

Louis V. Cammarata

12 Chatham Street • Cambridge, MA 02139 • 857-707-8309 • louis_cammarata@g.harvard.edu • [Personal website](#)

EDUCATION

Harvard University

PhD, Statistics, GPA: 3.95/4.00

Dissertation: “Connecting the Dots: Network Testing, Community Estimation, and Genomic Applications”
Advised by Professor Tracy Ke (Harvard Statistics) and Professor Caroline Uhler (MIT EECS)

Cambridge, MA
Expected May 2024

Massachusetts Institute of Technology, Institute for Data, Systems, and Society

MSc, Technology and Policy, GPA: 5.00/5.00, 2018 Best Thesis Award

Cambridge, MA
May 2018

École Polytechnique

MSc, Biological Engineering, GPA: 3.92/4.00

BSc, Mathematics and Sciences, GPA: 3.91/4.00

Palaiseau, FRANCE
May 2016
May 2015

FELLOWSHIPS & AWARDS

Bok Center Statistics Pedagogy Fellowship , Harvard University	2021
Bok Center Certificate of Distinction in Teaching Award , Harvard University	2019, 2020, 2021
Keystone Symposia Travel Fellowship , Keystone Symposia	2019
Technology & Policy Program Best Thesis Award , Massachusetts Institute of Technology	2018
Outstanding Investment Award , École Polytechnique	2015

PUBLICATIONS & PREPRINTS

Statistical Theory & Methods

Cammarata, L.V., Jin, J. and Ke, Z.T., 2024. Dynamic network analysis under smooth community evolution and potentially erratic degree changes. Manuscript in preparation.

- Develop minimax optimal dynamic mixed-membership estimation and embedding algorithm using spectral methods in the degree-corrected mixed membership stochastic block model
- Apply algorithm to international trade networks and dynamic human contact networks

Cammarata, L.V. and Ke, Z.T., 2023. Power enhancement and phase transitions for global testing of the mixed membership stochastic block model. *Bernoulli*, 29(3), pp.1741-1763.

- Derived fundamental statistical limit of global detection of network communities (i.e., testing whether network has more than one community) and designed a novel statistically optimal hypothesis test

Applied Machine Learning & Computational Biology

Cammarata, L.V., Shivashankar, G.V. and Uhler, C., 2024. Adhesome Receptor Clustering is Accompanied by the Colocalization of the Associated Genes in the Cell Nucleus. *bioRxiv*, pp.2023-12.

- Characterize map between protein assemblies on cell membrane and 3D organization of genome in nucleus, specifically for adhesome in IMR90 fibroblasts using multiple genomic/epigenomic data modalities (RNA-seq, ChIP-seq, Hi-C, FISH)

Braunger*, J.M., **Cammarata***, L.V., Sornapudi, T.R., Uhler, C. and Shivashankar, G.V., 2024. Transcriptional changes are tightly coupled to chromatin reorganization during cellular aging. *Aging Cell*, 23(3), p.e14056.

- Developed novel time-course prize-collecting Steiner tree algorithm to identify age-associated transcription factors and investigated coupling between gene transcription and spatial gene clustering in aging (using RNA-seq, ChIP-seq, Hi-C)
- Media coverage by the [Eric and Wendy Schmidt Center](#)
- Co-first authors marked with *

Zhang, J., **Cammarata, L.V.**, Squires, C., Sapsis, T.P. and Uhler, C., 2023. Active learning for optimal intervention design in causal models. *Nature Machine Intelligence*, 5(10), pp.1066-1075.

- Developed a consistent causal active learning strategy to identify optimal interventions in linear causal models with known causal graph for the discrepancy between the post-interventional mean of the distribution and a desired target mean

Belyaeva*, A., **Cammarata***, L., Radhakrishnan*, A., Squires, C., Yang, K.D., Shivashankar, G.V. and Uhler, C., 2021. Causal network models of SARS-CoV-2 expression and aging to identify candidates for drug repurposing. *Nature Communications*.

- Developed drug repurposing pipeline using overparametrized representation learning, network analysis and causal structure learning and applied it to identify *in silico* candidate drug targets for treatment of COVID-19
- Media coverage in [MIT News Office](#) and other specialized online media
- Co-first authors marked with *

Delaney*, C., Schnell*, A., **Cammarata***, L., Yao-Smith, A., Regev, A., Kuchroo, V.K. and Singer, M., 2019. COMET: a tool for marker-panel selection from single-cell transcriptomic data. *Molecular Systems Biology*.

- Developed COMET, a computational tool for combinatorial marker detection from single-cell transcriptomic data available as a [Python package](#) and leveraged tool to identify B cell subpopulations
- Co-first authors marked with *

Other Applied Statistics

Payzin-Dogru*, D., Wilson*, S.E., Blair, S.J., Erdogan, B., Hossain, S., **Cammarata, L.**, Matos, J.C.V., Wong, A.Y., Losner, J., Min, S., Singer, H. and Whited, J.L. (2021). Nerve-mediated amputation-induced stem cell activation primes distant appendages for future regeneration events in axolotl. *bioRxiv preprint*.

- Performed power analysis to guide experimental design and conducted statistical analysis of final experimental data

RELATED PROFESSIONAL EXPERIENCE

PathAI

Biomedical Data Science PhD Intern

Boston, MA

Jun – Aug 2022

- Built Deep Learning model in Python in team of 3 computational biologists and 1 expert pathologist to find predictive biomarkers of patients' treatment response from 1K+ histopathology images

Google

Data Science PhD Intern (gTrade)

Virtual/Mountain View, CA

May–Aug 2020

- Developed random effects model to predict competition price on Google Ads Exchange with Gibbs sampling on big data sets
- Implemented model and sent it for experiments on small percentage of display adds traffic to assess conversion performance

Goldman Sachs

Summer Quantitative Analyst (Franchise Analytics team)

New York City, NY

Jun–Aug 2017

- Designed statistical similarity model to score US corporate bonds and support relative value trading operations

TEACHING EXPERIENCE

Harvard University

Statistics Teaching Fellow

Cambridge, MA

Sep 2019 – Present

- Teach STAT303 – The Art and Practice of Teaching and Communicating Statistics (with Prof. Joe Blitzstein and Prof. Morgane Austern) to first-year Statistics PhD students in Fall 2021 and Spring 2022
- Taught STAT210 – Probability I (Fall 2019, Fall 2020 with Prof. Joe Blitzstein), STAT212 – Probability II (Spring 2020 with Prof. Subhabrata Sen) and STAT131 – Time Series (Spring 2020 with Prof. Tracy Ke) to classes of ~30-80 students

The Jubilee Institute | MIT Science and Technology Initiative Global Teaching Lab

Amman, JORDAN

High School Mathematics Teacher

Jan 2017

- Designed and taught 5-session introductory "Randomness & Probability" course to 6 cohorts of 25 students (10th grade)

ON-CAMPUS LEADERSHIP

MIT Volunteer Consulting Group | Massachusetts Institute of Technology

Cambridge, MA

Summer 2023 Project Leader

Feb – Jun 2023

- Framed customer relationship strategy case with nonprofit client; led team of 6 consultants during 6-week engagement

Winter 2023 Consultant

Jan – Feb 2023

- Collaborated in team of 6 consultants to shape market expansion strategy for a series A biotech company valued at \$100M via market research and interviews with 20+ key opinion leaders; delivered final recommendation to CEO

Harvard GSAS Consulting Club | Harvard University
Vice President of 2022 Harvard/MIT Case Competition

- Organized 12-day flagship event involving 100+ participants in cooperation with consulting firms and industry experts

Cambridge, MA
Sep 2021 – May 2022

Harvard Statistics Graduate Committee | Harvard University
Vice President

- Coordinate yearly Statistics PhD students retreat for ~70 students, faculty, and affiliates in Harvard's Statistics Department
- Organize bi-weekly Statistics Social Hours for Harvard Statistics community members
- Supervise mentoring of ~10 first-year Statistics PhD students by senior graduate students

Cambridge, MA
Sep 2019 – May 2022

PolitiX (student non-partisan policy club) | École Polytechnique
President

- Organized monthly conferences with politicians, CEOs, and academics for 500+ students – “Outstanding Investment Award”

Palaiseau, FRANCE
Jan 2015–Mar 2016

SELECTED CONFERENCE PRESENTATIONS

Cammarata, L. Transcriptional changes are tightly coupled to chromatin reorganization during cellular aging. Oral presentation delivered at the EMBO Workshop on Nuclear Mechanogenomics, Pula, Italy, April 2024.

Cammarata, L. Adhesome Receptor Clustering is Accompanied by the Colocalization of the Associated Genes in the Cell Nucleus. Poster presented at the EMBO Workshop on Nuclear Mechanogenomics, Pula, Italy, April 2024.

Cammarata, L. Adhesome receptor clustering is accompanied by the co-localization of adhesome genes in the cell nucleus. Oral presentation delivered at the 22nd International Conference on Systems Biology, Hartford, CT, October 2023.

Cammarata, L. Adhesome receptor clustering is accompanied by the co-localization of adhesome genes in the cell nucleus. Oral presentation delivered at the Broad Institute Cell Circuits and Epigenomics Seminar Series, Cambridge, MA, June 2022.

Cammarata, L. Power Enhancement and Phase Transitions for Network Testing. Oral presentation delivered at the Harvard Mini-workshop on Algebraic Statistics, Cambridge, MA, April 2022.

Cammarata, L. Drug Repurposing Pipeline Using Overparametrized Representation Learning and Causality. Oral presentation delivered at Purdue University Data Science Week, West Lafayette, IN (virtual), November 2021.

Cammarata, L. Drug Repurposing Pipeline Using Overparametrized Representation Learning and Causality. Oral presentation delivered at Barcelona Supercomputing Center (BSC), Barcelona, Spain (virtual), September 2021.

Cammarata, L. Phase Transitions in Network Global Testing. Oral presentation delivered at Joint Statistical Meetings (JSM), virtual, August 2021.

Cammarata, L. and Radhakrishnan, A. Drug Repurposing Pipeline Using Overparametrized Representation Learning and Causality. Oral presentation delivered at Max Delbrück Centrum BMSB Systems Biology Lecture series on “Multi-omics technology, computation and biology”, Berlin, Germany (virtual), July 2021.

Cammarata, L. and Radhakrishnan, A. Transport problems in biology: theoretical and applied insights. Oral presentation delivered at the Mila Biology + AI reading group, Montreal, Canada (virtual), June 2021.

Cammarata, L. and Belyaeva, A. Causal Network Models of SARS-CoV-2 Expression and Aging to Identify Candidates for Drug Repurposing. Oral presentation delivered at Machine Learning in Computational Biology (MLCB), virtual, November 2020.

Cammarata, L. COMET: Combinatorial Marker Detection from Single-Cell Transcriptomic Data. Spotlight oral presentation delivered at Machine Learning in Computational Biology (MLCB), Vancouver, Canada, December 2019.

Cammarata, L. COMET: Combinatorial Marker Detection from Single-Cell Transcriptomic Data. Poster presented at NeurIPS, Vancouver, Canada, December 2019.

Cammarata, L. COMET: Combinatorial Marker Detection from Single-Cell Transcriptomic Data. Poster presented at Next-Generation Genomics Conference, New York City, NY, August 2019.

Cammarata, L. COMET: Combinatorial Marker Detection from Single-Cell Transcriptomic Data. Poster presented at Keystone Symposia on Cancer Immunotherapy: Mechanistic Insights to Improve Clinical Benefits (C2), Whistler, Canada, March 2019.

Cammarata, L. Inferring Total Queueing Time Using Only Elapsed Time to Date. Oral presentation delivered at INFORMS Annual Meeting, Houston, TX, October 2017.