

Stanislav Bratchikov

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Research Experience

Broad Institute of MIT and Harvard, Cambridge, MA

Jul 2024 – Present

Computational Associate

- Developed and maintained computational pipelines for RNA-Seq and Tandem Mass Tag proteomics and metabolomics analysis used across multiple laboratory projects
- Responsible for quality control, data analysis, and visualization
- Implemented workflows that standardized omics data processing and interpretation
- Worked with wet lab biologists helping in data analysis and visualizations

Stanford School of Medicine (remote)

May 2024 – Jun 2024

Intern

- Assessed machine learning model performance for tumor microenvironment deconvolution using statistical validation methods

Northwestern University, Pulmonary Department

Nov 2022 – Jul 2024

Post-baccalaureate Researcher

- Led year-long project implementing automated flow cytometry pipeline using gradient boosting models, achieving 1400-fold speedup in data analysis
- Benchmarked differential gene expression methods for single-cell RNA-seq analysis in collaborative project with University of Warsaw
- Analyzed spatial transcriptomics data (Nanostring CosMx, 10x Xenium) contributing to technology adoption decisions

BostonGene Corporation, Boston, MA

Aug 2021 – Aug 2022

Junior Bioinformatician, Molecular Oncology Department

- Developed machine learning classifier for cancer-associated fibroblast deconvolution in bulk RNA-seq data to improve patient outcome prediction
- Results presented at OpenBio 2022 and submitted to AACR 2024

Education

Lomonosov Moscow State University – Moscow, Russia

2018 – 2022

BS in Biophysics, GPA: 3.7/4.0

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

Publications & Presentations

Robust Generation of Oxygen at the Surface of Human Cells via Plasma Membrane-Targeted SNORCL. Hercher T.W., To T.L., McCoy J., Wu A., Bratchikov S., Durham T., Vantaku V.R., Parangi S., Mootha V.K. *In preparation.*

Manuscripts

Developing and validating a machine learning model to predict successful next-day extubation in the ICU. Fenske S.W., Peltekian A., Kang M., Markov N.S., Zhu M., Grudzinski K., Bak M.J., Pawlowski A., Gupta V., Mao Y., Bratchikov S., Stoeger T., Rasmussen L.V., Choudhary A.N., Misharin A.V., Singer B.D., Budinger G.R.S., Wunderink R.G., Agrawal A., Gao C.A., and the NU SCRIPT Study Investigators. *medRxiv* 2024.06.28.24309547. *Scientific Reports*, *Accepted after revision*

Machine learning classifier for automated flow cytometry analysis (Bratchikov S., et al.). Presented at: Systems Biology for Infectious Diseases (2023), Northwestern Research Day (2023), Molecular Mechanisms of Lung Disease Conference (2023)

Posters

OpenBio 2022: **RNA Expression-Level Heterogeneity in Cancer-Associated Stromal Cell Populations**

Talks

Leadership & Service

Hackathon Organizer, Broad Institute

2025

- Led industrial partnerships (EvoluntaryScale, Ginkgo Bioworks, Google) and event planning for institute-wide hackathon
- Coordinated between academic and industry stakeholders to facilitate collaborative problem-solving initiatives

Steering Committee Member, CodeRATS

Aug 2024 – Present

- Support researchers at Broad Institute with coding through project planning, social events, and community building initiatives

NIAID Codeathon Assistant

Sep 2023

- Prepared flow cytometry datasets and supported 25 researchers from leading US institutions during 3-day collaborative coding event

Mentor, Kimberly Querrey Summer Research Program

Summer 2023

- Supervised diverse group of high school and undergraduate students in reproducible programming and flow cytometry analysis

Skills & Achievements

Python, R, LaTeX, Git, Bash, High Performance Computing

Programming

Omics data analysis (RNA-Seq, spatial transcriptomics, proteomics, database, metabolomics), UniParc database, gradient boosting, random forests, VAEs, statistical modeling

Methods

Boston Marathon finisher (2025)

Athletics

English (2023 IELTS 7.5)

Languages