

Stanislav Bratchikov

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Research Experience

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| Jul 2024 – Present | Broad Institute of MIT and Harvard , Cambridge, MA
<i>Computational Associate II</i> <ul style="list-style-type: none">• 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 |
| May 2024 – Jun 2024 | Stanford School of Medicine (remote)
<i>Intern</i> <ul style="list-style-type: none">• Assessed machine learning model performance for tumor microenvironment deconvolution using statistical validation methods |
| Nov 2022 – Jul 2024 | Northwestern University, Pulmonary Department
<i>Post-baccalaureate Researcher</i> <ul style="list-style-type: none">• 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 |
| Aug 2021 – Aug 2022 | BostonGene Corporation , Boston, MA
<i>Junior Bioinformatician, Molecular Oncology Department</i> <ul style="list-style-type: none">• 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

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| 2018 – 2022 | Lomonosov Moscow State University – Moscow, Russia
BS in Biophysics, <i>GPA: 3.7/4.0</i>
Thesis: Heterogeneity of cell populations in tumor environment at the RNA expression level. |
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Publications & Presentations

Manuscripts	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. <i>In preparation.</i> 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. <i>medRxiv</i> 2024.06.28.24309547. <i>In revision.</i>
Posters	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)
Talks	OpenBio 2022: RNA Expression-Level Heterogeneity in Cancer-Associated Stromal Cell Populations

Leadership & Service

2025	Hackathon Organizer, Broad Institute <ul style="list-style-type: none">• Led industrial partnerships and event planning for institute-wide hackathon• Coordinated between academic and industry stakeholders to facilitate collaborative problem-solving initiatives
Aug 2024 – Present	Steering Committee Member, CodeRATS <ul style="list-style-type: none">• Support researchers at Broad Institute with coding through project planning, social events, and community building initiatives
Sep 2023	NIAID Codeathon Assistant <ul style="list-style-type: none">• Prepared flow cytometry datasets and supported 25 researchers from leading US institutions during 3-day collaborative coding event
Summer 2023	Mentor, Kimberly Querrey Summer Research Program <ul style="list-style-type: none">• Supervised diverse group of high school and undergraduate students in reproducible programming and flow cytometry analysis

Skills & Achievements

Programming	Python, R, LaTeX, Git, Bash, High Performance Computing
Methods	Omics data analysis (RNA-Seq, spatial transcriptomics, proteomics, database, metabolomics), UniParc database, gradient boosting, random forests, VAEs, statistical modeling
Athletics	Boston Marathon finisher (2025)
Languages	English (2023 IELTS 7.5)