

Dr. Elena Marchetti

Postdoctoral Research Fellow — Computational Systems Biology



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Research Interests

- Computational systems biology
- Single-cell transcriptomics & multi-omics integration
- Machine learning for genomics
- Gene regulatory network inference
- Statistical modeling of biological dynamics
- Algorithm development for high-dimensional biomedical data
- Cancer systems biology
- Drug response prediction

Education

Ph.D. in Bioinformatics Meridian University, Cambridge, MA 2017–2022
Dissertation: *Probabilistic Graphical Models for Inference of Cell-Type-Specific Regulatory Networks from Heterogeneous Genomic Data*
Advisor: Prof. Samuel Okafor

M.S. in Computational Biology Apex Institute of Technology, Boston, MA 2015–2017
Thesis: *Bayesian Nonparametric Methods for Clustering Single-Cell Expression Profiles*
GPA: 3.94/4.00

B.S. in Biology, Minor in Computer Science Nimbus College, Amherst, MA 2011–2015
summa cum laude, Phi Beta Kappa
GPA: 3.88/4.00

Postdoctoral Research Experience

Postdoctoral Research Fellow Meridian University, Department of Computational Biology 2022–Present

Supervisor: Prof. Samuel Okafor

- Lead development of **NetRegulus**, an open-source R/Python toolkit for joint inference of gene regulatory networks from paired scRNA-seq and scATAC-seq data (2,400+ GitHub stars, 18 contributors).
- Designed novel transfer-learning framework that leverages bulk transcriptomic cohorts to improve single-cell network reconstruction accuracy by 34% over baseline methods.
- Established collaboration with Vertex Data Science on scalable GPU-accelerated implementations of network inference algorithms.
- Mentor three Ph.D. students and two undergraduate researchers; co-advised one M.S. thesis.
- Authored or co-authored 8 peer-reviewed publications (5 as first or co-first author) in high-impact

journals.

- Delivered 6 invited talks at international conferences and university seminar series.

Grants & Fellowships

Year	Title	Funding Agency	Amount
2024	Early Career Investigator Award: Multi-scale Network Modeling of Tumor Microenvironment Evolution	National Bioscience Initiative (NBI)	\$75,000
2024	Conference Support Grant	International Society for Computational Biology	\$1,800
2023	Postdoctoral Research Fellowship	Meridian Research Foundation	\$60,000
2023	Computational Resources Allocation (500,000 GPU-hours)	Vertex Innovation Cloud Program	In-kind
2022	Outstanding Dissertation Award & Publication Stipend	Meridian University Graduate School	\$3,500
2022	Travel Fellowship	Cold Spring Harbor Laboratory	\$2,200

Teaching Experience

Instructor of Record Meridian University Spring 2024

BIOL 450: Introduction to Bioinformatics (enrollment: 48)

Designed syllabus, delivered lectures, created 5 computational lab modules, and developed automated grading pipeline. Received average teaching evaluation score of 4.7/5.0.

Guest Lecturer Apex Institute of Technology Fall 2023

CS 580: Machine Learning in Genomics

Delivered three lectures on autoencoder architectures for dimensionality reduction in single-cell data, with accompanying Jupyter-based problem sets.

Head Teaching Assistant Meridian University 2020–2022

BIOL 300: Statistical Methods in Biology & CS 410: Algorithms for Bioinformatics

Led weekly discussion sections (25–35 students), held office hours, graded assignments and exams, and mentored junior TAs.

Workshop Organizer Meridian University 2023, 2024

Single-Cell Genomics Data Analysis Bootcamp

Developed and ran two annual 3-day hands-on workshops (60+ participants each) covering preprocessing, clustering, trajectory inference, and regulatory network analysis in R and Python.

Peer-Reviewed Publications

Denotes co-first authorship. H-index: 9 (Nexa Scholar, June 2025).

- [1] **Marchetti, E.**, Chen, R., Park, S., & Okafor, S. (2024). Joint inference of gene regulatory networks from paired single-cell multi-omics data using coupled latent variable models. *Meridian Journal of Computational Biology*, 45(3), 210–234.
- [2] **Marchetti, E.***, Torres, L.*, & Kim, J. (2024). Transfer learning improves cell-type-specific regulatory network reconstruction in rare populations. *Cell Systems*, 15(8), 892–908.
- [3] Park, S., **Marchetti, E.**, & Okafor, S. (2024). A unified probabilistic framework for integrative analysis of transcriptomic and epigenomic single-cell data. *Nature Computational Science*, 4, 456–470.
- [4] **Marchetti, E.**, & Nguyen, T. (2023). Bayesian nonparametric clustering of single-cell expression profiles

with automatic determination of the number of cell types. *Journal of Quantitative Biosciences*, 38(4), 567–589.

- [5] Torres, L., **Marchetti, E.**, & Walsh, P. (2023). Deciphering tumor microenvironment heterogeneity through multi-omics network analysis. *Cancer Systems Biology*, 12(2), 145–167.
- [6] **Marchetti, E.**, Okafor, S., & Rivera, D. (2022). NetRegulus: an open-source toolkit for gene regulatory network inference from heterogeneous genomic data. *Bioinformatics Advances*, 2(1), btac045.
- [7] Chen, R., Park, S., **Marchetti, E.**, & Okafor, S. (2022). Graph neural networks for cell-type-specific enhancer-promoter interaction prediction. *Proceedings of the International Symposium on Systems Biology (ISsB 2022)*, 88–99.
- [8] **Marchetti, E.**, & Okafor, S. (2021). A nonparametric Bayesian approach to inferring dynamic gene regulatory networks from pseudotemporally ordered single-cell data. *Meridian Journal of Computational Biology*, 42(6), 789–812.
- [9] Walsh, P., **Marchetti, E.**, & Liu, Y. (2021). Integrating ChIP-seq and RNA-seq data for context-specific regulatory network reconstruction. *Bioinformatics*, 37(18), 2901–2910.
- [10] **Marchetti, E.**, Kim, J., & Singh, A. (2020). Variational autoencoders for nonlinear dimensionality reduction in single-cell RNA-seq data. *Proceedings of the Machine Learning in Computational Biology Workshop (MLCB 2020)*, 45–56.

Conference Presentations & Invited Talks

Invited Seminar Department of Genetics, Apex Institute of Technology, March 2025
“From Cells to Circuits: Multi-Scale Network Modeling of Gene Regulation.”

Invited Talk International Symposium on Systems Biology (ISsB), Boston, MA, July 2024
“Coupled Latent Variable Models for Paired Single-Cell Multi-Omics Data.”

Platform Presentation Annual Meeting of the Society for Computational Biology, Seattle, WA, May 2024
“Transfer Learning Improves Regulatory Network Inference in Rare Cell Populations.”

Poster Cold Spring Harbor Laboratory Meeting on Single-Cell Analyses, Cold Spring Harbor, NY, October 2023
“NetRegulus: A Scalable Toolkit for Single-Cell Regulatory Network Inference.”

Invited Seminar Vertex Data Science Research Seminar Series, San Francisco, CA, September 2023
“Advances in Probabilistic Modeling of Single-Cell Genomics Data.”

Platform Presentation Machine Learning in Computational Biology (MLCB), Virtual, December 2022
“Bayesian Nonparametric Clustering with Automatic Cell-Type Number Determination.”

Invited Talk Meridian Systems Biology Symposium, Cambridge, MA, October 2022
“Gene Regulatory Network Inference from Heterogeneous Genomic Data.”

Professional Service

Journal Reviewer *Meridian Journal of Computational Biology* (2023–Present), *Journal of Quantitative Biosciences* (2023–Present), *Bioinformatics Advances* (2024–Present), *PLOS Computational Biology* (2024–Present).

Conference Organizing Committee International Symposium on Systems Biology (ISsB), 2024 & 2025.

Session Chair “Single-Cell Multi-Omics Methods,” Society for Computational Biology Annual Meeting, 2024.

Graduate Admissions Committee Department of Computational Biology, Meridian University, 2023–Present.

Outreach Volunteer instructor, Meridian Science Outreach Program: introducing computational biology to high school students from underrepresented backgrounds (2023, 2024).

Technical Skills

Programming	Python (numpy, scipy, pandas, scanpy, scvi-tools), R (Seurat, Monocle, glmnet, DESeq2), Julia, Bash
Bioinformatics	scRNA-seq, scATAC-seq, ChIP-seq, RNA-seq, multi-omics data integration, gene regulatory network inference
Machine Learning	PyTorch, scikit-learn, variational autoencoders, graph neural networks, Bayesian nonparametrics
Tools & Workflows	Git, Docker, Nextflow, Snakemake, Jupyter, Slurm, AWS (EC2, S3), Nexa Cloud Platform
Statistics	Bayesian inference, MCMC methods, hierarchical modeling, hypothesis testing, multiple testing correction
Visualization	matplotlib, seaborn, ggplot2, plotly, Adobe Illustrator
Languages	English (native), Italian (fluent), French (intermediate)

References

Available upon request.