PINAR DEMETCI

💻 pinardemetci.github.io ◇ ☎ +1.857.919.2448 ◇ ✉ pinardemetci@gmail.com

EDUCATION

Brown University Providence, RI **2018 - 2023 (Expected)**
Ph.D. Computer Science & Computational Biology (GPA: 3.90/4.00)
Dissertation: "Probabilistic and statistical algorithms for integrated analysis of single-cell multi-modal data"
Advisors: Ritambhara Singh, Ph.D. (primary), Sorin Istrail, Ph.D.

M.Sc. Computer Science (GPA: 4.00/4.00)
Thesis: "A combinatorial Bayesian algorithm to predict gene expression and identify of cis-eQTLs in higher order interactions"
Advisor: Sorin Istrail, Ph.D.

Olin College of Engineering Needham, MA **2013 - 2017**
B.Sc. Bioengineering (GPA: 3.67/4.00)

RESEARCH EXPERIENCE

Microsoft Research Redmond, WA & Cambridge, MA (Remote) **June 2022 - Present**
Research Intern
- Developing an optimal transport-based method for analysis of multi-modal chemical and genetic perturbation datasets.

Brown University Providence, RI **Sep 2018 - Present**
Graduate Research & Teaching Assistant
- 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].
- Served as the teaching assistant for "Advanced Algorithms in Computational Biology and Medical Bioinf." (Spring '19 & '21).

Microsoft Research Redmond, WA (Remote) **June 2020 - Sep 2020**
Research Intern
- Implemented a machine learning-based computational pipeline on Microsoft Azure for disease risk prediction and clinical and genomic marker identification.

Massachusetts Institute of Technology Cambridge, MA **May 2017 - Aug 2018**
Research Associate
- Served as the lab manager in Dr. Gene-Wei Li's quantitative biology lab. Investigated the mechanisms of bacterial regulatory network rewiring [Publication #2]. Developed in-lab RNA-seq analysis and image processing tools.

Olin College of Engineering Needham,MA **Sep 2015 - May 2017**
Undergraduate Research & Teaching Assistant
- Worked with Drs. Jean Huang and John Geddes on Lotka-Volterra-based dynamic modeling for bacterial communities undergoing perturbations.
- Served as a teaching assistant for the science course "Designing Better Drugs" and the entrepreneurship course "Products & Markets".
- Helped design an assistive software for blind navigation in Olin College Crowdsourcing and Machine Learning Lab.

REFEREED PUBLICATIONS

8. **P Demetci** , R Santorella, B Sandstede, R Singh. **Unsupervised integration of single-cell multi-omics datasets with disparities in cell-type representation** (2021). Peer-reviewed and accepted for publication at: *Proceedings of the 26th International Conference on Research in Computational Biology (RECOMB 2022).*
7. **P Demetci** , R Santorella, B Sandstede, W Stafford Noble, R Singh. **Gromov-Wasserstein optimal transport to align single-cell multi-omics data.** (2021). *Proceedings of the 25th International Conference on Research in Computational Molecular Biology (RECOMB 2021). (in press).*
6. **P Demetci** , R Santorella, B Sandstede, W Stafford Noble, R Singh. **SCOT: Single-cell multi-omics integration with optimal transport.** (2021). *Journal of Computational Biology. (in press).*
5. **P Demetci** , W Cheng, G Darnell, X Zhou, S Ramachandran, L Crawford. **Multi-scale genomic inference using biologically annotated neural networks.** (2020).*PLOS Genetics* 17(8): e1009754.
4. R Singh, **P Demetci** , G Bonora, V Ramani, C Lee, H Fang, Z Duan, X Deng, J Shendure, C Disteche, W Stafford Noble. **Unsupervised manifold alignment for single-cell multi-omics data.** (2020). *Proceedings of the 11th ACM International Conference on Bioinformatics, Computational Biology and Health Informatics. (ACM-BCB 2020).*
3. *B Alpay*, **P Demetci** , S Istrail,D Aguiar. **Combinatorial and statistical prediction of gene expression from haplotype sequence.** (2020). *Bioinformatics* 36 (Supplement - 1): i194 - i202.
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

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*

(*) Asterisk denotes equal contribution

PRE-PRINTS AND MANUSCRIPTS UNDER REVIEW

1. H Tran, H Janati, N Courty, R Flamary, I Redko, **P Demetci**,R. Singh. **Unbalanced CO-Optimal Transport.** (2022). Under review at: 36^{th} *Conference on Neural Information Processing Systems (NeurIPS 2022).*
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.*

SELECTED CONFERENCES & INVITED TALKS

Talk 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

Talk Title:"Biologically annotated neural networks for multi-scale genomic association discovery"

- **2022 Stanford University (Kundaje Lab)**: Invited Talk
- **2021 Translational Bioinformatics Seminar, Brown University**: Invited Talk
- **2019 Brown University CCV-Con**: Invited Talk

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

- **2022 International Conference on Research in Computational Biology (RECOMB)**: Oral Presentation
- **2021 Machine Learning in Computational Biology (MLCB) Conference**: Oral Presentation (25% acceptance rate)

Talk Title: "Gromov-Wasserstein optimal transport to align single-cell multi-omics data"

- **2021 International Conference on Research in Computational Biology (RECOMB):** Oral Presentation
- **2020 ICML Workshop on Computational Biology**: Spotlight Talk & Poster Presentation *(21% acceptance rate)*
- **2020 Machine Learning in Computational Biology (MLCB) Conference**: Oral Presentation *(15% acceptance rate)*
- **2020 Intelligent Systems in Molecular Biology (ISMB) Conference**: Poster Presentation *(25% acceptance rate)*
- **2020 Brown Unconference on Computational Intelligence and Applications**: Invited Talk
- **2020 University of Minnesota IMA – Workshop on Optimal Control, Optimal Transport, and Data Science:** Poster

AWARDS

2020	RECOMB Travel Fellowship
2020	ICML WCB Best Poster Award
2020	ICML WCB Fellowship
2018-Present	Brown Graduate Fellowship
2016	Meritorious Winner (top 10%) at COMAP MCM/ICM International Contest in Mathematical Modeling
2015-2017	Olin Alumni Merit Scholarship (towards living expenses)
2013-2017	Sunlin Chou International Scholarship (50% of tuition)
2013-2017	Olin Merit Scholarship (50% of tuition)
2013	Honorable Mention at First Step to Nobel Prize in Physics International Research Project Contest

PROFESSIONAL COMMUNITY SERVICE & MEMBERSHIP

2020-Present	Peer mentor for international graduate students at Brown University
2020-2021	Reviewer for *Journal of Computational Biology* and *Machine Learning in Computational Biology (MLCB)* conference
2020-2021	Subreviewer for *NeurIPS*, *ICML*, *RECOMB*, and *ISMB* conferences
2020-2021	Admissions committee member for the Computational Biology Ph.D. Program at Brown University
2020-2021	Member at the Society for Industrial and Applied Mathematics (SIAM).
2018-2021	Member at the International Society for Computational Biology (ISCB).
2018-2021	Member at the Graduate Women in Science and Engineering (GWiSE) at Brown University.

TECHNICAL SKILLS

Programming	Python, R, Java, C++, MATLAB, SQL, noSQL, CSS, HTML, bash
Platforms	UNIX, Google Cloud, slurm, High Performance Computing, Microsoft Azure, Docker, git
Frameworks	***Machine Learning:*** Python OT (POT), Tensorflow, PyTorch, Pyro, PyG, CUDA, sklearn ***Data Processing:*** NumPy, Numba, Pandas, SciPy, HDF5, skimage, openCV, Pillow ***Data Visualization:*** matplotlib, seaborn, ggplot, Bokeh, D3
Bioinformatics	Bioconductor, Scanpy, Seurat, Signac, VCFtools, BEDtools, GATK, Picard, Cromwell, PLINK, PyMOL, ImageJ