

Stanislav Bratchikov

EMAIL: sbratchi@broadinstitute.org

WEB: StanislavBratchikov.github.io

ADDRESS: 415 Main St, Cambridge, MA 02142

Education

2018 – 2022

Lomonosov Moscow State University – Moscow, Russia

BS in Biophysics

GPA: 3.7/4.0.

Thesis: Heterogeneity of cell populations in tumor environment at the RNA expression level.

Research experience

Jul 2024 –
Present

Broad Institute of MIT and Harvard, Boston, MA

Computational Associate II

- **RNA-Seq analysis and Tandem Mass Tag Proteomics analysis**

- Developing and maintaining computational pipelines using publicly available and in-house developed tools for the analysis of experiment data.
- Monitoring statistical aspects of study/experiment design, identification of appropriate tests and models, data analysis and visualization, assuring quality of data.

May 2024 – Jun
2024

Stanford School of Medicine

Intern

- **Machine learning models deconvolution**

- Assessing performance of machine learning models for tumor micro-environment deconvolution using statistical methods. Dr. Aaron Newman lab.

Nov 2022 – Jul
2024

Dr. S. Budinger, Dr. A. Misharin laboratories, 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.

- 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.

BostonGene Corporation, Boston, MA

Junior Bioinformatician, Molecular Oncology Department

Aug 2021 – Aug
2022

- 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.

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 **[Quantitative 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

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).