Oleksandr NARYKOV

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PERSONAL STATEMENT

I am a 6th year PhD student with the focus on machine learning and statistics with application to the biological and medical data, commited to conducting solid and reproducible research. I experienced working with diverse datasets, from clinical studies including several dozens of patients to large-scale biological databases, such as TCGA and GTEx. My versatile technical skill set helps me to make full use of available data, which makes me a good fit for data scientist position.

SKILLS

Machine Learning
Supervised, Semi-Supervised
Deep Learning, Clustering
scikit-learn, TensorFlow
pyTorch, OpenCV

Data Analysis
Data Mining, Data visualization
Network Science
pandas, SQL, jupyter, Cytoscape
bokeh, seaborn, ggplot2

Bioinformatics & Comp Bio
RNA-Seq, Gene Expression Analysis
and Pathway Analysis, Proteomics
BioPython, Bioconductor, bcbio-nextgen
SMART-seq, Drop-seq, SomaScan

Dev-Ops
Docker, Linux, bash

High Performance Computing
Hadoop, pySpark, GROMACS, NAMD

Software Engineering
Python, C++, R, C, Java, git

WORK EXPERIENCE

MAY 2019 — now

WORCESTER POLYTECHNIC INSTITUTE (WPI)
Research Assistant

ALT-IN Tool - machine learning model for prediction of gene isoforms interactions. It leverages existing interactome data and includes *alternative splicing-specific* information. I handled machine learning-related tasks, a part of data extraction and case study analysis, including **RNA-Seq**, and produces deliverables publicly available on https://github.com/korkinlab/altintool and https://hub.docker.com/r/narykov/alt-in.

Molecular dynamics of SARS-CoV-2 envelope - collaborative effort on bringing together accuate stoichiometry, geometry, and structural information on SARS-CoV-2 envelope. My responsibilities include part of the structural modeling of membrane (M) protein and system integration, as well as performing molecular dynamics simulations on **Frontera supercomputer** (https://frontera-portal.tacc.utexas.edu/).

Alternative splicing impact factor - the goal of this project is to distill quantitative measure of impact that **alternative splicing** has on protein function. My responsibilities include formulating a **mathematical description** of this concept and building **visualizations** that help people to extract information based on aforementioned measure. **Transcriptomics data** for case studies is based on **RNA-Seq** data from GTEx and TCGA repositories.

Clinical trials on treatment of Gulf War Illness - I was responsible for identifying gene set that exhibit response to accupuncture treatment based on **proteomics data**. I employed a range of **statistical methods** and successfully identified relevant genes. This discovery was further supported by literature search. I also conducted a preliminary work on **biomarkers identification**. This work was done as a part of a joint grant application.

JUN 2018 — AUG 2018

TUFTS MEDICAL CENTER CTSI
Research Intern

During my work in TMC **Clinical and Translational Science Institute** (CTSI) I foucsed on **pathway analysis** and **gene regulatory network reconstruction** algorithms in the context of **multi-omics** data integration. I reviewed existing methods and approaches, built Docker environment which included Hadoop, pySpark, TensorFlow, Anaconda and tested several computational methods.

JUN 2013 — MAY 2015

SAMSUNG R&D CENTER, Kyiv
Research Engineer

Designing machine learning models for the wearable devices. My responsibilities consisted of **Machine Learning, Image segmentation, Statistics, Time Series Analysis** and **Signal Processing**.

EDUCATION

2015-Now | PHD IN COMPUTER SCIENCE
Worcester Polytechnic Institute
GPA: 3.91

2013-2015 | MASTER DEGREE IN COMPUTER SCIENCE
National Technical University of Ukraine "Kyiv Polytechnic Institute", Institute of Physics and Technology