PINAR DEMETCI

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EDUCATION

Brown University Providence, RI
Ph.D. Computational Biology and Computer Science — GPA: 3.90/4.00 2018 - 2023 (Expected)
Dissertation: Probabilistic methods to enable integrated analysis of single-cell multi-modal data

M.Sc. Computer Science — GPA: 4.0/4.0
Thesis: Combinatorial Bayesian algorithm to identify cis-regulatory eQTLs in higher order interactions

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

EXPERIENCE

Brown University September 2018 - Present
Graduate Research & Teaching Assistant Providence, RI

- **(2019 - Present)** Working under the supervision of Ritambhara Singh, Ph.D. on unsupervised algorithms for integrated analysis of single-cell multi-omics data.
- **(2019 - 2021)** Worked with Sorin Istrail, Ph.D. on (1) combinatorial and statistical methods to predict gene expression from haplotypes and identifying cis-regulatory elements in higher order interactions. Served as their graduate teaching assistant in "Advanced Algorithms in Computational Biology and Medical Bioinformatics"
- **(2018 - 2019)** Worked with Lorin Crawford, Ph.D. on Bayesian approaches for multi-scale genomic association and genetic architecture discovery.

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

- Implemented a computational pipeline for precision medicine applications on Microsoft Azure platform. Implemented Bayesian machine learning algorithms for predicting phenotypes and finding genetic and clinical biomarkers of disease.

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

- Worked in the quantitative biology laboratory with Gene-Wei Li, Ph.D. Investigated gene regulatory network rewiring in bacterial model organisms and assisted with various quantitative biology projects in the lab. Contributed to an interactive RNA-seq differential expression analysis and visualization pipeline. Served as the lab manager and environmental, health, and safety officer.

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

- Worked with Jean Huang, Ph.D. and John Geddes, Ph.D. on dynamical modeling of bacterial communities under environmental perturbations.
- Worked with Paul Ruvolo, Ph.D. on sensory substitution system for assisting visually impared users with shopping. Collaborated with Bose Corporation on user interaction research.

Design That Matters Jan 2016 - Oct 2016
Student Engineer Salem, MA

- Engineered a newborn warmer that works efficiently with phototherapy device Otter, targeting the developing world. Conducted user interviews in Vietnam.

Daktari Diagnostics Jan 2015 - Dec 2015
Student Engineer Cambridge, MA

- Developed a bioimaging software for sickle-cell disease diagnotics purposes; served as the technical lead.

AWARDS

2020	ICML WCB Fellowship
2020	ICML WCB Best Poster Award
2016	Meritorious Winner: MCM/ICM International Contest in Mathematical Modeling (Top 10%)
2015-2017	Olin Alumni Merit Scholarship
2013-2017	Sunlin Chou International Scholarship (50% tuition)
2013-2017	Olin Merit Scholarship (50% tuition)
2013	Honorable Mention (Instrumentation): First Step to Nobel Prize in Physics
2013	First Place: MEF Contest in Research Projects

PUBLICATIONS AND PRE-PRINTS

* Denotes equal contribution

1. **P Demetci***, R Santorella*, B Sandstede, W Stafford Noble, and R Singh. Gromov-Wasserstein optimal transport to align single-cell multi-omics data (2021). *International Conference on Research in Computational Molecular Biology (RECOMB).*
2. 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)*
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.
4. **P Demetci**, W Cheng, G Darnell, X Zhou, S Ramachandran, and L Crawford. Multi-scale genomic inference using biologically annotated neural networks (2021). *under review at PLOS Genetics.*
5. D Parker*, **P Demetci***, G W Li. Rapid accumulation of motility-activating mutations in resting liquid culture of *Escherichia coli* (2019). *Journal of Bacteriology*
6. **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*

CONFERENCES AND INVITED TALKS

Presenters underlined, * Denotes equal contribution to the work,

2020 **Machine Learning in Computational Biology (MLCB): Oral Presentation**
(**Acceptance rate:** 15%)
Gromov-Wasserstein optimal transport to align single-cell multi-omics data
P Demetci*,R Santorella*, B Sandstede, W S Noble, and R Singh

2020 **Workshop on Optimal Control, Optimal Transport & Data Science: Invited Poster**
University of Minnesota - Institute for Mathematics and Its Applications
Gromov-Wasserstein optimal transport to align single-cell multi-omics data
P Demetci*,R Santorella*, B Sandstede, W S Noble, and R Singh

2020 **ICML Workshop on Computational Biology: Spotlight Talk & Poster Presentations**
(**Acceptance rate:** 21%)
Gromov-Wasserstein optimal transport to align single-cell multi-omics data
P Demetci* [spotlight], R Santorella* [poster], B Sandstede, W S Noble, and R Singh

2020 **ISMB (MLCSB track): Spotlight Talk & Poster Presentations** (**Acceptance rate:** 25%)
Gromov-Wasserstein optimal transport to align single-cell multi-omics data
P Demetci*[poster], R Santorella* [spotlight], B Sandstede, W S Noble, and R Singh

2020 **ISMB Proceedings (Variant Interpretation Track): Oral Presentation**
(**Acceptance rate:** 19%)

Combinatorial and statistical prediction of gene expression from haplotype sequence
B Alpay*, **P Demetci**, S Istrail, and D Aguiar.

2020 **ACM-BCB: Oral Presentation**
Unsupervised manifold alignment for single-cell multi-omics data
R Singh, **P Demetci**, G Bonora, V Ramani, C Lee, H Fang, Z Duan, X Deng, J Shendure, C Disteche, and W Stafford Noble.

2020 **Brown Unconference on Computational Intelligence and Applications: Invited Talk**
Gromov-Wasserstein optimal transport to align single-cell multi-omics data
P Demetci*, R Santorella*, B Sandstede, W S Noble, and R Singh

2019 **Brown Center for Computation & Visualization Conference: Invited Talk**
Biologically Annotated Neural Networks for Multi-Scale Genomic Discovery in GWAS
P Demetci, W Cheng, S Ramachandran, and L Crawford

2016 **Frontiers in Education (FIE): Oral Presentation** (**Acceptance rate:** 48%)
Internationalization and Externalization in the Classroom:
P Demetci, C Nichols, YV Zastavker, JD Stolk, A Dillon, and M Gross

2016 **NEMPET: Poster Presentation**
Bioinformatic comparison of phototropic communities that degrade cellulose and fix nitrogen
P Demetci, M Sheets, A Knapp, L Amaral-Zettler, and J J Huang

2015 **Closing the Gap: Oral Presentation**
Project EyeHelper: Assistive navigation for blind shopping
P Demetci, A Johnson, M Ruehle, and P Ruvolo

TEACHING EXPERIENCE

Graduate Teaching Assistant at Brown University

- **CSCI2820 Advanced Algorithms in Comp. Bio. & Medical Bioinfo.** (Spring 2019 & 2021)
  Instructor: Sorin Istrail, Ph.D.

Undergraduate Teaching Assistant at Olin College of Engineering

- **SCI1240: Designing Better Drugs with Laboratory** (Fall 2015)
  Instructor: Joanne Pratt, Ph.D.

PROFESSIONAL MEMBERSHIPS & COMMUNITY ACTIVITIES

2020 - Present	Computational Biology Ph.D. Program Admissions Committee
2020 - 2021	Reviewer for MLCB 2020 and associate (sub-) reviewer for RECOMB 2021 & ICML 2021
2020 - Present	Peer Mentor for International Graduate Students at Brown University
2020 - Present	Student Member at Society for Industrial and Applied Mathematics (SIAM)
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

TECHNICAL SKILLS

Languages	Python, R, MATLAB, Java, C++, SQL, HTML, CSS, JavaScript
Frameworks	Pandas, Numpy, Tensorflow, PyTorch, Pyro, HDF5, Bioconductor, Seurat
Software	VCFtools, BCFtools, Cromwell, GATK, Picard, PLINK, Cytoscape, QIIME, VAMPS
Environments	Linux, MacOS, slurm, High Performance Computing. Google Cloud, Microsoft Azure
Laboratory	DNA & RNA extraction, PCR & qPCR, RNA library preperation, Ribo-seq, Western blot, Molecular transformation & transfection, Protein assay, Microscopy, SEM, Cell culture, Anaerobic culture, HPLC, Rheology