

# Ayse Berceste Dincer

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## EDUCATION

### University of Washington

*Ph.D. in Computer Science*

Seattle, WA

*Expected 2022*

### University of Washington

*M.S. in Computer Science*

Seattle, WA

*2019*

- GPA: 3.87/4.00
- Anne Dinning-Michael Wolf Endowed First-Year Fellowship
- Highlighted Coursework: Machine Learning, Statistical Methods in CS, Computational Biology, Data Visualization

### Bilkent University

*B.S. in Computer Engineering*

Ankara, Turkey

*2017*

- GPA: 4.00/4.00 (Class and Faculty Rank: 1st)
- Comprehensive Fellowship (4 years)

## RESEARCH EXPERIENCE

### Research Assistant

*AIMS Lab, University of Washington*

2017 – Present

*Seattle, WA*

- Advised by Prof. Su-In Lee
- Developed and applied machine learning techniques to solve biological problems with a focus on cancer and Alzheimer's disease

### Undergraduate Researcher

*Bioinformatics and Computational Genomics Group, Bilkent University*

Autumn 2016

*Ankara, Turkey*

- Advised by Prof. Can Alkan
- Developed algorithms for structural variant detection in human DNA

## UNDERGRADUATE INTERNSHIP EXPERIENCE

### Summer Intern

*SRDC (Software Research & Development Consultancy)*

Summer 2016

*Ankara, Turkey*

- Collected data from medical devices and developed a mobile application for medical data monitoring

### Summer Intern

*TÜBİTAK Software Technologies Research Institute*

Summer 2015

*Ankara, Turkey*

- Developed mobile applications for tracking and tracing medical devices and cosmetic products

### Summer Intern

*TÜBİTAK Software Technologies Research Institute*

Summer 2014

*Ankara, Turkey*

- Studied web design using WordPress
- Explored software management activities focused on Agile Project Management and Test-Driven Development

### Summer Intern

*Akgün (Medical) Software Inc.*

Summer 2014

*Ankara, Turkey*

- Studied automated testing

## PROJECTS

### Deep learning of interpretable modules for Alzheimer's disease

2020 – Present

- Collaborated with Prof. Sara Mostafavi from the University of Washington
- Developed a framework for learning interpretable and deconfounded expression embeddings for the aging human brain
- Investigated the associations between transcriptomic heterogeneity and Alzheimer's disease neuropathology

### An integrative method for learning interpretable communities of biological pathways

2020 – Present

- Collaborated with Nicasia Beebe-Wang from the University of Washington
- Developed an integrative web tool using community detection algorithms to reconcile biological pathways from different databases by revealing informative groups with distinct biological functions

## Adversarial Deconfounding Autoencoder for learning robust gene expression embeddings 2019 – 2020

- Developed a novel unsupervised deep learning approach for learning deconfounded embeddings
- Published in Proceedings of ECCB 2020 | Contributed Talk at ISMB MLCSB 2020

## DeepProfile: Interpretable deep learning of latent variables for 18 human cancers 2018 – Present

- Collaborated with Prof. Kamila Naxerova from Massachusetts General Hospital, Center for Systems Biology
- Developed an interpretable deep learning framework for learning gene expression embeddings
- Investigated the molecular mechanisms behind patient-level heterogeneity for 18 cancer types
- Highlighted as a spotlight talk at MLCB 2019 | ICML CompBio Workshop 2018

## Explorator: Undergraduate Senior Design Project 2016 – 2017

- Developed a platform to generate personalized travel plans by collecting data from social media platforms
- Received Sibel Özelçi Best Senior Design Project Award

## PUBLICATIONS AND PREPRINTS

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- **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) Conference*.
- **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) Conference*.
- **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. *International Conference on Machine Learning (ICML) Workshop on Computational Biology*.
- 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

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### Teaching Assistant Autumn 2020

University of Washington

Seattle, WA

- Computational Biology (CSE527)

### Teaching Assistant Autumn 2019

University of Washington

Seattle, WA

- Computational Biology (CSE527)

### Undergraduate Tutor and Grader Autumn 2016

Bilkent University

Ankara, Turkey

- Introduction to Programming for Engineers (CS114)

## CONTRIBUTED TALKS

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- 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

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**Languages:** Python, Java, R, MATLAB, C/C++, HTML/CSS, SQL

**Developer Tools:** Jupyter Notebooks, Git, Android Studio, PyCharm, IntelliJ, Eclipse, Visual Paradigm

**Packages:** NumPy, Pandas, Scikit-learn, SciPy, Keras/TensorFlow, Statsmodels, Matplotlib