

Oleksandr NARYKOV



Final year Ph.D. candidate specialized in developing machine learning methods and statistical approaches for biological and medical applications, with six years of research experience and two years of industry R&D experience.

CONTACT INFORMATION

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EDUCATION

2015-Now | **PH.D.** IN COMPUTER SCIENCE, *Worcester Polytechnic Institute*, GPA: 3.91/4.0
2013-2015 | **M.S.** IN COMPUTER SCIENCE, *National Technical University of Ukraine Kyiv Polytechnic Institute*
2009-2013 | **B.S.** IN COMPUTER SCIENCE, *National Technical University of Ukraine Kyiv Polytechnic Institute*

TECHNICAL SKILLS

Machine Learning Tools

scikit-learn, PyTorch, Weka
AWS SageMaker, Keras, OpenCV

Databases

mySQL, Oracle, MongoDB
Hadoop, Neo4j

Bioinformatics Tools

Bioconductor, bcbio-nextgen, GSEA
Modeller, Chimera, Cytoscape

Dev-Ops

Docker, Linux, bash

High-Performance Computing

Hadoop, MPI, SLURM

Software Engineering

Python, C++, R, C#, Java, git, googletest, unittest

Web Technologies

C#, JavaScript, HTML

Biological Databases

TCGA, NCBI, GTEx, KEGG

Statistical Tools

scipy, statsmodels, PyMC3, R Stats

RESEARCH AND TEACHING EXPERIENCE

MAY 2019
now

WORCESTER POLYTECHNIC INSTITUTE (WPI)

Research Assistant

Developed **Machine Learning** models for the biological data (**RNA-Seq**, **protein interactomes**, **protein structures**, **clinical trials**). My responsibilities include mentoring bachelor students.

- Developed a **machine learning** models for the prediction of gene isoforms interactions for **ALT-IN Tool** project. These model leverage existing interactome data and include **alternative splicing**-specific information. I handled machine learning-related tasks, a part of data extraction and case study analysis, including **RNA-Seq**, and produced deliverables publicly available on <https://github.com/korkinlab/altintool> and <https://hub.docker.com/r/narykov/alt-in>.
- Identified **biomarkers** that predicts response to the treatment in **Clinical trials on Gulf War Illness treatment** based on **SomaScan** proteomics data, evaluated different intra- and interplate normalization strategies, employed a range of **statistical methods** to validate results.
- Led collaborative efforts of WPI team on **molecular dynamics of SARS-CoV-2 envelope** project. Completed a part of the structural modeling of the membrane (M) protein and system integration, performed **molecular dynamics simulations** on **Frontera supercomputer** (<https://frontera-portal.tacc.utexas.edu/>).
- Developed a **computational model** of Alternative Splicing impact on protein function that combines **RNA-Seq** expression levels and binding sites changes for **Alternative splicing impact factor (AS-IF)** project.
- **scRNA-Seq pseudo-bulk analysis (mentoring)** - navigated B.S. students through the data choice and pipeline building for the **scRNA-Seq** in project dedicated to extracting alternative splicing from the **scRNA-Seq** data using deep-learning-based clustering.
- Modeled intra- and host-viral **homology-based** protein complexes of COVID-19 viral protein and analysis of their potential interactors for **SARS-CoV-2 structural genomics and interactomics** project.

AUG 2015
MAY 2019

WORCESTER POLYTECHNIC INSTITUTE (WPI)

Teaching Assistant

Taught undergraduate and graduate students for four years at CS department.

Assisted with **Algorithms Design and Analysis** (graduate and undergraduate), **AI**, Computer Networks, **Databases**, OOP Design. Was responsible for seminars, creating quizzes, reviewing assignments, and proctoring.

- Employed a hybrid approach that combined high-quality seed modules obtained via consensus clustering from multiple algorithms (Walktrap, SPICi, DIAMOND), follow-up module recovery protocol via Infomap algorithm, and subsequent trimming for topology-based disease modules discovery **DREAM Challenge 2016** from **multi-omics** network data. Our team reached the top 3 during the leaderboard stage.

JUN 2018 | TUFTS MEDICAL CENTER CTSI
AUG 2018 | *Research Intern*

Selected and integrated **Pathway Analysis** and **Gene Regulatory Network** reconstruction algorithms into **multi-omics** data platform. Reviewed existing methods and approaches, built a Docker environment that included Hadoop, pySpark, TensorFlow, and Anaconda, performed testing.

JUN 2013 | SAMSUNG R&D CENTER, Kyiv
MAY 2015 | *Machine Learning Engineer*

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

- Developed gesture recognition algorithms based on multimodal data from smartphone sensors (camera, proximity sensor, touch screen) for **gesture recognition engine**.
- Constructed **Machine Learning** solutions for sport activity recognition and vehicle recognition (e.g., bicycle, car, train) based on smartphone and smartwatch sensors. Created energy-efficient lightweight model based on **Dynamic Time Warp distance**.

PUBLICATIONS

1. **O. Narykov**, S. Srinivasan, D. Korkin "Computational protein modeling and the next viral pandemic" *Nature Methods*, 18, 444445 (2021) <https://doi.org/10.1038/s41592-021-01144-0> (Impact Factor: 34.975)
2. **O. Narykov**, N. T. Johnson, D. Korkin "Predicting protein interaction network perturbation by alternative splicing with semi-supervised learning" *Cell Reports*, 37.8 (2021) <https://doi.org/10.1016/j.celrep.2021.110045> (Impact Factor: 10.394)
3. 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> (Impact factor: 5.127) **Cover feature**
4. **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> (Impact Factor: 6.937)
5. 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> (Impact Factor: 34.975)
6. 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> **Cover feature**

IN PREPARATION

1. W. Pezeshkian[†], F. Grünwald[†], **O. Narykov**[†], S. Lu, T. A Wassenaar, S. J. Marrink, D. Korkin "Molecular architecture of SARS-CoV-2 envelope by integrative modeling" (2021) *BioRxiv* <https://doi.org/10.1101/2021.09.15.459697>
2. **O. Narykov**, E. Kokkotou, D. Korkin "Proteomics of the Gulf War Syndrome pain studies"
3. **O. Narykov**, N. T. Johnson, D. Korkin "Alternative splicing impact factor"

[†] - equal contribution

MEDIA COVERAGE

- Structural Genomics of SARS-CoV-2: [WPI](#), [Wall Street Journal](#), [Boston Herald](#), [Boston.com](#), [NBC Boston](#)
- Finalist Team in XPRIZE Pandemic Response Challenge: [XPRIZE](#)

REFEREED PRESENTATIONS

1. **O. Narykov**, W. Pezeshkian, F. Grünwald, S. Lu, T. A Wassenaar, S. J. Marrink, D. Korkin. Integrative Modeling of SARS-CoV-2 Envelope structure. *ASBMB PDB50 Symposium*, May 2021
2. **O. Narykov**, N. T. Johnson, D. Korkin. Functional dynamics of protein interactome induced by alternative splicingAn in silico approach. *CSHL Global Regulation of Gene Expression*, March 2020
3. **O. Narykov**, N. T. Johnson, D. Korkin. Determining rewiring effects of alternatively spliced isoforms of protein-protein interactions using a computational approach. *RNA Therapeutics*, June 2018

SCHOLARSHIPS

- Graduate Student Travel Scholarship, WPI, 2018 • Academic Excellence Scholarship, NTUU "KPI", 2010

LEADERSHIP

- **Mentoring** B.S. students. • **President** of the cultural club at WPI during 2017-2019.