

Hakime Öztürk

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 [hkmztrk](#)  [scholar](#)

RESEARCH INTERESTS Computational and functional genomics, cheminformatics, machine learning (ML), deep learning (DL), natural language processing (NLP)

PROFESSIONAL EXPERIENCE

Postdoctoral researcher

German Cancer Research Center (DKFZ), Heidelberg, Germany Dec 2019 – today
[Computational Genomics and System Genetics](#), (Supervisor: Prof. Oliver Stegle)

- Designed and implemented a deep learning based model that integrates multi-modal data such as whole-genome/exome sequencing (WGS/WXS) variant annotations and transcriptomics (RNA-seq) using contrastive learning to derive insights into patient representations in cancer research.
- Developed XGBoost and Convolutional Neural Network (CNN) based methodologies to decode the genomic sequence grammar involved in TAD (Topologically Associating Domain) boundary formation, proficiently utilizing Hi-C, DNase-seq, and ChIP-seq data.
- Contributed to the development and analysis of a set neural network based, novel and flexible deep learning based strategy to conduct rare variant association testing (RVAT) on UK-Biobank.
- Supervised a MSc and a PhD student, each for a three-month internship, on applied ML in genomics.

Instructor, DKFZ & Universität Heidelberg, Germany

2020 – 2023

- Served as a lecturer in "Computational Single-cell and Multi-omics" courses organized by our group since 2020. Prepared and conducted the corresponding workshop on 10X Genomics scRNA-seq data.

Graduate student researcher, Boğaziçi University, Turkey

2012 – 2019

Department of Computer Engineering

- Developed multiple NLP inspired ML/DL models for predicting drug-target binding affinity, notably DeepDTA, one of the first sequence-based CNN-based DL models tailored for this specific task.
- Collaborated with researchers from diverse research fields, resulting in the publication of two works in biomedical NLP, and one focused on biological networks in the context of breast cancer.
- Supervised more than six undergraduates in their senior theses on cheminformatics.

Teaching Assistant, Dept. of Computer Eng., Boğaziçi University, Turkey

2018 – 2019

- Prepared and conducted lab courses for "Introduction to Programming (C)" and "Introduction to Programming (R)".

Data Analyst, Boğaziçi University Technology Transfer Office (TTO), Turkey

2016 – 2018

- Generated university ranking and scientific impact reports through automatized data collection and analysis using Python.

EDUCATION

Ph.D., Computer Engineering | Cheminformatics, Boğaziçi University, Turkey

2014 – 2019

Thesis: [Text-based Machine Learning Methodologies for Modelling Drug-Target Interactions](#)

M.S., Computer Engineering | Cheminformatics, Boğaziçi University, Turkey

2012 – 2014

Thesis: [Analysing Drug Targets Using Ligand Similarity](#)

B.S., Computer Engineering, Dokuz Eylül University, Turkey

2008 – 2012

SKILLS

- Proficient in Python (10+ years), R (5 years) with solid experience in Unix/Linux environments.

- Skilled in machine/deep learning frameworks such as PyTorch, PyTorch Lightning, Keras, and XGBoost with an experience in multi-GPU computing.
- Advanced experience in high-performance computing (HPC) environments (e.g LSF) and bioinformatic workflow management tools (e.g. Snakemake).
- Fluent in development environments and version control systems including Jupyter, RStudio, VS-Code, and Git.
- Proficient in applying cutting-edge data science techniques to tackle computational genomics and cheminformatics challenges. Well-versed in handling diverse data types, including WXS/WGS, transcriptome (RNA-seq, scRNA-seq), and regulatory genomics (ChIP-seq, DNase-seq, Hi-C, methylation).
- Effective communicator skilled at fostering collaboration among researchers with diverse backgrounds.

SELECTED PUBLICATIONS

- [1] Clarke, B., Holtkamp, E., **H. Öztürk**, M. Muck, M. Wahlberg, K. Meyer, F. Munzlinger, F. Brechtmann, F. R. Holzwimmer, J. Gagneur and O. Stegle. Integration of variant annotations using deep set networks boosts rare variant association genetics. (*under review, Nature Genetics*), 2023
- [2] Özcelik, R., **H. Öztürk**, A. Özgür and E. Ozkirimli. ChemBoost: A chemical language based approach for protein-ligand interaction prediction *Molecular Informatics*, 2021
- [3] **Öztürk, H.**, A. Özgür, P. Schwaller, T. Laino and E. Ozkirimli. Exploring Chemical Space using Natural Language Processing Methodologies for Drug Discovery. *Drug Discovery Today*, 2020
- [4] **Öztürk, H.**, A. Özgür, and E. Ozkirimli. DeepDTA: Deep Drug-Target Binding Affinity Prediction. *Bioinformatics*, 2018
- [5] **Öztürk, H.**, A. Özgür, and E. Ozkirimli. A novel methodology on distributed representations of proteins using their interacting ligands. *Bioinformatics*, 2018
- [6] Cilek, E. E., **H. Öztürk**, and B. G. Dedeoglu. Construction of miRNA-miRNA networks revealing the complexity of miRNA-mediated mechanisms in trastuzumab treated breast cancer cell lines. *PloS one*, 2017

SELECTED TALKS

- **Variant impact based patient similarity networks for cancer subtype analysis** 31st Conference on Intelligent Systems for Molecular Biology and the 22nd European Conference on Computational Biology (ISMB/ECCB), 2023, France.
- **Genomic Language Models** Heidelberg Life Science Lab, 2021, Germany.
- **WideDTA: prediction of drug-target binding affinity** 27th Conference on Intelligent Systems for Molecular Biology and the 18th European Conference on Computational Biology (ISMB/ECCB), 2019, Switzerland.
- **A Hitchhikers' Guide to Drug Discovery** Gebze Teknik University, 2019, Turkey.
- **DeepDTA: Deep Drug-Target Binding Affinity Prediction** 17th European Conference on Computational Biology (ECCB), 2018, Greece.
- **A novel methodology on distributed representations of proteins using their interacting ligands** 26th Conference on Intelligent Systems for Molecular Biology (ISMB), 2018, USA.

AWARDS & VOLUNTEER ACTIVITIES

- Selected as Georg Forster Fellow by Alexander von Humboldt Stiftung in 2020. (Declined due to another funding.)
- Received the Best Doctoral Dissertation Award by Bogazici University in 2020.
- Mentored a female STEM student during her transition from MSc to PhD through [moveMINT in Hochschule Mannheim](#).
- Served as a voluntary mentor to more than 15 female mentees in numerous [DjangoGirls](#) workshops.
- Served as a reviewer for journals including: Nature Communications Biology, Nature Communications Chemistry, Bioinformatics, BMC Bioinformatics, Briefings in Bioinformatics, Journal of Chemical Information and Modeling and more, as well as international conferences such as ISMB.