

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.

EDUCATION

Ph.D. IN COMPUTER SCIENCE, *Worcester Polytechnic Institute*, GPA: 3.91/4.0 Expected graduation: Feb 2022
M.S. IN COMPUTER SCIENCE, *National Technical University of Ukraine Kyiv Polytechnic Institute* Graduated: Jun 2015
B.S. IN COMPUTER SCIENCE, *National Technical University of Ukraine Kyiv Polytechnic Institute* Graduated: Jun 2013

TECHNICAL SKILLS

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| • Machine Learning Tools | scikit-learn, pandas, PyTorch, Weka, AWS SageMaker, Keras, OpenCV |
| • Bioinformatics & Comp Bio | GATK, Bioconductor, bcbio-nextgen, GROMACS, SMART-seq, SomaScan |
| • Data Visualization | Matplotlib, bokeh, seaborn, ggplot2, Cytoscape, D3 |
| • Statistical Packages | scipy, statsmodels, PyMC3, R Stats |
| • High-Performance Computing | SLURM, Hadoop, MPI |
| • Dev-Ops | Docker, Linux, bash |
| • Software Engineering | Python, C++, R, C#, Java, git, googletest, unittest |
| • Web Applications | C#, JavaScript, HTML |
| • Biological Databases | TCGA, NCBI, GTEX, KEGG |
| • Others | MS Office, Adobe Illustrator |

RESEARCH AND TEACHING EXPERIENCE

Research Assistant, WORCESTER POLYTECHNIC INSTITUTE (WPI) MAY 2019-*now*

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** model for the 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 produced deliverables publicly available on <https://github.com/korkinlab/altintool> and <https://hub.docker.com/r/narykov/alt-in>.
- Identified **biomarkers** that predict response to the treatment in **clinical trials on Gulf War Illness** based on **SomaScan** proteomics data, evaluated different intra- and interplate normalization strategies, and employed a range of **statistical methods**.
- Led collaborative efforts of WPI team on **molecular dynamics simulations of SARS-CoV-2 envelope**, 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 AS 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.

Teaching Assistant, WORCESTER POLYTECHNIC INSTITUTE (WPI) AUG 2015 - MAY 2019

Taught undergraduate and graduate students for four years at C.S. department. Assisted with **Algorithms Design and Analysis** (graduate and undergraduate), **A.I.**, 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.

Intern, TUFTS MEDICAL CENTER CTSI

JUN 2018- AUG 2018

- 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.

Machine Learning Engineer, SAMSUNG R&D CENTER

JUN 2013- MAY 2015

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 splicing: An 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

AWARDS

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

LEADERSHIP

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