PINAR DEMETCI

💻 pinardemetci.github.io ◇ ☎ 857 · 919 · 2448 ◇ ✉ pinardemetci@gmail.com

SUMMARY & INTERESTS

I am interested in developing probabilistic and statistical algorithms tailored to the unique challenges of high-dimensional biological data. My overall research goal is to facilitate the study of complex cellular regulatory mechanisms and their influence on phenotypic variation in health and (especially heterogenous) disease, specifically to find therapeutic targets. My long-term career goal is to establish myself as a leading interdisciplinary researcher and an effective academic mentor at the intersection of machine learning and computational genomics

Methodological interests: representation learning, manifold learning, optimal transport, transfer learning, Bayesian nonparametrics, Bayesian inference, variable selection, interpretability methods in machine learning.
Application domain interests: regulatory genomics, precision medicine, single-cell genomics, multi-modal data integration, cancer, neurodenegerative diseases

EDUCATION

Brown University Providence, RI
Ph.D. Computer Science and Computational Biology — GPA: 3.90/4.00 2023 (Expected)
Advisors: Ritambhara Singh, Ph.D. (primary) and Sorin Istrail, Ph.D.
Dissertation: “Probabilistic and statistical algorithms for integrated analysis of single-cell multi-omics data”

M.Sc. Computer Science — GPA: 4.0/4.0
Advisor: Sorin Istrail, Ph.D.
Thesis: “Combinatorial Bayesian algorithms to identify cis-regulatory eQTLs in higher order interactions”

Olin College of Engineering Needham, MA
B.Sc. Bioengineering — GPA: 3.67/4.00 2017

RESEARCH EXPERIENCE

Microsoft Research June 2022 - Present
Research Intern Redmond, WA & Cambridge, MA (remote)

- Developing optimal transport-based methods to study multi-modal chemical and genetic perturbation datasets.

Brown University Sept 2018 - Present
Graduate Research Assistant Providence, RI

- Developing statistical and probabilistic algorithms for integrated analysis of single-cell multi-modal data, with applications in regulatory genomics. [Publications #4, #6, #7, #8]
- Previously worked on neural network interpretability methods with Bayesian variable selection for applications to genome-wide association studies [Publication #5].

Microsoft Research June 2020 - September 2020
Research Intern Redmond, WA (remote)

- Implemented a Bayesian inference and machine learning pipeline on Microsoft Azure for disease risk prediction and clinical and genomic marker identification.

Massachusetts Institute of Technology (MIT) June 2017 - August 2018
Research Associate Cambridge, MA

- Served as the lab manager in Gene-Wei Li lab. Investigated bacterial regulatory network rewiring [Publication #2]. Contributed to RNA-seq analysis tools in Python and image processing tools in MATLAB.

Olin College of Engineering Sep 2015 - May 2017
Undergraduate Research & Teaching Assistant Needham, MA

- Worked with Drs. Jean Huang and John Geddes on Lotka-Volterra-based dynamic modeling for bacterial communities undergoing perturbations.
- Designed an assistive software for blind navigation in Olin College Crowdsourcing and Machine Learning (OCCaM) Lab.

PEER-REVIEWED PUBLICATIONS

(*) Denotes equal contribution, Undergraduate mentees underlined

8. **P Demetci**, R Santorella, B Sandstede, and R Singh (2022). Unsupervised integration of single-cell multi-omics datasets with disparities in cell type representation. *International Conference on Research in Computational Biology (RECOMB 2022). Springer Lecture Notes in Computer Science.* 306:3-19. doi: 10.1007/978-3-031-04749-7_1.
    - Also to appear as (extended paper): **P Demetci**, R Santorella, M Chakravarthy, B Sandstede, W Stafford Noble, and R Singh (2022). SCOTv2: Single-cell multi-omic alignment with disproportionate cell-type representation. *Journal of Computational Biology (in press).*
7. **P Demetci***, R Santorella*, B Sandstede, W Stafford Noble, and R Singh (2021). Gromov-Wasserstein optimal transport to align single-cell multi-omics data *International Conference on Research in Computational Molecular Biology (RECOMB 2021).*
    - Also appeared at (abstract): *the 37th International Comference on Machine Learning (ICML) Workshop on Computational Biology (2020).*
6. **P Demetci***, R Santorella*, B Sandstede, W Stafford Noble, and R Singh (2021). SCOT: Single-Cell multi-omic integration with Optimal Transport *Journal of Computational Biology.* 29(1):3-18. doi: 10.1089/cmb.2021.0446
5. **P Demetci**, W Cheng, G Darnell, X Zhou, S Ramachandran, and L Crawford. Multi-scale genomic inference using biologically annotated neural networks (2021). *PLOS Genetics.* 17(8): e1009754. doi: 10.1371/journal.pgen.1009754
4. R Singh, **P Demetci**, G Bonora, V Ramani, C Lee, H Fang, Z Duan, X Deng, J Shendure, C Disteche, and W Stafford Noble. Unsupervised manifold alignment for single-cell multi-omics data (2020). *ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM BCB).* doi: 10.1145/3388440.3412410
3. B Alpay*, **P Demetci***, S Istrail, and D Aguiar. Combinatorial and statistical prediction of gene expression from haplotype sequence (2020). *Bioinformatics.* 36:Supplement-1: i194-i202. doi: 10.1093/bioinformatics/btaa318
2. D Parker*, **P Demetci***, G W Li. Rapid accumulation of motility-activating mutations in resting liquid culture of *Escherichia coli* (2019). *Journal of Bacteriology.* 201(19):e00259-19. doi: 10.1128/JB.00259-19
1. **P Demetci**, C Nichols, Y V Zastavker, J D Stolk, A Dillon, M Gross. Externalization and internalization in the classroom: How do they emerge and why is it important? (2016). *IEEE Frontiers in Education Conference.* doi: 10.1109/FIE.2016.7757463

PRE-PRINTS AND MANUSCRIPTS IN PREPARATION

1. QH Tran, H Janati, N Courty, R Flamary, I Redko, **P Demetci**, R Singh. Unbalanced CO-Optimal Transport (2022). *Under review for the Proceedings of the 34th Conference on Neural Information Processing Systems (NeurIPS 2022).* arXiv pre-print: arxiv.org/abs/2205.14923
2. **P Demetci**, I Redko, R Singh. Simultaneously aligning cells and genomic features of single-cell multi-omics data with co-optimal transport. *In preparation.*

AWARDS

2022	Rising Star in Electrical Engineering and Computer Science (UT Austin)
2022	RECOMB Travel Fellowship
2020	ICML WCB Best Poster Award
2020	ICML WCB Fellowship
2016	Meritorious Winner: COMAP MCM/ICM Contest in Mathematical Modeling (Top 10%)
2015-2017	Olin Alumni Merit Scholarship (towards living expenses)
2013-2017	Sunlin Chou International Scholarship (50% tuition)
2013-2017	Olin Merit Scholarship (50% tuition)

SELECTED CONFERENCES AND INVITED TALKS

Title: "Unsupervised integration of single-cell multi-omics datasets with disparities in cell-type representation"

2022 RECOMB Proceedings: Oral Presentation *(Acceptance Rate: 20%)*
RECOMB: International Conference on Research in Computational Molecular Biology

2021 Machine Learning in Computational Biology (MLCB): Oral Presentation *(Acceptance R.: 25%)*

Title: "Enabling integrated analysis of single-cell multi-omics data with optimal transport"

2021 NeurIPS Workshop on Optimal Transport in Machine Learning: Keynote Talk

2021 University of Connecticut Bioinformatics Seminar: Invited Talk

Title: "Biologically Annotated Neural Networks for Multi-Scale Genomic Discovery in GWAS"

2022 Stanford University (Kundaje Lab): Invited Talk

2021 Translational Bioinformatics Seminar, Brown University: Invited Talk

2019 Brown Center for Computation & Visualization Conference – CCV-Con: Invited Talk

Title: "Gromov-Wasserstein Optimal Transport to Align Single-cell Multi-omics Data"

2021 RECOMB Proceedings: Oral Presentation *(Acceptance Rate: 19%)*

2021 Machine Learning in Computational Biology (MLCB): Oral Presentation *(Acceptance R.: 15%)*

2020 Workshop on Optimal Control, Optimal Transport & Data Science: Invited Poster
at University of Minnesota – Institute for Mathematics and Its Applications (IMA)

2020 ICML Workshop on Computational Biology: Spotlight Talk & Poster *(Acceptance Rate: 21%)*

2020 Intelligent Systems in Molecular Biology (ISMB – MLCB track): Oral & Poster Presentations *(Acceptance rate: 25%)*

2020 Brown Unconference on Computational Intelligence and Applications: Invited Talk

Title: "Internalization and externalization in the classroom: How do they emerge and why is it important?"

2016 Frontiers in Education – FIE: Oral Presentation *(Acceptance rate: 48%)*

TEACHING EXPERIENCE

Graduate Teaching Assistant at Brown University

- **CSCI2820 Advanced Algorithms in Comp. Bio. & Medical Bioinfo.** (Spring 2019 & 2021)
  Instructor: Sorin Istrail, Ph.D.
  Guest-lectured three times, held recitation sessions and office hours, wrote and graded assignments.

Undergraduate Teaching Assistant at Olin College of Engineering

- **SCI1240: Designing Better Drugs with Laboratory** (Fall 2015)
  Instructor: Joanne Pratt, Ph.D.
  Assisted in the classroom, wrote and graded assignments

PROFESSIONAL COMMUNITY SERVICE & MEMBERSHIPS & LEADERSHIP

2020 - 2022	Reviewer for Journal of Computational Biology, and MLCB 2020 and 2021 conferences.
2020 - 2021	Sub-reviewer for ICML, NeurIPS, and RECOMB conferences.
2020 - 2021	Computational Biology Ph.D. Program Admissions Committee Member (Brown University)
2020 - Present	Peer Mentor for International Graduate Students at Brown University
2020 - Present	Student Member at Society for Industrial and Applied Mathematics (SIAM) and AnitaB.org.
2018 - Present	Student Member at International Society for Computational Biology (ISCB)
2018 - Present	Member at Models, Inference, and Algorithms (MIA) at Broad Institute of MIT and Harvard
2018 - Present	Member at Graduate Women in Science and Engineering (GWiSE) at Brown University

MENTORSHIP

- Zheyuan Zhou (Masters student in Computer Science, Brown University)
- Hossam Zaki (Class of 2022, Brown University) → now MD-PhD student at Brown University
- Samantha Hong (Brown U. Class of 2023, Computational Biology)
- Momoka Kobayashi (Brown University, Class of 2023, Biomedical Engineering and Computer Science)
- Chris Chae (Brown U. Class of 2023, Computer Science)
- Manav Chakravarthy (Brown University, Class of 2024, Computer Science and Economics)

TECHNICAL SKILLS

Languages	Python, R, Java, C++, MATLAB, SQL, HTML, CSS, JavaScript
Frameworks	Pandas, Numpy, Tensorflow, PyTorch, Pyro, HDF5, Docker, Bioconductor, Seurat
Environments	Linux, UNIX, slurm, High Performance Computing, Google Cloud, Microsoft Azure
Bioinformatics	VCFtools, BCFtools, Cromwell, GATK, Picard, PLINK, Cytoscape, QIIME, VAMPS