

Ph.D. candidate in Computational Biology with extensive industry software engineering experience and a very strong publication record in discovering pathogenesis and immune response mechanisms in pulmonary diseases. I excel in applying machine learning tools (newly published or custom built) to high-resolution and multimodal data, such as single-cell RNA-seq, spatial transcriptomics or EHR data, to deliver high-quality analytics, interpretability and interactive visualizations. My interest is to use vast amount of published data via novel machine learning models to estimate causal relationships within and between cells. This will inform the search for new therapeutic targets and biomarkers, and will guide future experiments to fill the gaps.

Education

Ph.D. in Computational Biology , Northwestern University, Chicago, USA Driskill Graduate Program in Life Sciences	2022–2025 (anticipated)
M.S. in Bioinformatics , Newcastle University, Newcastle upon Tyne, UK <i>With distinction</i>	2017–2018
Undergraduate coursework in Biology, Genetics, Moscow State University, Moscow, Russia	2003–2006


Work Experience

Post-Baccalaureate Research Fellow, Bioinformatics , Division of Pulmonary and Critical Care Medicine, Feinberg School of Medicine, Northwestern University, Chicago, USA	2019–2022
<ul style="list-style-type: none"> Analyze scRNAseq and other high-throughput data from human samples and mouse experiments Clean and analyze clinical EHR data from patient cohorts Deliver analytical insights to principal investigators in presentations and data exploration tools Develop and maintain data processing pipelines, data exchange and management infrastructure Write and publish scientific manuscripts Read literature to stay up-to-date with new computational tools for -omics analyses 	
Head of maintenance tools development group , Yandex, Moscow, Russia	2014–2017
<ul style="list-style-type: none"> Manage a team of engineers: mentoring, resolving conflicts, improving performance, code review, hiring Develop, design and support tools for system administrators and other employees 	
Full-stack software engineer , Yandex, Moscow, Russia	2007–2014
<ul style="list-style-type: none"> Identify employees' workflows bottlenecks for automation Develop, design and support web-services and console tools for system administrators and other employees 	
Software engineer , Art. Lebedev Studio, Moscow, Russia	2006–2007
Develop and support web-sites and a content management system.	

Computational skills

Programming languages:

Python, R, Java, C++, Ruby, Perl. Linux. Latex. SQL. HTML, JavaScript.





Github: <https://github.com/mxposed> 

Techniques:

Machine learning, deep learning (torch, jax), statistics, bayesian modeling, scRNAseq (scanpy, Seurat), bioinformatics tools, interactive visualizations (d3.js, plotly), pipelines (nextflow, snakemake).

Key publications

(* denotes equal contribution)

Markov NS , [...], Wunderink RG, Budinger GRS, Singer BD, Morales-Nebreda L, NU SCRIPT Study Investigators.	2024
A distinctive evolution of alveolar T cell responses is associated with clinical outcomes in unvaccinated patients with SARS-CoV-2 pneumonia. <i>Nature Immunology</i> . 10.1038/s41590-024-01914-w 	
Gao CA*, Markov NS* , Stoeger T*, [...], Misharin AV, Singer BD, NU SCRIPT Study Investigators.	2023
Machine learning links unresolved secondary pneumonia to mortality in patients with severe pneumonia, including COVID-19. <i>The Journal of Clinical Investigation (JCI)</i> . 10.1172/JCI170682 	
Sikkema L, Ramírez-Suástegui C, Strobl DC, Gillett TE, Zappia L, Madissoon E, Markov NS , [...], Theis FJ.	2023
An integrated cell atlas of the lung in health and disease. <i>Nature Medicine</i> . 10.1038/s41591-023-02327-2 	
Speir ML, Bhaduri A, Markov NS , [...], Papatheodorou I, Pollen AA, Raney BJ, Seninge L, Kent WJ, Haeussler M.	2021
UCSC Cell Browser: visualize your single-cell data. <i>Bioinformatics</i> . 10.1093/bioinformatics/btab503 	
Grant RA*, Morales-Nebreda L*, Markov NS* , [...], Budinger GRS, Misharin AV, Singer BD, Wunderink RG.	2021
Circuits between infected macrophages and T cells in SARS-CoV-2 pneumonia. <i>Nature</i> . 10.1038/s41586-020-03148-w 