Stanislav Bratchikov

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Research Experience

Jul 2024 – Present

Broad Institute of MIT and Harvard, Boston, MA
Computational Associate II

- Developed and maintained computational pipelines for RNA-Seq and Tandem Mass Tag proteomics and metabolomics analysis used across multiple laboratory projects
- Responsible for statistical design, quality control, data analysis, and visualization
- Implemented reproducible workflows that standardized omics data processing and interpretation for mitochondrial biology research

May 2024 – Jun 2024

Stanford School of Medicine (remote)
Intern

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

Nov 2022 – Jul 2024

Northwestern University, Pulmonary Department
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

Aug 2021 – Aug 2022

BostonGene Corporation, Boston, MA
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

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.

Publications & Presentations

Manuscripts

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

Posters	Machine learning classifier for automated flow cytometry analysis (<u>Bratchikov S.</u>, 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**

- 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**

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

Sep 2023   **NIAID Codeathon Assistant**

- 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**

- 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, metabolomics), gradient boosting, random forests, VAEs, statistical modeling
Athletics	Boston Marathon finisher (2025)
Languages	English (2023 IELTS 7.5)