

TUNC MOROVA

✉ morovatunc@gmail.com
☎ +17788141190
📍 Vancouver, Canada
🐼 mortunco

Education

University of British Columbia 2019 to Current
PhD Bioinformatics
Thesis title: Deciphering non-coding driver mutations in prostate cancer.

Koc University 2015 to 2018
MSc Biomedical Science and Engineering 2018
Thesis title: Androgen receptor binding sites are highly mutated in prostate cancer. GPA: 3.51

Marmara University 2010 to 2015
BSc Bioengineering 2015
GPA: 3.49

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, Jupyter Lab
MACHINE LEARNING: Linear Regression, Logistic Regression, Random Forest Classification and Regression

Awards

University of British Columbia
President's Academic Excellence Initiative PhD Award
2020-2022 - \$3000 CAD

University of British Columbia ·
Faculty of Science Graduate Award
2019-2022 - \$16,000 CAD

University of British Columbia ·
International Tuition Award
2019-2022 - \$15,000 CAD

The Gauthier Family Endowment ·
Shaun Kenneth Gauthier (Shaun G) Scholarship in Cancer Research
2020 - \$1,500 CAD

· NSERC-CREATE Scholarship
2019 - \$32,000 CAD

Koc University
2016 Fall Semester Outstanding Teaching Award
2017 - \$846 USD on Jan 2016

TUBITAK ·
TUBITAK (The Scientific and Technological Research Council of Turkey) Project Scholarship
2015-2018 - \$103,242 on Jan 2018

References

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

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

I am an enthusiastic graduate student with 7 years of field experience in bioinformatics and data science, with an excellent track 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.

Employment

University of British Columbia Vancouver, Canada
Research Assistant - Vancouver Prostate Centre 2019 to Current

- Joined Hach Laboratory to develop computational algorithms for cancer genomics.
- Developed scalable and streamlined pipelines to process various genomic data.
- Wrote and contributed 5 peer-reviewed publications in prestigious journals.
- Managed laboratory high performance cluster storage (~25 Tb).
- Created SOPs for data storage and submission.
- Mentored, trained and interviewed new PhD and Masters students.
- Organized laboratory social vents, "Lab-outs", which we experienced a new restaurant ever month.

Project #1: Characterization of Androgen Receptor enhancer regions:

- Built scalable computational analysis workflow (Snakemake) to process and summarize capture based STARRseq into tabular data format.
- Created the first functional map of AR enhancers using STARRseq experimental method under the supervision of Dr. Nathan A. Lack.
- Interrogated 96 genomic features using Random Forest Classifier to identify confounding factors that determine active enhancers in R.
- Published co-first author paper (Morova, Huang, Ozturan and Lingadahalli et al, 2021 - PMID: 33975627) in Genome Biology (Impact factor: 17.9).
- Participated international collaborators using the established the STARRSeq method in Lack Laboratory (Linder et al, 2022- PMID: 35754340).
- Summarized the recent advancements about prostate cancer enhancers in a review article (Ozturan and Morova et al, 2022 - PMID: 35269520).

Project #2: Development of snpSTARRseq to measure impact of non-coding variants on enhancer activity

- Designed novel variant-aware version of STARRseq method for functional characterization of the variants supervised by Dr. Nathan A. Lack.
- Developed analysis pipeline to reconstruct DNA sequences using Python language under the supervision of Dr. Faraz Hach.
- Deposited analysis code in (github.com/mortunco/snp-starrseq) with a quick tutorial.
- Performed quality control, hypothesis testing and visualization using R language to identify candidate variants.
- Led, wrote and first authored the manuscript of the project. Accepted for publication in Nucleic Acid Research (NAR).
- Using findings from snpSTARRseq, contributed to (Baca et al , 2022 - PMID: 36071171) published in Nature Genetics (impact factor: 41.38).

Project #3: Characterization of Androgen Receptor enhancer regions:

- Led and performed the analysis of prostate cancer based hyper-dimensional single cell dataset (32 time points, 23,000 genes and >100,000 cells).
- Built an efficient computational pipeline for filtration, marker selection and trajectory analysis to decipher prostate cancer plasticity in R (Seurat, - Monocle) and Python (Scanpy, PAGA, CellRank).

Koc University Istanbul, Turkey
Research Assistant 2015 to 2018

- Joined Lack Laboratory to characterize prostate cancer mutations.
- Learned core bioinformatics skills such as (data visualization and wrangling, command line interface, version control and etc)
- Took "Introduction to Python" and implemented sequencing alignment (Needleman–Wunsch algorithm) using dynamic programming.
- Took "Applied Machine Learning in Biology and Finance" course and benchmarked multiple algorithms on prostate cancer gene expression data.

Thesis Project: Androgen receptor binding sites are heavily mutated

- Analyzed International Cancer Genome Consortium (2648 patients) whole genome sequences to investigate androgen receptor binding mutations.
- Developed and optimized scalable mutation calling pipeline to process 64 Tb patient samples in Snakemake workflow framework.
- Embedded downstream analysis pipeline in Docker to share with collaborators. Deposited under (github.com/mortunco/project_dockerv2).
- Executed mutation calling pipeline in Slurm, Sun Grid Engine and AWS high performance computing instances.
- Wrote the resulting publication (Morova et al, 2020 - PMID: 32047165) in Nature Communications under the supervision of Dr. Nathan A. Lack.

Side Projects

- Analyzed CRISPR-based knockdown experiment to characterize essential epigenetic markers in stem cell and brain cancer research.
- Conducted data cleaning, hypothesis testing and visualization of a data table with >50 columns and 2400 rows in R language. Visualized findings in interactive dashboards using Plotly. (Yediyer-Bayram et al, 2022 - PMID: 35973998, Ozyerli-Goknar, 2022 - In print: Cell death and differentiation).
- Consulted analysis of various genomic assays RNAseq (Ebrahimi et al 2019, PMID - 30962627) and ChIPseq (Ozgun et al, 2021 - PMID: 34318896).

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

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.