Stanislav Bratchikov

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Research Experience

Jul 2024 –

Broad Institute of MIT and Harvard, Cambridge, MA

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

May 2024 - Jun

Stanford School of Medicine (remote)

2024

Intern

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

Nov 2022 - Jul

Northwestern University, Pulmonary Department

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

Aug 2021 - Aug

BostonGene Corporation, Boston, MA

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

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

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., <u>Bratchikov S.</u>, Durham T., Vantaku V.R., Parangi S., Mootha V.K. *In preparation*.

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., <u>Bratchikov S.</u>, 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*

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 (EvolutinaryScale, Ginkgo Bioworks, Google) and event planning for institute-wide hackathon
- Coordinated between academic and industry stakeholders to facilitate collaborative problemsolving 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, database, metabolomics), Uni-Parc database, gradient boosting, random forests, VAEs, statistical modeling

Athletics

Boston Marathon finisher (2025)

Languages

English (2023 IELTS 7.5)