





# Ozan Göçmen

 **Work :** Ege University, Bioengineering Department , 35100, Izmir, Türkiye

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**Date of birth:** 05/02/2000 **Nationality:** Turkish

## ABOUT ME

Single cell sequencing lover :) , my predominantly interests include developing a bioinformatics pipeline for immunotherapy applications on the cancer treatment. I have dynamic knowledge in the fields of bioengineering and biotechnology, strong interdisciplinary communication, problem solving skills, and ethical values as a part of team leading scientific developments. I am growing to be an expert who can generate ideas and work from the perspective of data science and machine learning benefits for bioengineering. So, my adventure continues by learning the horizon that bioinformatics provides to bioengineers. I am highly suitable for remote working on projects.

## EDUCATION AND TRAINING

[ 06/2024 – Current ]

### Master's Student of Bioengineering/Biotechnology

**Ege University Graduate School of Natural and Applied Sciences** <https://ebp.ege.edu.tr/DereceProgramlari/Detay/2/60456/4702/932001>

**City:** Izmir | **Country:** Türkiye | **Field(s) of study:** Bioengineering ; Biotechnology | **Level in EQF:** EQF level 7

[ 16/08/2019 – 2024 ]

### Department of Bioengineering

**Ege University** <https://biyomuhendislik.ege.edu.tr/eng-/Homepage.html>

**Address:** Ege University, 35100, Izmir, Türkiye | **Field(s) of study:** Bioengineering | **Level in EQF:** EQF level 6

## WORK EXPERIENCE

[ 01/03/2022 – 01/06/2024 ]

### Intern Researcher

**Ege University Department of Bioengineering** <https://www.linkedin.com/company/bmglab/>

**City:** Izmir | **Country:** Türkiye

#### Bioinformatics and Molecular Genetics Laboratory

As an intern researcher in Dr. Yasin Kaymaz's candidate antigen enrichment project, I worked on integrating scRNAseq data for CAR T cell therapy against non-small cell lung cancer. I downloaded and analyzed publicly available scRNAseq data using Seurat and Scanpy. We developed a target enrichment scheme that integrates, filters, normalizes, and prepares data for differential gene expression analysis. This robust pipeline, managed with Snakemake, uses HierFIT for hierarchical classification of tumor and normal cell types.

1. Programming Languages(R, Python and Bash Scripting)
2. Biological Data Analysis
3. Next-Generation Sequencing
4. Single-cell RNA Sequencing

[ 09/2023 – 12/2023 ]

### Bioinformatics Trainee

**Ege University Faculty of Medicine** [https://med.ege.edu.tr/files/med/icerik/id\\_22939\\_doc\\_dr\\_ayse\\_caner.pdf](https://med.ege.edu.tr/files/med/icerik/id_22939_doc_dr_ayse_caner.pdf)

**City:** Izmir | **Country:** Türkiye

#### Cancer Biology and Immunology Department

As a trainee of Cancer Biology and Immunology Department, I overcame bioinformatics challenges in the search for circularRNA molecules that could be biomarkers in Head & Neck squamous cell carcinoma. I sequenced the RNAs collected from carcinoma tissues with Oxford Nanopore Technologies devices that allow long reads. By developing bioinformatic algorithms, I quantified the data and detected circRNAs that could be biomarkers by collapsing their isoforms.

- Nanopore Sequencing
- circularRNA's
- NGS

[ 07/2023 – 09/2023 ]

### Research Intern

**City:** Izmir | **Country:** Türkiye

**Links:** <http://proton.tools.ibg.edu.tr:8001/new-run> | <https://www.notion.so/ozangocmen/PROT-ON-Tutorials-49a95ad303ea4d75b2757f492db84d8d>

### **Karaca Computational Structural Biology Laboratory**

As an intern of the Karaca Computational Structural Biology lab, I contributed to develop novel techniques and tools to rapidly build high-accuracy structural models and help overcome the bottleneck in structural biology. During my time in the lab, I was work on the use and development of the tool called Prot-ON in protein-protein, protein-nucleic acids, protein-ligand complexes. Also I integrated to AlphaFold protein complexes predictions and Prot-ON for efficient protein engineering and drug discovery efforts.

- AlphaFold
- PDB
- Docking
- PyMol
- HTML/CSS/Javascript

[ 01/2023 – 04/2023 ]

### **External Project Intern**

#### **Boehringer Ingelheim**

**City:** Remote | **Business or sector:** Human health and social work activities

#### **Computational Biology Department**

I worked on computational biology and bioinformatics methods development for reproducible science in single cell with Computational Biology community at Boehringer Ingelheim.

1. Programming Languages(R, Python and Bash Scripting)
2. High Performance Computing and Cloud Computing
3. Biological Data Analysis
  - a. Common Factor Analysis
  - b. Permutation Test
  - c. Weighted one sided T test
  - d. Bhattacharya Distance
  - e. Hierarchical Gaussian Regression model (ML approach)

[ 12/2022 – 04/2023 ]

### **Intern**

#### **Genfoquest Analytica Informatics**

**City:** Izmir | **Country:** Türkiye

Genfoquest Analytica Informatics is a data science initiative focused on bioinformatics. As a part of the bioinformatics team we developed algorithms, software, and user-friendly applications for analyzing various types of data in the fields of comparative genomics, transcriptomics, proteomics, pharmacogenomics, epigenetics, and molecular phylogenetics. I had the opportunity to take part as an intern in the joint project with Boehringer Ingelheim.

1. Software Development
2. Database Management (SQL)
3. Workflow Management Tools(Snakemake and Nextflow)
4. Biological Data Analysis(NGS, scRNA-seq, ATAC-seq, Spatial)

[ 06/2021 – 12/2021 ]

### **Core Team Member**

#### **Google Developer Students Club**

**City:** Izmir | **Country:** Türkiye

At the Ege University, I took a role as a GDSC core member to disseminate Google technologies on various topics such as artificial intelligence, machine learning, cloud computing, web3.0.

## **LANGUAGE SKILLS**

**Mother tongue(s):** Turkish

**Other language(s):**

**English**

**LISTENING C1 READING C1 WRITING C1**

**SPOKEN PRODUCTION C1 SPOKEN INTERACTION C1**

*Levels: A1 and A2: Basic user; B1 and B2: Independent user; C1 and C2: Proficient user*

## DIGITAL SKILLS

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### My Digital Skills

Python | R | Bash | Linux | SQL | Docker | Git | Tensorflow | PyMOL | Scikit-Learn |  
Scanpy | Pyro | PyTorch | SwissADME | PDB

## NETWORKS AND MEMBERSHIPS

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[ 04/2022 – Current ]

**Member** International Society for Computational Biology (ISCB)

## PROJECTS

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[ 09/2023 – 12/2023 ]

### Identification of Circular RNAs as Biomarkers in Head and Neck Cancer Cells and Investigation of the Effects of Radiotherapy on These Biomarkers

Head and neck squamous cell carcinomas (HNSCC) cause over 300,000 deaths annually. Early detection is crucial for effective treatment, necessitating reliable biomarkers. This project investigates circular RNAs (circRNAs) as potential biomarkers in HNSCC using SCC-15 carcinoma and hTERT-OME epithelial cell lines. Total RNA will be isolated, enriched for circRNAs, and analyzed via qRT-PCR and ONT to identify differentially expressed circRNAs and their post-radiotherapy expression levels.

[ 07/2023 – 09/2023 ]

### PROT-ON: A structure-based detection of designer PROTein interface MutatiONs

Mutation-induced changes in protein-protein interfaces often cause severe diseases, leading to the development of computational tools to predict their impact. FoldX and EvoEF1 are notable for their speed and accuracy. Building on these, we developed the PROT-ON framework to identify critical protein interface mutations for designing new protein binders.

[ 10/2022 – 04/2023 ]

### Development of methodological software to map cancer-specific T cell phases across multiple indications with single-cell RNA sequencing data

Our software product aims to profile cancer-specific T cell states in multiple indications. It will provide an accessible and analytical approach for processing single-cell transcriptomic sequencing data, including common factor analysis interpretations and unsupervised machine learning methods. The product, which is being developed in R&D, is intended for use in clinical studies for research purposes and will be integrated into common health practices for its potential social impact.

[ 03/2022 – 12/2022 ]

### Enrichment of Alternative Target Antigen Pool for CAR T cell therapy Against Non-Small Cell Lung Cancer with Single Cell Genomic Data

In this project, which was developed jointly with the medical faculty hospital, we applied the SeqWell single cell sequencing method to lung cancer tissues, which was performed for the first time in Turkey. At the bioinformatics part, we aimed to collect and reprocess public lung cancer single cell transcriptomic datasets also with our datasets which are over the 100 distinct dataset to identify the tumor-specific antigens for CAR T therapy in NSCLC.

## HONOURS AND AWARDS

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[ 20/03/2023 ]

**2209B - Industry Oriented Research Project Support Programme for Undergraduate Students**  
**Awarding institution:** THE SCIENTIFIC AND TECHNOLOGICAL RESEARCH COUNCIL OF TURKEY

The aim of the program is to provide undergraduate students studying at universities; to encourage research through industry-oriented projects. I am entitled to be supported with my "Development of methodological software to map cancer-specific T cell phases across multiple indications with single-cell RNA sequencing data" project.

[ 20/04/2022 ]

**2247C STAR - Intern Researcher Scholarship** **Awarding institution:** THE SCIENTIFIC AND TECHNOLOGICAL RESEARCH COUNCIL OF TURKEY

It is aimed to provide scholarship support for undergraduate students who take part in research projects carried out at TUBITAK Centers and Institutes or supported by TUBITAK. I worked as a researcher in Dr. Yasin Kaymaz's project "Enrichment of Alternative Target Antigen Pool for CAR T

cell therapy Against Non-Small Cell Lung Cancer with Single Cell Genomic Data" and was awarded this scholarship.

[ 09/2019 ] **Undergraduate Student Scholarship Awarding institution:** Republic of Turkey Ministry of Youth and Sports

CONFERENCES AND SEMINARS

[ 11/05/2024 – 12/05/2024 ] **9th National Bioengineering Conference** Izmir, TR

I presented my project, titled "cellstatemapp: Developing software to map cancer-specific immune cell dynamics across multiple indications with single cell RNA sequencing (scRNA-seq) data," at the prestigious 9th National Bioengineering Student Congress hosted by Ege University on May 11-12.

Link: <https://www.9biyomuhkongre.com/>

PUBLICATIONS

[ 2024 ] **[Development of methodological software to map cancer-specific T cell phases across multiple indications with single-cell RNA sequencing data](#)**  
**Reference:** Gocmen, O., Kocakaya, E., & Kaymaz, Y. (2024). 9th National Bioengineering Congress.