

# Stanislav Bratchikov

EMAIL: [stanislav.bratchikov@northwestern.edu](mailto:stanislav.bratchikov@northwestern.edu)

WEB: [StanislavBratchikov.github.io](https://StanislavBratchikov.github.io)

ADDRESS: 303 E. Superior St., Chicago, IL, 60611

## Education

2018 – 2022     **Lomonosov Moscow State University** – Moscow, Russia  
BS in Biophysics  
Mentors: Dr. Alexander Bagaev, Dr. Dmitriy Nechipurenko, *GPA: 3.7/4.0*.  
Thesis: Heterogeneity of cell populations in tumor environment at the RNA expression level.

## Research experience

Nov 2022 – Present     **Dr. Alexander Misharin laboratory, Pulmonary Department, Northwestern University**

*Post-baccalaureate researcher*

### - Automated flow cytometry pipeline

- Led a **year-long project** to implement an innovative automated flow cytometry data analysis pipeline using gradient boosting models, significantly reducing (**1400-fold speedup**) data analysis time for wet bench researchers.
- By automating the data processing and classification steps, the pipeline improved workflow efficiency and allowed for quicker access to critical insights.
- This work was used for **multiple projects** within the laboratory.
- **First author paper** based on this work is in progress.

### - Differential gene expression methods benchmarking

- **Worked** with **computational biology group** from the university of Warsaw on a large **collaborative project** focusing on the analysis of single cell RNA-seq data from hundreds of patients.
- Benchmarked traditional approaches for differential gene expression methods vs deep learning-based approaches.
- The results of this work were essential for downstream tasks in this project.
- **Publication is expected** in 2024.

### - Single cell spatial transcriptomics analysis

- **Researched** spatial transcriptomics platforms (Nanostring CosMx, 10x Xenium) that **helped** bringing these technologies to the **laboratory**.
- Utilized various best-practice computational tools and techniques to decipher spatial patterns and identify potential biomarkers associated with pulmonary diseases, assessed publicly available datasets.

### - Single cell RNA-seq data analysis

- Analyzed single-cell data from pulmonary samples to gain insights into cellular heterogeneity and molecular changes in disease conditions.
- Employed bioinformatics tools to preprocess and interpret single-cell RNA sequencing data, revealing critical cellular subpopulations and their functional roles.

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Aug 2021 – Aug  
2022

**BostonGene Corporation, Boston, MA**

*Junior Bioinformatician, Molecular Oncology Department*

- **Cell type deconvolution of cancer- associated fibroblasts in bulk RNA-seq data using machine learning methods with the goal to improve outcome prediction in cancer patients**

- Led development of a project classifying fibroblasts in tumor microenvironments using machine learning and gene expression signatures, which resulted in my **thesis**.
- Presented work at OpenBio 2022.
- Work on this project was **continued** and results were submitted to [AACR 2024](#).

- **Machine learning models validation**

Developed a script to validate machine learning models that deconvolve sample cells' percentages based on sequencing data.

- **Enhanced cross-team communication**

Developed standard report form of RNA samples analysis to share results efficiently across multiple bioinformatics teams.

- **Reproducible programming and RNA-seq analysis**

Performed code debugging, analysis, and filtration of RNA-seq lab samples.

July 2021 – Aug  
2021

**BostonGene Corporation, Boston, MA**

*Applied machine learning research intern, Molecular Oncology Department*

Analyzed myeloid-derived suppressor cells in patient samples, generated gene signatures for cell type identification, enhancing the production ML model.

## Posters, manuscripts, talks

Posters

Machine learning classifier for automated and scalable analysis of clinical flow cytometry samples.[\[Link to Poster PDF\]](#)

2023 Systems biology for infectious diseases annual conference, Northwestern university

2023 Molecular Mechanisms of Lung disease annual meeting, University of Helmholtz - Northwestern university [conference](#)

2023 The 17th Annual Lewis Landsberg [Research Day](#), Northwestern university

Manuscripts

Bratchikov S., Misharin A., et al; (in progress) Automated and Scalable Analysis of Clinical Flow Cytometry Samples Using Machine Learning Approaches

Talks

OpenBio 2022, RNA Expression-Level Heterogeneity in Cancer-Associated Stromal Cell Populations within the Tumor Microenvironment.

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## Mentorship and service

- Sep 2023 **NIAID sponsored [Codeathon](#) assistant**  
Prepared data for the event, enabling use of flow cytometry data. Collaborated with **25 researchers** from leading US institutions for a 3-day event. Supported multiple teams and contributed to a project predicting ICU outcomes ([Project 2](#)).
- Summer 2023 **Kimberly Querrey [summer research program](#)**  
**Supervised** a diverse multinational **group** of highschool and undergraduate students. Helped students with limited code experience to learn fundamentals of reproducible programming and conduct research. **Mentored** project on performing flow cytometry analysis.

## Courses and workshops

- 2020-2022 **[AI Masters](#), machine learning courses**  
Went through extensive selection (100/5000 people), and took classes from academia and industry leaders in
- Machine learning (A. Djakonov, Lomonosov Moscow State University)
  - Data engineering (P. Klemenkov, NVIDIA)
  - Statistics (V. Panov, Computer Science department, Higher School of Economics),
  - Linear algebra (I. Oseledets, Skoltech)
  - Linux, Bash and Git
- 10-17 Feb 2022 **Winter Computer Science School**  
*Computer Science department, Higher School of Economics, Moscow*
- Fall semester 2021 **Quantative genetics course by prof. Yuri Aulchenko [certificate](#)**  
*Moscow Institute of Physics and Technology, Moscow*  
Gained entry into genetics courses, being among the 35 students selected. Topics included Genes in populations, Complex traits genetics, Genome Wide Associated Studies.
- 23-27 Aug 2021 **Summer School on Machine Learning in Bioinformatics [certificate](#)**  
*Computer Science department, Higher School of Economics, Moscow*  
Took diverse workshops on various topics related to the use of machine learning in bioinformatics by academia leaders from leading US and European institutions.

## Software development

- 2023 **Open-source contribution**  
Introduced enhanced way of data extraction in leading flow cytometry gating app. An open-source plugin called "Labeler" with this functionality will be released for wide use [here](#).

## Skills

- Programming Python (4 years), R (2 years), C/C++ (1 year), LATEX, Git, Bash, high performance computing.
- Theory Gradient boosting, random forests, variational autoencoders; probability theory, stochastic processes.
- Languages English (7.5 IELTS total band score).