TUNC MOROVA

✉ morovatunc@gmail.com
☎ +17788141190
📍 Vancouver, Canada
🐦 tuncmorova
🐙 mortunco

Skills

PROGRAMMING LANGUAGES:
Python, R
FRAMEWORKS: NumPy, Pandas,
Tidyverse, SQL
SOFT SKILLS: Project Management,
Problem solving, Leadership,
Collaboration, Dependability
DATA VISUALISATION: matplotlib,
seaborn, ggplot, Rshiny, Plotly
OTHER TECH SKILLS: Git, AWS,
CLI, VSCode, ML (Linear
Regression, Random Forest
Regression and Classification),
RstudioServer, Jupyter Lab, Slurm

Awards

President's Academic Excellence
Initiative PhD Award
· University of British Columbia
2020-2022

Faculty of Science Graduate Award ·
University of British Columbia
2019-2022

International Tuition Award ·
University of British Columbia
2019-2022

Shaun Kenneth Gauthier (Shaun G)
Scholarship in Cancer Research
· The Gauthier Family Endowment
2020

NSERC-CREATE Scholarship
2019

2016 Fall Semester Outstanding
Teaching Award
· Koc University
2017

TUBITAK (The Scientific and
Technological Research Council of
Turkey) Project Scholarship
· TUBITAK
2015-2018

References

Dr. Nathan Lack
Principle Investigator (Lack Laboratory)
Vancouver Prostate Centre
2660 Oak St, Vancouver, BC V6H 3Z6, Canada,
nlack@prostatecentre.com

Dr. Faraz Hach ·
Principle Investigator (Hach Laboratory)
Vancouver Prostate Centre
2660 Oak St, Vancouver, BC V6H 3Z6, Canada,
faraz.hach@ubc.ca

I am an enthusiastic graduate student with 7 years of field experience in bioinformatics and data science, with an excellent tract record of publications in high impact journals. With my data analysis and visualization skills, I can confidently unravel the mysteries of multi-dimensional datasets. I would like to pursue my career in the field of data science where I can utilize my computational, machine learning and statistical skills to understand the complex nature of big data sets.

Education

University of British Columbia
2019 to Current
PhD Bioinformatics
Joined Hach Laboratory to develop computational algorithms for cancer genomics. Developed streamlined variant calling and single cell analysis pipelines in Snakemake workflow environment. Became proficient in data visualisation, cleaning and wrangling with R (ggplot2/tidyverse) and Python (pandas/numpy/searborn/matplotlib). Wrote and contributed 9 peer-reviewed publications in prestigious journals. Mentored new PhD and Masters students.

Koc University
2015 to 2018
MSc Biomedical Science and Engineering 2018
Analyzed International Cancer Genome Consortium (2648 patients) whole genome sequence data to investigate androgen receptor binding site mutations. Utilized slurm, SGE and AWS instances for high performance computing. Developed analysis pipelines to perform analysis of CRISPR-screens, RNA-seq and ChIP-seq data sets. Became proficient in Unix Command line. Implemented computational analysis pipelines in Docker and Singularity containers for reproducibility.

Marmara University
2010 to 2015
BSc Bioengineering 2015

Employment

Collins Laboratory - Vancouver Prostate Centre
Visiting Scholar
Feb. 2022 to Aug. 2022
Led the analysis of prostate cancer xenograft based single cell dataset (>100,000 cells). Developed streamlined computational pipeline for filtration, marker selection and trajectory analysis to decipher prostate cancer plasticity in single cell resolution.

4Global
Intern
Aug. 2018 to Sept. 2018
Obtained hands on experience on SQL queries. Optimized the performance of 4Global database. Conducted code review and user interface testing.

Alkan Laboratory - Bilkent University
Ankara, Turkey
Visiting Scholar
Sept. 2017 to Jan. 2018
Conducted the first genome assembly of *Alburnus tarichi* using PacBio Long Reads

Epigenetix
Istanbul, Turkey
Intern
June 2015 to Sept. 2015
Analyzed microarray data sets with custom R scripts. Parted ways with graphical user interface and switched to Linux command line interface forever.

Publications

Optimized high-throughput screening of non-coding variants identified from genome-wide association studies
2022
Under revision in Nucleic Acids Research. First author. One of the three PhD thesis project publications which I led the experimental design, statistical analysis and wrote the manuscript with Dr. Lack. Developed novel computational method to reconstruct sequencing fragments to increase experimental accuracy.

Genetic determinants of chromatin reveal prostate cancer risk mediated by context-dependent gene regulation.
2022
Nature Genetics. Contributing second author in multi-national collaboration (Harvard/USA, UBC/CAN, NKI, NL). Using my previously published method, (NAR submission), I investigated prostate cancer risk-associated mutations. Analyzed and visualized results from 12 top candidates.

EPIKOL, a chromatin-focused CRISPR/Cas9-based screening platform, to identify cancer-specific epigenetic vulnerabilities
2022
Nature Cell death & Disease. Contributing second author. Side-project during PhD degree. Developed analysis methods for processing CRISPR/Cas9-based knockdown screens. Using my streamlined analysis pipeline >50 samples have been processed, analyzed and visualized.

Androgen Receptor-Mediated Transcription in Prostate Cancer
Cells. Co-first author to invitational review article. Covered the recent advancements in Androgen Receptor enhancer literature.

Functional mapping of androgen receptor enhancer activity.
2021
Genome Biology. Co-first author. Led the statistical and computational analysis of this work. Gathered existing public datasets and coordinated the collaboration of machine learning section. Conducted Random Forest Classification and Feature Importance analysis on 102 distinct genomic features to understand the grammar of Androgen Receptor enhancers.

Epigenetic-focused CRISPR/Cas9 screen identifies ASH2L as a regulator of glioblastoma cell survival
2022
Accepted Cell death and differentiation. Follow-up study that implemented my computational method from (EPIKOL publication).

Androgen receptor-binding sites are highly mutated in prostate cancer.
2020
Nature Communications. First author. Resulting publication of my MSc thesis. Interrogated whole genome sequencing data of 2048 patients from multiple for somatic mutations. Became proficient in fundamental data analysis and genomic skills.

Bromodomain inhibition of the coactivators CBP/EP300 facilitate cellular reprogramming
2019
Nature Chemical Biology. Contributing second author. Side-project during MSc degree. Processed and visualized tabular RNAseq and ChIPseq datasets (25,000-1,000,000 rows for each sample) in the published work.