Nikolay S. Markov

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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

Ph.D. in Computational Biology, Northwestern University, Chicago, USA — 2022–2025 (expected in December)
Driskill Graduate Program in Life Sciences

M.S. in Bioinformatics, Newcastle University, Newcastle upon Tyne, UK — 2017–2018
With distinction

Undergraduate coursework in Biology, Genetics, Moscow State University, Moscow, Russia — 2003–2006

Work Experience

Ph.D. researcher, Division of Pulmonary and Critical Care Medicine, Feinberg School of Medicine, Northwestern University, Chicago, USA — 2022–present
- Analyzed scRNAseq and EHR data jointly to understand patient response to severe pneumonia, including COVID-19
- Acquired external funding for the project (competitive AHA predoctoral fellowship)
- Consulted Northwestern students and faculty on deep learning, data science and data visualization
- Presented and published our research in 3 peer-reviewed papers

Research data analyst, bioinformatics, Division of Pulmonary and Critical Care Medicine, Feinberg School of Medicine, Northwestern University, Chicago, USA — 2019–2022
- Analyzed scRNAseq and other high-throughput data from human samples and mouse experiments
- Cleaned and analyzed clinical EHR data from patient cohorts
- Delivered analytical insights to principal investigators in presentations and data exploration tools
- Developed and maintained data processing pipelines, data exchange and management infrastructure

Head of maintenance tools development group, Yandex, Moscow, Russia — 2014–2017
- Managed a team of 6 engineers: hiring, mentoring, resolving conflicts, improving performance
- Developed, designed and supported tools for system administrators and other employees

Full-stack software engineer, Yandex, Moscow, Russia — 2007–2014
- Identified employees' workflows bottlenecks for automation
- Developed, designed and supported web-services and console tools for system administrators and other employees

Software engineer, Art. Lebedev Studio, Moscow, Russia — 2006–2007
Developed and supported web-sites and a content management system

Key publications

(* denotes equal contribution)

Markov NS*, Esposito AJ*, […], Perlman H, Lam AP, Gottardi CJ, Budinger GRS, Misharin AV, Hinchcliff ME. 2025
Profibrotic monocyte-derived alveolar macrophages as a biomarker and therapeutic target in systemic sclerosis-associated interstitial lung disease. *bioRxiv*. https://doi.org/10.1101/2025.08.07.669006

Luecken MD, Gigante S, Burkhardt DB, Cannoodt R, Strobl DC, **Markov NS**, […], Theis FJ, Krishnaswamy S. 2025
Defining and benchmarking open problems in single-cell analysis. *Nature Biotechnilogy*. https://doi.org/10.1038/s41587-025-02694-w

Markov NS, […], 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. *Nature Immunology*. 10.1038/s41590-024-01914-w

Gao CA*, **Markov NS***, Stoeger T*, […], Misharin AV, Singer BD, NU SCRIPT Study Investigators. 2023
Machine learning links unresolving secondary pneumonia to mortality in patients with severe pneumonia, including COVID-19. *The Journal of Clinical Investigation (JCI)*. 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. *Nature Medicine*. 10.1038/s41591-023-02327-2

Speir ML, Bhaduri A, **Markov NS**, […], Pollen AA, Raney BJ, Seninge L, Kent WJ, Haeussler M. 2021
UCSC Cell Browser: visualize your single-cell data. *Bioinformatics*. 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. *Nature*. 10.1038/s41586-020-03148-w