

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 and private multimodal data via novel machine learning models to improve our understanding of common diseases and factors that determine patient individual outcomes.

## Technical expertise

### • Machine learning

Deep learning frameworks (torch, jax), large language models, multimodal fusion, embedding representations, bayesian modeling

### • Software & tools

Python, R, SQL, Linux, computational clusters, interactive visualizations, pipelines

### • Healthcare data

Electronic health records (EHR), clinical notes analysis, single-cell RNA-seq, spatial transcriptomics, imaging data, statistics

### • Leadership

Cross-functional collaboration, project management, team management, mentorship, scientific communication

## Education







<b>Ph.D. in Computational Biology</b> , Northwestern University, Chicago, USA Driskill Graduate Program in Life Sciences	2022–2025 (expected in December)
<b>M.S. in Bioinformatics</b> , 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

<b>Ph.D. researcher</b> , Division of Pulmonary and Critical Care Medicine, Feinberg School of Medicine, Northwestern University, Chicago, USA <ul style="list-style-type: none"> <li>Analyzed scRNAseq and EHR data jointly to understand patient response to severe pneumonia, including COVID-19</li> <li>Acquired external funding for the project (competitive AHA predoctoral fellowship)</li> <li>Consulted Northwestern students and faculty on deep learning, data science and data visualization</li> <li>Presented and published our research in 3 peer-reviewed papers</li> </ul>	2022–present
<b>Research data analyst, bioinformatics</b> , Division of Pulmonary and Critical Care Medicine, Feinberg School of Medicine, Northwestern University, Chicago, USA <ul style="list-style-type: none"> <li>Analyzed scRNAseq and other high-throughput data from human samples and mouse experiments</li> <li>Cleaned and analyzed clinical EHR data from patient cohorts</li> <li>Delivered analytical insights to principal investigators in presentations and data exploration tools</li> <li>Developed and maintained data processing pipelines, data exchange and management infrastructure</li> </ul>	2019–2022
<b>Head of maintenance tools development group</b> , Yandex, Moscow, Russia <ul style="list-style-type: none"> <li>Managed a team of 6 engineers: hiring, mentoring, resolving conflicts, improving performance</li> <li>Developed, designed and supported tools for system administrators and other employees</li> </ul>	2014–2017
<b>Full-stack software engineer</b> , Yandex, Moscow, Russia <ul style="list-style-type: none"> <li>Identified employees' workflows bottlenecks for automation</li> <li>Developed, designed and supported web-services and console tools for system administrators and other employees</li> </ul>	2007–2014
<b>Software engineer</b> , Art. Lebedev Studio, Moscow, Russia Developed and supported web-sites and a content management system	2006–2007

## Key publications

(\* denotes equal contribution)

Luecken MD, Gigante S, Burkhardt DB, Cannoodt R, Strobl DC, <b>Markov NS</b> , [...], Theis FJ, Krishnaswamy S. Defining and benchmarking open problems in single-cell analysis. <i>Nature Biotechnology</i> . <a href="https://doi.org/10.1038/s41587-025-02694-w">https://doi.org/10.1038/s41587-025-02694-w</a> 	2025
<b>Markov NS</b> , [...], Budinger GRS, Singer BD, Morales-Nebreda L, NU SCRIPT Study Investigators. 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 	2024
Gao CA*, <b>Markov NS*</b> , Stoeger T*, [...], Misharin AV, Singer BD, NU SCRIPT Study Investigators. Machine learning links unresolving secondary pneumonia to mortality in patients with severe pneumonia, including COVID-19. <i>The Journal of Clinical Investigation (JCI)</i> . 10.1172/JCI170682 	2023
Sikkema L, Ramírez-Suástegui C, Strobl DC, Gillett TE, Zappia L, Madissoon E, <b>Markov NS</b> , [...], Theis FJ. An integrated cell atlas of the lung in health and disease. <i>Nature Medicine</i> . 10.1038/s41591-023-02327-2 	2023
Speir ML, Bhaduri A, <b>Markov NS</b> , [...], Pollen AA, Raney BJ, Seninge L, Kent WJ, Haeussler M. UCSC Cell Browser: visualize your single-cell data. <i>Bioinformatics</i> . 10.1093/bioinformatics/btab503 	2021
Grant RA*, Morales-Nebreda L*, <b>Markov NS*</b> , [...], Budinger GRS, Misharin AV, Singer BD, Wunderink RG. Circuits between infected macrophages and T cells in SARS-CoV-2 pneumonia. <i>Nature</i> . 10.1038/s41586-020-03148-w 	2021