Tessa Durakis Green

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Education

Harvard Medical School   Boston, MA

PhD, Biophysics: Methods and applications of single-cell transcriptomics   October 2023

Massachusetts Institute of Technology   Cambridge, MA

B.S., Physics: Cumulative GPA 4.9/5.0   February 2016

Research Experience

Marks and Sander Labs, Department of Systems Biology   October 2017 – October 2023

Methods for perturbation analysis

- 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.

Cell-cell communication in triple-negative breast cancer

- 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.

Transcriptomics for asthma-exacerbated respiratory disease

- 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.

Additional responsibilities

- Ran lab journal club in 2020–2021; oversaw transition to a fully remote invited 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

Patient-Led Research Collaborative   Remote

Machine learning consultant   October 2023 – January 2024

- Identified patient subgroups based on binary self-reported symptom data, comparing across machine learning methodologies. Manuscript in preparation.

Teaching Experience

Harvard Medical School   Boston, MA

Research Mentor   June 2018–August 2018

Direct supervisor

- 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.

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
- "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. Nature Methods 2024. Also published and presented at NeurIPS Learning Meaningful Representations of Life Workshop December 2022 under Green et al. *: co-first authors
- "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 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
- 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)