20 gene-edited pigs", Nature Medicine (2020): 1-13.

19. William F. Mueller, Petra Jakob, **Han Sun**, Sandra Clauder-Münster, Sonja Ghidelli-Disse, Diana Ordonez, Markus Boesche, Marcus Bantscheff, Paul Collier, Bettina Haase, Vladimir Benes, Malte Paulsen, Peter Sehr, Joe Lewis, Gerard Drewes, Lars M. Steinmetz. "Loss of N-glycanase 1 Alters Transcriptional and Translational Regulation in K562 Cell Lines." G3: Genes, Genomes, Genetics (2020).

20. Arne H. Smits, Frederik Ziebell, Gerard Joberty Nico Zinn, William F. Mueller, Sandra Clauder-Munster, Paola Grandi, Petra Jakob, Anne-Marie Michon, **Hanice Sun**, Karen Tessmer, Tilmann Burckstummer, Marcus Bantscheff, Lars M. Steinmetz, Gerard Drewes, and Wolfgang Huber. "Biological plasticity rescues target activity in CRISPR knock outs.", Nature Methods 2019 Oct 28:1-7.

21. Suo, Lun, Yu Xiao Zhou, Li Ling Jia, Hai Bo Wu, Jin Zheng, Qi Feng Lyu, Li Hua Sun, **Han Sun**, and Yan Ping Kuang. "Transcriptome profiling of human oocytes experiencing recurrent total fertilization failure." Scientific Reports 8, no. 1 (2018): 17890.

22. **Han Sun**, Chen Chen, Baofeng Lian, Menghuan Zhang, Xiaojing Wang, Bing Zhang, Yixue Li, Pengyuan Yang, and Lu Xie. 2015. "Identification of HPV Integration and Gene Mutation in HeLa Cell Line by Integrated Analysis of RNA-Seq and MS/MS Data." Journal of Proteome Research 14 (4): 1678–86, **co-first author**.

23. **Han Sun**, Chen Chen, Meng Shi, Dandan Wang, Mingwei Liu, Daixi Li, Pengyuan Yang, Yixue Li, and Lu Xie. 2014. "Integration of Mass Spectrometry and RNA-Seq Data to Confirm Human Ab Initio Predicted Genes and lncRNAs." Proteomics 14 (23-24): 2760–68, **co-first author**.

24. **Han Sun**, Xiaobin Xing, Jing Li, Fengli Zhou, Yunqin Chen, Ying He, Wei Li, et al. 2013. "Identification of Gene Fusions from Human Lung Cancer Mass Spectrometry Data." BMC Genomics 14 Suppl 8 (December): S5, **co-first author**.

25. Zhen-Hao Liu, Bao-Feng Lian, Qiong-Zhu Dong, **Han Sun**, Jin-Wang Wei, Yuan-Yuan Sheng, Wei Li, et al. 2018. "Whole-Exome Mutational and Transcriptional Landscapes of Combined Hepatocellular Cholangiocarcinoma and Intrahepatic Cholangiocarcinoma Reveal Molecular Diversity." Biochimica et Biophysica Acta 1864 (6 Pt B): 2360–68.

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27. Wei Li, Jian Yu, Baofeng Lian, **Han Sun**, Jing Li, Menghuan Zhang, Ling Li, Yixue Li, Qian Liu, and Lu Xie. 2015. "Identifying Prognostic Features by Bottom-up Approach and Correlating to Drug Repositioning." PloS One 10 (3): e0118672.

28. Jing Li, Jia Jia, Hong Li, Jian Yu, **Han Sun**, Ying He, Daqing Lv, et al. 2014. "SysPTM 2.0: An Updated Systematic Resource for Post-Translational Modification." Database: The Journal of Biological Databases and Curation 2014 (April): bau025.

29. Yulin Dai, Shengdi Li, Xiao Dong, **Han Sun**, Chao Li, Zhi Liu, Beili Ying, Guohui Ding, and Yixue Li. 2013. "The de Novo Sequence Origin of Two Long Non-Coding Genes from an Inter-Genic Region." BMC Genomics 14 (Suppl 8): S6.

30. Li Xia, Tong-Dan Wang, Shao-Ming Shen, Meng Zhao, **Han Sun**, Ying He, Lu Xie, et al. 2013. "Phosphoproteomics Study on the Activated PKCδ-Induced Cell Death." Journal of Proteome Research 12 (10): 4280–4301.

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33. Xiao Chang, Yun Li, Jie Ping, Xiao-Bin Xing, **Han Sun**, Peng Jia, Chuan Wang, Yuan-Yuan Li, and Yi-Xue Li. 2011. "EcoBrowser: A Web-Based Tool for Visualizing Transcriptome Data of Escherichia Coli." BMC Research Notes 4 (October): 405.

34. Xiao-Bin Xing, Qing-Run Li, **Han Sun**, Xing Fu, Fei Zhan, Xiu Huang, Jing Li, et al. 2011. "The Discovery of Novel Protein-Coding Features in Mouse Genome Based on Mass Spectrometry Data." Genomics 98 (5): 343–51.