

Education

Harvard Medical School PhD, Biophysics: Methods and applications of single-cell transcriptomics	Boston, MA October 2023
Massachusetts Institute of Technology B.S., Physics: Cumulative GPA 4.9/5.0	Cambridge, MA February 2016

Research Experience

Marks and Sander Labs, Department of Systems Biology <i>Methods for perturbation analysis</i> <ul style="list-style-type: none">Developed and studied statistical tools for perturbation quantification in single cell -omics and evaluation metrics for machine learning in the single cell transcriptomics space.Created database of single-cell perturbation datasets with harmonized annotations to serve as a resource for machine learning.Contributed to ongoing collaborative package for single cell perturbation analysis. <i>Cell-cell communication in triple-negative breast cancer</i> <ul style="list-style-type: none">Applied matrix decomposition methods to study cell-cell interactions in single cell transcriptomics of triple negative breast cancer, predicting interactions underlying treatment resistance.Managed regular grant reports for external funding, including written quarterly reports and presentations to the grant organization and to other members of international collaborative Wellcome-LEAP grant. <i>Transcriptomics for asthma-exacerbated respiratory disease</i> <ul style="list-style-type: none">Developed machine learning methods for joint latent space discovery using single cell RNA counts and single cell protein measurements.Performed bioinformatic analysis of single-cell RNA-sequencing data of activating B cells, including pseudotemporal analysis.Led time-course gene expression study to discover drug response markers in asthma. <i>Additional responsibilities</i> <ul style="list-style-type: none">Ran lab journal club in 2020–2021; oversaw transition to a fully remote invited speaker seriesSummer 2023: Managed two postdocs initiating study of spatial immuno-histochemistry of breast cancerWriting 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	October 2017 – October 2023
Patient-Led Research Collaborative <i>Machine learning consultant</i> <ul style="list-style-type: none">Identified patient subgroups based on binary self-reported symptom data, comparing across machine learning methodologies. Manuscript in preparation.	Remote October 2023 – January 2024

Teaching Experience

Harvard Medical School Research Mentor <i>Direct supervisor</i> <ul style="list-style-type: none">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 <i>Arabidopsis thaliana</i>.”	Boston, MA June 2018–August 2018
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- Student placed in the top 5 papers and top 10 presentations at the 2018 MIT CEE Research Science Institute.

MIT

Cambridge, MA

Research Science Institute, Center for Excellence in Education

June 2017 – August 2017

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.

Leadership Experience

Harvard

Cambridge, MA

Graduate Student Union Finance and Benefits Committee

June 2020 – March 2023

- Wrote policies to equitably allocate over \$400k in benefits to Harvard students; served as lead for healthcare benefits throughout 2020–2023.
- Co-chaired the Finance and Benefits committee for 2022, in which we streamlined benefits processing, hired and managed more than 30 temporary employees, interfaced with Harvard's Office of Employee-Labor Relationships, and allocated \$1.47M to 1000+ student workers.

Publications and Presentations

Papers

- "Optimal distance metrics for single-cell RNA-seq populations." Y. Ji, **T.D. Green**, S. Peidli, M. Bahrami, M. Liu, L. Zappia, K. Hrovatin, C. Sander, F. Theis. bioRxiv. <https://doi.org/10.1101/2023.12.26.572833>
- "scPerturb: Harmonized single-cell perturbation data." S. Peidli*, **T.D. Green***, C. Shen, T. Gross, J. Min, S. Garda, B. Yuan, L. J. Schumacher, J. P. Taylor-King, D. S. Marks, A. Luna, N. Blüthgen, C. Sander. bioRxiv. <https://doi.org/10.1101/2022.08.20.504663>. Accepted by Nature Methods August 2023; revised version available by request. Also published and presented at NeurIPS Learning Meaningful Representations of Life Workshop December 2022 under Green et al. *: co-first authors
- "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

- 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

Proficient knowledge in: 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)