# 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.

## Education

**Ph.D. in Computational Biology**, Northwestern University, Chicago, USA          2022–2025 (anticipated in June)
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,          2022–2025
Feinberg School of Medicine, Northwestern University, Chicago, USA
- Analyzed scRNAseq and EHR data jointly to understand patient response to severe pneumonia, including COVID-19
- Acquired external funding for the project (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

**Post-baccalaureate research fellow, bioinformatics**, Division of Pulmonary and Critical Care Medicine,          2019–2022
Feinberg School of Medicine, Northwestern University, Chicago, USA
- 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

## 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          <span>(* denotes equal contribution)</span>

**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 ⟳