Tessa Durakis Green

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Education	
Harvard Medical School	Boston, MA
PhD, Biophysics: Methods and applications of single-cell transcriptomics	March 2024
Massachusetts Institute of Technology	Cambridge, MA
B.S., Physics: Cumulative GPA 4.9/5.0	February 2016
Experience	
KiraGen Bio	Boston, MA
Machine learning scientist, head of immunoinformatics	July 2024 –
present	2
 Sole dry-lab member of small company (<10) working to optimize selection that protect CAR-T cells from the tumor microenvironment and enable efficient that strategy for immunoinformatics, including machine learning microsoftener-based architecture for integration of sequencing and functiona Establishing and managing external partnerships for model development at Collaborating with wet lab team to ensure experimental high-throughput set 	on of large N gene knockouts icacy against solid tumors. nodel development with l data. nd sequencing creens align with AI modeling
needs.	
• Developing and implementing computational pipelines for analysis of CAI microenvironment response, and guide RNA selection	R-T cell function, tumor
Patient-Led Research Collaborative	Remote
Machine learning consultant	October 2023 – January 2024
• Identified patient subgroups based on binary self-reported symptom data, o	comparing across machine
learning methodologies. Manuscript in preparation.	
Marks and Sander Labs, Department of Systems Biology	Harvard Medical
School	
PhD Researcher	October 2017 – October 2023
 Methods for perturbation analysis Developed and studied statistical tools for perturbation quantification in sin 	ngle cell -omics and evaluation
metrics for machine learning in the single cell transcriptomics space.	
 Created database of single-cell perturbation datasets with harmonized anno machine learning. 	otations to serve as a resource for
• Contributed to ongoing collaborative package for single cell perturbation a	nalysis.
Cell-cell communication in triple-negative breast cancer	-
• Applied matrix decomposition methods to study cell-cell interactions in sin negative breast cancer, predicting interactions underlying treatment resista	ngle cell transcriptomics of triple nce.
• Managed regular grant reports for external funding, including written quar the grant organization and to other members of international collaborative	terly reports and presentations to Wellcome-LEAP grant.
Transcriptomics for asthma-exacerbated respiratory disease	8
 Developed machine learning methods for joint latent space discovery using single cell protein measurements. 	g single cell RNA counts and
 Performed bioinformatic analysis of single-cell RNA-sequencing data of a pseudotemporal analysis. 	ctivating B cells, including
• Led time-course gene expression study to discover drug response markers	in asthma.
Additional responsibilities	
• Ran lab journal club in 2020–2021; oversaw transition to a fully remote in	vited speaker series

• Summer 2023: Managed two postdocs initiating study of spatial immuno-histochemistry of breast cancer

- Writing lead for the scPerturb paper; project manager for the scPerturb contribution to pertpy (open source software package for single cell perturbation analysis)
- Managed ongoing international collaboration between multiple data generation and data analysis teams
- Conceived of and directed high school research student on the project "Using Single-Cell RNA Sequencing Data to Study Plastid Differentiation Dynamics with Nucleus-Encoded Plastid Gene Expression in Arabidopsis thaliana." Student placed in the top 5 papers and top 10 presentations at the 2018 MIT CEE Research Science Institute.

Harvard Graduate Student Union

Finance and Benefits Committee (Co-lead 2022)

• Wrote policy for and managed allocation of \$1.47M in student benefits, streamlined processing, and hired/managing 30+ employees.

MIT

Research Science Institute, Center for Excellence in Education

Cambridge, MA June 2017 – August 2017

June 2020 – March 2023

Cambridge, MA

Academic Tutor

- Taught science communication in a classroom setting to sixteen advanced high school science students.
- Provided guidance to students throughout month-long mentorship placements at biology labs
- Worked one-on-one with students to refine writing and presentation skills and helped them to write a scientific paper and give a ten-minute talk at the conclusion of the program.

Publications and Presentations

Papers

- "scPerturb: Harmonized single-cell perturbation data." S. Peidli*, **T.D. Green*** et al. Nature Methods 2024. Also published and presented at NeurIPS Learning Meaningful Representations of Life Workshop December 2022 under Green et al. *: co-first authors"
- Multi-method phenotyping of Long COVID patients using high-dimensional symptom data." **T.D Green** et al, Research Square 2024.
- "Pertpy: an end-to-end framework for perturbation analysis." L. Heumos, Y. Ji, L. May, **T.D. Green** et al, bioRxiv 2024 (in review at Nature Methods).
- "Optimal distance metrics for single-cell RNA-seq populations." Y. Ji, T.D. Green et al. bioRxiv 2023.
- "Scalable nonparametric Bayesian models that predict and generate genome sequences." A. Amin, E.N. Weinstein, J. Disset, T. Green, D. Marks. NeurIPS Learning Meaningful Representations of Life Workshop, 2020.

Posters

- "Prediction of cell-cell communication directly from scRNA-seq latent spaces", **T.D. Green**, L.J. Schumacher, D.S Marks, C. Sander. NeurIPS Learning Meaningful Representations of Life Workshop, 2021.
- "Joint modeling for discovery of causal molecular mechanisms in disease", **T. Green**, K. Buccheit, T. Laidlaw, and D. Marks. Presented at Janelia Women in Computational Biology conference, Nov. 2019.

Patent

Green, T. D. "Design for Electricity Transportation and Storage System," US Patent number 8,723,371, May 2014. A modification of flow battery design that would enable simultaneous storage and transport of energy

Honors and Awards

• Lynch Fellowship (2018, Harvard Medical School) • Phi Beta Kappa (2016, MIT) • Sigma Pi Sigma Physics Honors Society (2016, MIT) • Thiel Fellowship (2011, declined to pursue traditional education)

Skills

Programming Languages: Python, R, bash

Computational Skills: Machine Learning (Pytorch, scikit-learn, pyro), data science in R and Python (pandas), Unix/Linux based systems for cluster computing, single cell analysis in R (Seurat) and Python (scanpy)