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 machine learning for biosciences.

EDUCATION

Ph.D. in Computer Science (Anticipated) 2020 - 2025
Stanford University
GPA: 4.0/4.0

M.Eng. in Computer Science & Molecular Biology 2019 - 2020
B.S. in Computer Science & Molecular Biology 2015 - 2019
Massachusetts Institute of Technology
GPA: 4.8/5.0

EXPERIENCE

Ph.D. Student Researcher Aug 2021 - Current
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 deficiencies 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 a 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 a novel model-based *in silico* 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, standardized cell-type annotations and cell embeddings. Developed and deployed a high-throughput analysis pipeline via Kubernetes.
- Identified genetic features and cell states relevant to cardiac disease progression using deep learning models on multimodal single-cell data across patients of varying cardiac disease states.

Undergraduate Researcher Jan 2018 - Sept 2020
Alexander Gusev, Harvard Medical School
Manolis Kellis, MIT

- Created a novel statistical method (PLASMA) to identify causal regulatory 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.

Undergraduate Researcher Jan 2017 - Sept 2018

Bonnie Berger, MIT

- Developed k-mer-based machine-learning methods for modeling RNA-Protein interactions.
- Deployed workflows to train and infer protein-RNA affinity across multiple large-scale databases.

PAPERS

* *indicates equal contribution*

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.

POSTERS

Wang AT, Shetty AH, [et al., including Gusev A]. "Allele-Specific QTL Fine-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.

FELLOWSHIPS & AWARDS

Stanford Bowes Bio-X Fellowship 2023 - 2026
Interdisciplinary research fellowship with 20 admits per year.

Stanford School of Engineering Fellowship 2020 - 2021
Institute-awarded funding for Stanford Ph.D. first-year rotations.

Harvard Herchel Smith Graduate Fellowship (Declined) 2020 - 2022
Awarded to five students in the entire Harvard University admitted Ph.D. class.

Roger Williams Award, IGES 2019 2019
Awarded for best oral presentation by a trainee at the IGES 2019 Annual Meeting conference. Talk: "Allele-Specific QTL Fine-Mapping with PLASMA."

Eta Kappa Nu (HKN) Member 2019
National IEEE Electrical Engineering and Computer Science honor society.

USA Biology Olympiad, Bronze Medalist
National high school competition for biology.

SKILLS

Machine Learning: deep learning, generative modeling, mechanistic interpretability, convex optimization, linear algebra

Probability & Statistics: regression models, mixture models, Bayesian graphical models, variational Bayes, Monte Carlo methods, stochastic calculus

Biology: genomics, single-cell assays, cell biology, transcription factors

Numerical & Machine Learning Software: PyTorch, Tensorflow, Keras, Numpy, Pandas, Polars

Biostatistical Software: R, Seurat, Signac

Other: Python, Snakemake, Kubernetes, Google Cloud

TEACHING

Course Assistant Jan 2023 - Dec 2024
CS161 Design and Analysis of Algorithms, Stanford University

Course Assistant Apr 2023 - Jun 2023
CS273B Deep Learning in Genomics and Biomedicine, Stanford University

Course Tutor, Eta Kappa Nu Program Sep 2018 - May 2019
6.046 Design and Analysis of Algorithms, MIT