Pinar Demetci

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SKILLS

PROGRAMMING

• **Experienced:** Python, R, Java, Matlab, UNIX shell, High Performance Computing, Cloud Computing
• **Others:** C++, JavaScript, mySQL, noSQL
• **Common packages / tools:** Numpy, Pandas, Tensorflow, Tensorflow Probability, PyTorch, Pyro, Scikit-learn, HDF5, Bioconductor, Seurat, glm, SAMtools, BEDtools, VCFtools, PLINK.

RELEVANT COURSEWORK

Computational Biology • Statistical Inference • Analysis of Algorithms • Advanced Algorithms in Bioinformatics • Deep Learning in Genomics • Data Science • Software Design • Quantitative Biology • Human Population Genomics • Cancer Biology • Microbiology • Biochemistry • Cellular & Molecular Mechanisms of Diseases

AWARDS & RESEARCH OUTCOME

MERITORIOUS WINNER

2016 MCM Interdisciplinary Contest in Mathematical Modeling

HONORABLE MENTION

2013 First Step to Nobel Prize in Physics (project titled "Non-Contact Manipulation: Optical Tweezing for Single Cells")

PAPERS

P Demetci, B Alpay, S Istrail, D Aguiar. "Combinatorial methods for predicting gene expression from genetic data" RECOMB 2020 (in review).

D Parker*, P Demetci*, GW Li. "Rapid accumulation of motility-activating mutations in resting liquid culture of Escherichia coli." Journal of Bacteriology. 2019. *Equal contribution

P Demetci, C Nichols, Y V Zastavker, J D Stolk, A Dillon, M Gross. Internalization and externalization in the classroom: How do they emerge and why is it important? IEEE FIE 2016.

INVITED TALKS & CONFERENCES

Invited Talk, CCV-Con '19: "Biologically Annotated Neural Networks for Multi-Scale Genomic Association Discovery".

Poster Presentation, NEMPET '16 "Bioinformatic Comparison of Phototrophic Communities that Degrade Cellulose and Fix Nitrogen"

Invited Talk, Closing the Gap '15 "Project Eye-Helper: Assistive Navigation for Blind Shopping"

MEMBERSHIPS & SERVICE

• International Society for Computational Biology (ISCB)
•Models, Inference, and Algorithms (MIA) at Broad Institute
• Reviewer for Journal of Computational Biology (November 2019)

RESEARCH INTERESTS

Developing machine learning methods and combinatorial algorithms for genomic data analysis, with a focus on interpretability.

EDUCATION

PH.D. COMPUTATIONAL BIOLOGY (COMPUTER SCIENCE TRACK)

Sep 2018 - May 2023 (expected) | Brown University, RI, USA
• 2018-2020 Brown Graduate Fellowship

M.S. COMPUTER SCIENCE • GPA: 4.00/4.00

Sep 2018 - May 2020 (expected) | Brown University, RI, USA
• Thesis: "Bayesian neural networks and combinatorial methods for genomic association discovery in trait and eQTL mapping."

B.S. BIOENGINEERING • GPA: 3.67/4.00

Sep 2013 - May 2017 | Olin College of Engineering, MA, USA
• 2016-2017 Olin Alumni Merit Scholarship
• 2013-2017 Sunlin Chou International Scholarship
• 2013-2017 Olin Merit Scholarship

EXPERIENCE

GRADUATE RESEARCH & TEACHING ASSISTANT at Brown University

September 2018 – Present | Providence, RI

- Working with Dr. Lorin Crawford on a biologically annotated, interpretable Bayesian neural network models for multi-scale discovery in genome-wide association studies (applications with UK Biobank). Manuscript in progress.
- Research rotation completed with Dr. Ritambhara Singh on evaluating manifold alignment algorithms for single cell assays and developing a deep learning model for cancer pharmacogenomics (TCGA & GDSC datasets).
- Rotation research completed with Dr. Sorin Istrail on combinatorial algorithms for detecting genomic signatures of gene expression variation in GTEx dataset (manuscript submitted to RECOMB 2020).
- Teaching assistant for CSCI 2820: Advanced Algorithms in Medical Bioinformatics and Computational Biology (Spring 2019).

RESEARCH SUPPORT ASSOCIATE at Massachusetts Institute of Tech

May 2017 – August 2018 | Cambridge, MA

- Investigated regulatory network remodeling in *E.coli* deletion strains in different environmental conditions, which involved bioinformatic analyses and wet lab experimentation. Published in Journal of Bacteriology.
- Contributed to an interactive data visualization pipeline in Python for RNA-seq differential expression analysis and a NoSQL database of RNA-seq and Ribo-Seq data.

RESEARCH ASSISTANT at Olin College Huang Microbiology Lab

January 2016 – May 2017 | Needham, MA

- Conducted bacterial community network analyses, metagenomic analyses, Lotka-Volterra based mathematical modelling for perturbation experiments on environmental bacterial communities, in collaboration with Woods Hole Marine Biological Laboratories. Presented at 2016 NEMPET Conference.

ENGINEERING CAPSTONE at Daktari Diagnostics

Jan 2016 – Oct 2016 | Cambridge, MA

- Worked as technical lead to implement a bioimaging system for a low-cost sickle cell diagnostic test, using computer vision tools in Python.

RESEARCH ASSISTANT at Olin Crowdsourcing & Machine Learning Lab

May 2015 – Aug 2015 | Needham, MA

- Implemented software features for aiding visually impaired users with navigation. In collaboration with Bose Corporation, designed and conducted user interviews to get feedback on the features implemented. Invited talk at Closing the Gap Conference, 2015.