Stanislav Bratchikov

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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.

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* Analysed different types of myeloid derived suppressor cells for deconvolution in patient samples, collected gene signatures for cell type identification. This work provided insights for enhancing current 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.

Mentorship and service

Sep 2023 **NIAID sponsored Codeathon assistant**
Participated in preparing data before the codeathon. My work **enabled** the use of flow cytometry data associated with patients for this event. Worked together with **25 researches** from leading US universities and laboratories for 3 days. Provided support to multiple teams and contributed (Project 2) to a project on predicting intensive care unit outcome using information on multi-cellular programs and pathogen infiltration.

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 (A. Trunov).

10-17 Feb 2022 **Winter Computer Science School**
Computer science department, Higher school of economics, Moscow

Fall semester 2021 **Quantative genetics course by prof. Yurii 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

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 machine learning: gradient boosting algorithms, random forests, variational autoencoders; probability theory, stochastic processes.

Languages English (7.5 IELTS total band score).