

# Ahmet Arda Ceylan

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🎓 [Google Scholar](https://scholar.google.com/citations?user=...)

## Education

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### Bilkent University

M.Sc. of Computer Science

September 2024 - Present

Ankara, Turkey

- **Relevant Coursework:** Deep Learning, Neural Networks, Generative Networks, Bioinformatics
- **Advisor:** Assoc. Prof. Ercument Cicek

### Bilkent University

B.Sc. of Computer Science

September 2020 - July 2024

Ankara, Turkey

- **Relevant Coursework:** Data Structures and Algorithms, Machine Learning, Genomics, Data Privacy

## Publications & Preprints

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### LYCEUM: Learning to Call Copy Number Variants on Low Coverage Ancient Genomes

Mehmet Alper Yilmaz †, **Ahmet Arda Ceylan** †, Gun Kaynar, A. Ercument Cicek

Bioinformatics, Volume 41, Issue Supplement 1, Pages 285–293 (2025) · doi.org/10.1093/bioinformatics/btaf244

Accepted to ISMB-ECCB 2025 (Liverpool)

LYCEUM is a machine learning framework designed to accurately call copy number variants (CNVs) in ancient genomes sequenced at low coverage. By leveraging signal properties specific to degraded DNA and integrating coverage-aware learning strategies, LYCEUM significantly improves CNV detection performance, enabling more reliable genomic analysis in ancient DNA research.

### ExactCN: Learning to Estimate Exact Copy Number on Whole-Exome Sequencing Data

Erfan FarhangKia †, **Ahmet Arda Ceylan** †, Mert Gençtürk, Mehmet Alper Yilmaz, Furkan Karademir, and A. Ercument Cicek

Under Review at ISMB 2026 · bioRxiv preprint

A deep learning framework for precise integer copy-number estimation from WES data, combining convolutional layers for local read-depth feature extraction with transformer encoders to capture genomic context and reduce WES biases. Achieved substantial performance improvement over state-of-the-art CNV callers (RMSE reduced from 0.310 to 0.079).

### CHALLENGER: Detecting CNVs in Challenging Genes from Whole-Genome Sequencing

Mehmet Alper Yilmaz, **Ahmet Arda Ceylan**, and A. Ercument Cicek

· bioRxiv preprint

A masked-language-modeling-based system for detecting CNVs in difficult genomic regions using short-read WGS depth signals. Enabled short-read-based CNV models to recover variant signatures that traditionally require long-read sequencing, improving detection in highly duplicated genes such as SMN1/SMN2, AMY1/2, and NPY4R.

## Research Projects

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### Beacon Defense Mechanism

Implemented reward functions, evaluation pipelines, and visualization tools.

A reinforcement-learning-based strategy for dynamically protecting genomic privacy in Beacon-sharing platforms. Designed to defend against membership inference attacks by training PPO agents that adapt decisions to distinguish legitimate users from adversaries. (Genome Biology, <https://link.springer.com/article/10.1186/s13059-025-03871-5>)

### Read Depth Bert: Foundation Model for Read Depth Signals

Solely responsible for model design, implementation, training, and evaluation.

A BERT-based foundation model for reconstructing whole-genome sequencing (WGS) read-depth signals and learning meaningful representations. Enables downstream tasks such as CNV calling, read-depth simulation, and copy-number-variation simulation.

### MediXAI: Explainable AI for Mammography

Contributed to model evaluation and explainability implementation.

An application for automating mammography assessments using explainable ML models to support collaborative diagnosis between clinicians and AI. Achieved 88% accuracy and 62% F1 score using attention mechanisms and Grad-CAM for interpretability.

### DocsAsPR: Automated Technical Documentation Update from Pull Requests

Contributed to the framework development, multi-agent system design, and evaluation pipeline.

Proposed an automated documentation framework using LLM agents and retrieve-then-rerank pipelines on PRs. Achieved 0.68 MRR and 57% Precision@1 on Jest and HuggingFace, significantly outperforming baselines.

### Turkish Diabetes Database CNV Analysis

Contributed to data preprocessing and variant calling pipeline implementation.

Conducted CNV analysis on genomic data from 863 Turkish diabetes patients and matched controls using ECOLE, identifying structural variants and biomarkers associated with disease susceptibility and progression.

## Anatolian Ancient Genomes CNV Analysis

Contributed to variant calling pipeline implementation using LYCEUM.

Performed CNV analysis on nearly 60 low-coverage ancient genomes spanning the Neolithic to Bronze Age from Anatolian archaeological sites. Utilized the LYCEUM deep learning framework to detect CNVs despite severe DNA degradation and low coverage.

## NIH RhCMV/SIV Vaccine Analysis

Responsible from preprocessing, feature selection, interpretability modeling, and visualization.

Analyzed RNA sequencing data from 123 rhesus macaques to identify biomarkers associated with protection against RhCMV/SIV vaccines. Applied interpretable ML under supervision of Prof. Jan Komorowski to uncover time-series gene-expression signatures and regulatory networks.

## Teaching Experience

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### Bilkent University

Ankara, Türkiye

Teaching Assistant - **CS464** Introduction to Machine Learning

Spring 2025

Teaching Assistant - **CS201** Introduction to Data Structures and Algorithm Analysis

Fall 2025

Teaching Assistant - **CS319** Object Oriented Software Engineering

Fall 2024

Teaching Assistant - **CS101** Algorithms and Programming I

Fall 2024

## Academic Service

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Research in Computational Molecular Biology (**RECOMB**) Conference

Reviewer, 2025,2026

UCLA Computational Genomics Summer Institute (**CGSI**)

Paper Presenter, 2025

Google DeepMind MenaML (**MenaML**)

Poster Presenter, 2025

Research in Computational Molecular Biology (**RECOMB**) Conference

Volunteer, 2023

## Honors & Awards

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**TUBITAK BiGG Seal of Excellence** (Scientific and Technological Research Council of Türkiye)

2025

Awarded \$20k funding for Remind, an AI-based project proposal for mitigating cognitive decline.

**Outstanding Teaching Assistant Award**

2025

Selected as the "Outstanding Teaching Assistant" among 110 assistants at Bilkent University CS Department.

## Experiences

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### Cicek Lab, Bilkent University

Jan 2024 – Present

Research Assistant

Ankara, Türkiye

- Worked on transformer-based models for CNV calling on noisy genomic signals. Developed reinforcement-learning-based defense mechanisms for genomic data beacons.

### Komorowski Lab, Uppsala University

Jul 2023 – Nov 2023

Research Assistant

Uppsala, Sweden

- Conducted interpretable ML research on RNA-seq data related to SIV vaccine studies under Prof. Jan Komorowski. Identified candidate biomarker networks associated with vaccine protection.

### Synthetic Biology Research, Bilkent University

Jan 2023 – Jul 2023

iGEM Team Member

Ankara, Türkiye

- Worked on SMA therapeutic strategies by enhancing SMN1 expression via transfection of self-amplified transcripts into neurons under Assoc. Prof. Urartu Şeker.

### InfoDif Technology

Jun 2022 – Sep 2022

Summer Intern – Machine Learning Research

Ankara, Türkiye

- Implemented ML and computer vision algorithms for defense-related applications.

### Kolaysoft Technology

Jul 2021 – Sep 2021

Summer Intern – Software Developer

Ankara, Türkiye

- Developed backend components for web applications using Java Spring Boot.

## Skills

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**Computer:** C++, C (Pthread), Java, Python, Spring Boot, React/React Native, MySQL, Assembly, Algorithms & Complexity Analysis, SystemVerilog, TensorFlow, NumPy, PyTorch, Lex, Yacc, gnomAD, Galaxy, Ensembl

**Languages:** Turkish (Native), English (Fluent, IELTS 7.5/9.0), German (Introductory)