Austin T. Wang

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ABOUT	Computer Science Ph.D. student with a strong interdisciplinary background in AI, machine learning, and quantitative biology. Extensive experience with large-scale data curation, training, evaluation, interpretation, and application of complex models. Currently working on deep learning for genomics; broadly interested in applying machine learning to real-world problems.		
EDUCATION	Ph.D. in Computer Science (Anticipated)2020 - 202Stanford UniversityGPA: 4.0/4.0		
	M.Eng. in Computer Science & Molecular Biology2019 - 202B.S. in Computer Science & Molecular Biology2015 - 201Massachusetts Institute of TechnologyGPA: 4.8/5.0		
EXPERIENCE	Ph.D. Student Researcher Aug 2021 - Curren Anshul Kundaje, Stanford University		
	• Formulated rigorous zero-shot and supervised benchmarks for DNA language models (DNALMs) emphasizing non-coding regulatory logic. Fine-tuned and evaluated multiple large DNA language model architectures. Identified def ciencies in performance and computational efficiency over alternative baseline models. Proposed improvements in modeling, data curation, and evaluation strategies for future DNALMs.		
	• Developed FiNeMo, a robust, high-performance method for identifying sequence motifs in neural network contribution scores. Formulated and implemented custom GPU-accelerated proximal gradient descent optimizer with hard convergence guarantees.		
	• Leveraged sequence-based deep learning models for chromatin accessibility to uncover unique cardiac developmental patterns across species. Developed novel model-based <i>in silico</i> genome transfer technique for comparing cross species regulatory syntax that overcomes large-scale genomic rearrangements		
	• Lead efforts for large-scale processing and analysis of over 300 single-cell RNA seq and ATAC-seq datasets into integrated atlases under the ENCODE consortium. Managed a team of over 10 analysts to produce high-quality, star dardized cell-type annotations and cell embeddings. Developed and deployed high-throughput analysis pipeline via Kubernetes.		
	• Identified genetic features and cell states relevant to cardiac disease progressic using deep learning models on multimodal single-cell data across patients of varying cardiac disease states.		
	Undergraduate Researcher Jan 2018 - Sept 202 Alexander Gusev, Harvard Medical School Manolis Kellis, MIT		
	• Created a novel statistical method (PLASMA) to identify causal regulator		

- genetic markers (QTL fine-mapping) with an order-of-magnitude improvement in power over previously existing techniques.
- Formulated allele-specific methods for fine-mapping single-cell QTLs and cell-type-specific colocalization with disease, with applications to Alzheimer's disease.

PAPERS * indicates equal contribution Liu BB*, Jessa S*, Kim SH*, Ng YT*, Higashino S, Marinov GK, Chen DC, Parks BE, Li L, Nguyen TC, Wang SK, Wang AT, Tan SY, Kosicki M, Pennacchio LA, Ben-David E, Pasca AM, Kundaje A, Farh KKH, Greenleaf WJ. "Dissecting regulatory syntax in human development with scalable multiomics and deep learning." bioRxiv. April 2025. Marderstein AR*, Kundu S*, Padhi EM*, Deshpande S, Wang AT, Robb E, Sun Y, Yun CM, Pomales-Matos D, Xie Y, Nachun D, Jessa S, Kundaje A, Montgomery SB. "Mapping the regulatory effects of common and rare non-coding variants across cellular and developmental contexts in the brain and heart." *bioRxiv*. February 2025. Wang AT*, Patel A*, Singhal A*, Pampari A, Kasowski M, Kundaje AB. "DART-Eval: A Comprehensive DNA Language Model Evaluation Benchmark on Regulatory DNA." Advances in Neural Information Processing Systems (NeurIPS). December 2024. Wang AT, Shetty AH, O'Connor E, Bell C, Pomerantz MM, Freedman ML, Gusev A. "Allele-Specific QTL Fine-Mapping with PLASMA." American Journal of Human Genetics. February 2020. https://doi.org/10.1016/j.ajhg.2019.12.011 TALKS Wang AT*, Patel A*, Singhal A*, Pampari A, Kasowski M, Kundaje AB. "DART-Eval: A Comprehensive DNA Language Model Evaluation Benchmark on Regulatory DNA." MLCB 2024. Seattle, WA, September 5-6, 2024. Wang AT, Fan I, Red-Horse K, Kundaje AB. "Characterizing species-specific regulation of cardiac development with deep learning models." CSHL Biology of Genomes 2024. Cold Spring Harbor, NY, May 7-11, 2024. Wang AT, Park YP, [et al., including Kellis M, Gusev A]. "Single-cell eQTLs across 343 samples reveal neuronal and glial genetic drivers of psychiatric and neurodegenerative disorders." ASHG 2020 Annual Meeting. Online, October 27-30, 2020. Wang AT, Shetty AH, [et al., including Gusev A]. "Allele-Specific QTL Fine-Mapping with PLASMA." RECOMB/ISCB Conference on Regulatory & Systems Genomics. New York, NY, November 4-6, 2019. Wang AT, Shetty AH, [et al., including Gusev A]. "Allele-Specific QTL Fine-Mapping with PLASMA." IGES 2019 Annual Meeting. Houston, TX, October 12-14, 2019.Orenstein Y, Wang AT [presenter], Berger B. "Computational Modeling of Protein-RNA Interactions." ACM Conference on Bioinformatics, Computational Biology, and Health Informatics. Boston, MA, August 20-23, 2017. Wang AT, Shetty AH, [et al., including Gusev A]. "Allele-Specific QTL Fine-POSTERS Mapping with PLASMA." ASHG 2019 Annual Meeting. Houston, TX, October 15-19, 2019. McHugh KJ, Nguyen TD, [et al., including Wang AT, Langer R]. "Injectable microfabricated particles with pulsatile kinetics." Biomedical Engineering Society Annual Meeting. Minneapolis, MN, October 5-8, 2016. McHugh KJ, Nguyen TD, [et al., including Wang AT, Langer R]. "Injectable Microfabricated Particles with Pulsatile Release Kinetics." Controlled Release Society Annual Meeting & Exposition. Seattle, WA, July 17-20, 2016.

	Interdisciplinary research fellowship with 20 admits per year.	
	Stanford School of Engineering Fellowship Institute-awarded funding for Stanford Ph.D. first-year rotation	2020 - 2021 s.
	Harvard Herchel Smith Graduate Fellowship (Declined) Awarded to five students in the entire Harvard University admi	2020 - 2022 tted Ph.D. class.
	Roger Williams Award, IGES 2019 Awarded for best oral presentation by a trainee at the IGES 2 conference. Talk: "Allele-Specific QTL Fine-Mapping with PLA	2019 019 Annual Meeting ASMA."
	Eta Kappa Nu (HKN) Member National IEEE Electrical Engineering and Computer Science ho	2019 onor society.
	USA Biology Olympiad, Bronze Medalist National high school competition for biology.	
SKILLS	Machine Learning: deep learning, generative modeling, mechan convex optimization, linear algebra, fine-tuning	istic interpretability,
	Probability & Statistics: regression models, mixture models models, variational Bayes, Monte Carlo methods	, Bayesian graphical
	Numerical & Machine Learning Software: PyTorch, Tensorf Pandas, Polars	flow, Keras, Numpy,
	Other: Python, Snakemake, Google Cloud, AWS, R	
TEACHING	Course Assistant CS161 Design and Analysis of Algorithms, Stanford University	Jan 2023 - Dec 2024
	Course Assistant CS273B Deep Learning in Genomics and Biomedicine, Stanford	Apr 2023 - Jun 2023 University
	Course Tutor, Eta Kappa Nu Program 6.046 Design and Analysis of Algorithms, MIT	Sep 2018 - May 2019