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工作经历

高级 计算生物学者 **2020 –**
儿科系, 医学院, 斯坦福大学, **Anna Gloyn 教授**

博士后 **2015 – 2019**
遗传系, 医学院, 斯坦福大学, **Lars Steinmetz 教授**

学习经历

博士, 生物信息学 **2009 – 2014**
系统生物学重点实验室, 中科院上海生命科学院, 导师: 李亦学研究员 谢鹭研究员

学士, 软件工程 **2004 – 2008**
华东师范大学

科研专长

- Python, R, C/C++, FastAPI/FastHTML, high performance computing (HPC), 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, scanpy, seurat, docker/singularity, snakemake/nextflow) and Biostatistics (hypothesis testing, confidence interval, power calculation, and Bayesian inference)

开发过的软件和认证

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

项目经验

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, WGBS, 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.

Artificial intelligence to predict genetic ancestry, HLA types, and functional elements from DNA sequences

- Developed machine learning models to accurately predict genetic ancestry from genotyping data (gap).

- Reproduced the SpliceAI model and extended it with Transformer and Hyena architectures for both splice site and usage prediction (spredle).

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

- Implemented hierarchical, mixture-of-experts (MoE), and multi-task deep learning models for HLA imputation (hlarchical).

专利

- 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.

主要论文

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.

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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.

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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**.

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