# Umut Berkay Altıntaş

E mail: umutberkayaltintas@gmail.com
Mobile: +905396439832

## Objective

Utilizing advanced computational techniques is an inevitable skill set for academia. I have been well trained analysing multiple biological assays from multiple biological databases such as GEO, SRA, ENA, ENCODE and TCGA. I acquired and developed many skill sets during processing biological data, such as data collection from various sources, and designing analytical solutions for given problems, further visualizing the data in a presentable setting. Furthermore, I adore how machines can learn the biological data and tell us what is unseen. However, I am always enthusiastic about artificial intelligence but ethical enough to not let them lead.

## Education

University of British Columbia — Vancouver, CANADA

*PhD Bioinformatics;* — Present

- Investigating the function of cis-regulatory element networks on gene transcription.

Koç University — Istanbul, TURKEY

*MSc Computational Sciences and Engineering; CGPA: 3.95 / 4.00 (98.75 / 100)* — 2022

- Examining the androgen receptor cis-regulatory element network in prostate cancer cells and their intrinsic potentials to discover individual regulatory element's role in the network.

Middle East Technical University — Ankara, TURKEY

*BSc Molecular Biology and Genetics; CGPA: 3.22 / 4.00 (80.5 / 100)* — 2019

- Developing a Python based program which searches for similar genomic patterns of genomes of specified microorganism groups on ancient DNA data to draw a conclusion about the microbiome of the sample.

## Experiences

Lack Lab (Koç University, KU) — Istanbul, TURKEY

*Master Student* — Feb. 2020 – Present

- Examining the androgen receptor cis-regulatory element network in prostate cancer cells and their intrinsic potentials to discover individual regulatory element's role in the network.

CompEvo Team (Middle East Technical University, METU) — Ankara, TURKEY

*Special Project Student* — Dec. 2016 – Jun. 2019

- Developing a Python based program which searches for similar genomic patterns of genomes of specified microorganism groups on ancient DNA data to draw a conclusion about the microbiome of the sample.

GeoGenetics (University of Copenhagen, KU) — Copenhagen, DENMARK

*Intern* Jun. 2018 – Aug. 2018

- Determining pathogenic microorganism species that cause zoonotic disease in Sierra Leone and Congo Democratic Republic by analyzing metagenomic data of small mammals.

Aydın-Son Research Group (Middle East Technical University, METU) Ankara, TURKEY

*Special Project Student* Oct. 2018 – Jun. 2019

- Comparing brain transcriptomes of human and chimpanzee to suggest positively selected genes for advanced thinking ability of humans, and case analysis on WGS data of a patient with a rare genetic disease to report candidate disease associated variations.

## Skills

***Programming:*** *Python, Julia, R, C++, Java*

***Bioinformatic tools / Utilities / Libraries:*** *Snakemake, Pandas, Numpy, Seaborn, Matplotlib, Scipy, Sklearn, Tensorflow, Pytorch, NetworkX, AWK, Parallel, FastQC, AdapterRemoval, Cutadapt, SAMTools, Bowtie1/2, BWA, BLAST, MACS2/3, DeepTools, BedTools, GenomicInteractions, BPNet, rtNEAT, MGMapper, Kraken 2, UCSF Chimera, Jmol, AutoDockTools, SNPnexus, PredictSNP, DAVID*

***Software / OS:*** *PyCharm, RStudio, IntelliJ, MS Office tools, Adobe Photoshop, MS Windows, Unix/GNU/Linux, macOS*

***Molecular Biology Lab:*** *RT-PCR, PCR, Spectrophotometry, Polyacrylamide gel electrophoresis, Agarose gel electrophoresis, Nucleic acid isolation from a cell, Restriction enzyme digestion, Bacterial transformation, Thin layer chromatography, Gel permeation chromatography, Titration methods*

## Languages

Turkish (Native)

English (Fluent)

German (Beginner)

French (Beginner)

## Certificates & Conferences

***Awards:*** Academic Excellence Award 2022 (Koç University)

***Certificate of English proficiency:*** IELTS Apr. 2022 ( 7 )

***Certificate of Roll of METU:*** High Honor; 2018 - 2019

***Articles:*** Huang, C.-C. F., Lingadahalli, S., Morova, T., Ozturan, D., Hu, E., Yu, I. P. L., Linder, S., Hoogstraat, M., Stelloo, S., Sar, F., van der Poel, H., **Altintas, U. B.**, Saffarzadeh, M., Le Bihan, S., McConeghy, B., Gokbayrak, B., Feng, F. Y., Gleave, M. E., Bergman, A. M., … Lack, N. A. (2021). Functional mapping of androgen receptor enhancer activity. Genome Biology, 22(1), 149. https://doi.org/10.1186/s13059-021-02339-6