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

Publications

O. Narykov, N. T. Johnson, D. Korkin "Predicting protein interaction network perturbation by alternative splicing with semi-supervised learning" *In revision in Cell Reports*

O. Narykov, S. Srinivasan, D. Korkin "Computational protein modeling and the next viral pandemic" *Bioinformatics*, 18, 444445 (2019) https://doi.org/10.1038/s41592-021-01144-0

S. Srinivasan, H. Cui, Z. Gao, M. Liu, S. Lu, W. Mkandawire, **O. Narykov**, M. Sun, D. Korkin "Structural Genomics of SARS-CoV-2 Indicates Evolutionary Conserved Functional Regions of Viral Proteins." *Viruses*, 12, 360. (2020) https://doi.org/10.3390/v12040360

O. Narykov, D. Bogatov, D. Korkin "DISPOT: A simple knowledge-based protein domain interaction statistical potential." *Bioinformatics*, 35, 53745378 (2019) https://doi.org/10.1093/bioinformatics/btz587

S. Choobdar, M.E. Ashen [et al, including **O. Narykov**] "Assessment of network module identification across complex diseases." *Nature Methods* 16, 843852 (2019) https://doi.org/10.1038/s41592-019-0509-5

Z. Gao, S. Lu, **O. Narykov**, S. Srinivasan, D. Korkin, Chapter 7 in Virus Bioinformatics (1st ed.) D. Frishman, M. Marz, (Eds.). (2021) *Chapman and Hall/CRC* https://doi.org/10.1201/9781003097679