AYSE BERCESTE DINCER

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EDUCATION

University of Washington, Seattle, WA — Expected June 2022
Ph.D. in Computer Science
- GPA: 3.89/4.00
- Thesis: Developing machine learning techniques for solving biomedical problems

University of Washington, Seattle, WA — 2019
M.S. in Computer Science
- GPA: 3.87/4.00 (Accepted with Anne Dinning-Michael Wolf Endowed First-Year Fellowship)
- Highlighted Coursework: Machine Learning, Statistical Methods in CS, Computational Biology, Data Visualization

Bilkent University, Ankara, Turkey — 2017
B.S. in Computer Engineering
- GPA: 4.00/4.00
- Ranked 1^{st} in School of Engineering
- Accepted with Comprehensive Fellowship

RESEARCH EXPERIENCE

Research Assistant — 2021 – Present
Noble Lab, University of Washington, Seattle, WA
- Advised by Prof. William Stafford Noble
- Developed deep learning models by incorporating biological hypotheses into the prediction tasks
- Focused on developing deep learning models for denoising data and built transfer learning pipelines
- Led multidisciplinary collaborations to facilitate model application

Research Assistant — 2017 – 2020
AIMS Lab, University of Washington, Seattle, WA
- Advised by Prof. Su-In Lee
- Built unsupervised deep learning models for representation learning of high-dimensional biological data
- Incorporated explainable AI techniques to machine learning pipelines to draw generalizable insights
- Mentored junior graduate students and actively engaged in multidisciplinary collaborations

Undergraduate Researcher — 2016
Bioinformatics and Computational Genomics Group, Bilkent University, Ankara, Turkey
- Advised by Prof. Can Alkan
- Developed sequence alignment algorithms for variant detection in DNA

PROJECTS

A deep learning approach to denoising protein quantification measurements — 2021 – Present
- Developed a convolutional neural network model to eliminate quantitative bias from protein measurements
- Received best presentation award at ISMB/ECCB CompMS 2021 | Contributed talks at MLCB & ASMS 2021

An integrative method for learning interpretable communities of biological pathways — 2020
- Developed an integrative web tool using community detection algorithms to reconcile 4,847 biological pathways

Adversarial Deconfounding Autoencoder for learning robust embeddings — 2019 – 2020
- Developed an unsupervised deep learning approach for learning deconfounded embeddings
- Improved cancer subtype classification across different data domains
- Published in Proceedings of ECCB 2020 | Contributed talk at ISMB MLCSB 2020

DeepProfile: Interpretable deep learning of latent variables for 18 human cancers — 2018 – 2020
- Increased the robustness of variational autoencoders (VAEs) by designing an ensemble learning pipeline
- Collected and integrated gene expression measurements from 1,098 datasets and 18 cancer types
- Implemented regression models to predict patient survival and drug response

Explorator: Personalized travel plan recommender — 2016 – 2017
- Designed and implemented a mobile application for generating personalized optimal travel plans
- Created a recommendation system by collecting and integrating data from different social media platforms
- Received Sibel Ozelci Best Senior Design Project Award at Bilkent University CS Fair 2017

Publications and Conference Presentations

- **Dincer, A. B.**, Lu, Y. Y., & Noble, W. S. (2021). Inferring peptide coefficients from quantitative mass spectrometry data. *American Society for Mass Spectrometry (ASMS).*
- Qiu, W. Chen, H., **Dincer, A. B.**, Lundberg, S., Kaeberlein, M. & Lee, S. I. (2021). Interpretable machine learning prediction of all-cause mortality. *medRxiv* 2021.01.20.21250135.
- **Dincer, A. B.**, Janizek, J. D., & Lee, S. I. (2020). Adversarial Deconfounding Autoencoder for learning robust gene expression embeddings. *Bioinformatics*, 36(Supplement 2), i573–i582.
- Weinberger, E., **Dincer, A. B.** & Lee, S. I. (2020). HD-MD: Batch-effect-free embeddings of scRNA-seq data. *Machine Learning in Computational Biology (MLCB).*
- **Dincer, A. B.**, Janizek J. D., Celik, S., Hiranuma, N., Naxerova, K. & Lee, S. I. (2019). DeepProfile: Interpretable deep learning of latent variables from a compendium of expression profiles for 18 human cancers. *Machine Learning in Computational Biology (MLCB).*
- Janizek J. D., **Dincer, A. B**., Lundberg, S., Naxerova, K. & Lee, S. I. (2019). EXPRESS: Explainable prediction of anti-cancer drug synergy. *International Conference on Machine Learning (ICML) Workshop on Computational Biology.*
- **Dincer, A. B.**, Celik, S., Hiranuma, N., & Lee, S. I. (2018). DeepProfile: Deep learning of cancer molecular profiles for precision medicine. *Joint International Conference on Machine Learning (ICML) and International Joint Conferences on Artificial Intelligence (IJCAI) Workshop on Computational Biology.*

Teaching Experience

Teaching Assistant — Winter 2021
University of Washington, Seattle, WA
- Computational Genomics (CSE 529)

Teaching Assistant — Autumn 2021
University of Washington, Seattle, WA
- Machine Learning (CSE 446/546)

Teaching Assistant — Spring 2021
University of Washington, Seattle, WA
- Machine Learning for Big Data (CSE 547)

Teaching Assistant — Autumn 2020
University of Washington, Seattle, WA
- Computational Biology (CSE 527)

Teaching Assistant — Autumn 2019
University of Washington, Seattle, WA
- Computational Biology (CSE 527)

Undergraduate Tutor — Autumn 2016
Bilkent University, Ankara, Turkey
- Introduction to Programming for Engineers (CS 114)

Undergraduate Internship Experience

Software Engineering Intern — Summer 2016
SRDC (Software Research & Development Consultancy), Ankara, Turkey
- Collected data from medical devices and developed a mobile application for medical data monitoring

Software Engineering Intern — Summer 2015
TUBITAK Software Technologies Research Institute, Ankara, Turkey
- Developed mobile applications for tracking and tracing medical devices and cosmetic products

Software Engineering Intern — Summer 2014
TUBITAK Software Technologies Research Institute, Ankara, Turkey
- Studied web design using WordPress
- Explored software management activities focused on Agile Project Management and Test-Driven Development

Contributed Talks

- Machine Learning for Computational Biology (MLCB) 2021, “Inferring peptide coefficients from quantitative mass spectrometry data with deep learning.”
- American Society for Mass Spectrometry (ASMS) 2021, “Inferring peptide coefficients from quantitative mass spectrometry data.”
- International Conference on Intelligent Systems for Molecular Biology / European Conference on Computational Biology (ISMB/ECCB) Computational Mass Spectrometry (CompMS) 2021, “Inferring peptide coefficients from quantitative mass spectrometry data.”
- University of Washington Computational Molecular Biology (CMB) Program Virtual Retreat 2020, “Deep profiling of a compendium of expression data from 18 human cancers.”
- European Conference on Computational Biology (ECCB) 2020, “Adversarial Deconfounding Autoencoder for learning robust gene expression embeddings.”
- International Conference on Intelligent Systems for Molecular Biology (ISMB) Machine Learning in Computational and Systems Biology (MLCSB) 2020, “Adversarial Deconfounding Autoencoder for learning robust gene expression embeddings.”

TECHNICAL SKILLS

Languages: Python (proficient), Java, R, MATLAB, C/C++, HTML/CSS, SQL
Developer Tools: Jupyter Notebooks, Git, Android Studio, IntelliJ
Packages: NumPy, Pandas, Keras, TensorFlow, Scikit-learn, Matplotlib, Seaborn, SciPy, PyTorch, Statsmodels, PySpark