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
- Supported wet lab biologists with statistical analysis and visualizations including dimensionality reduction, phenotyping, and genotyping
- Performed longitudinal RNAseq statistical analysis using time series tools to research cell time dependent response to oxygen levels

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 for annotating Chronic Lung Allograft Dysfunction, 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 aimed to research influence of pathogen response in pneumonia patients outcomes
- Researched mechanism of splenic macrophages population maintenance using supervised and semi supervised clustering tools for FACS data
- Assessed publicly available spatial transcriptomics datasets (Nanostring CosMx, 10x Xenium) contributing to technology adoption decisions focusing on identification of potential biomarkers associated with pulmonary diseases assesing quiality of cell segmantation and transcript coverage.
- Analyzed single cell samples from Bronchoalveolar lavage fluid using automated SnakeMake pipeline and RNAseq large language model based cell annotation

BostonGene Corporation, Boston, MA   Aug 2021 – Aug 2022
Junior Bioinformatician, Molecular Oncology Department
- Analyzed single cell transcriptomics patient samples performing cell typing
- 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., <u>Bratchikov S.</u>, 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., <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. *Scientific Reports, Published after revision link:* https://rdcu.be/eAqfJ.

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)   Posters

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

Leadership & Service

Hackathon Organizer, Broad Institute   2025
- Led industrial partnerships (EvolutinaryScale, 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, metabolomics), gradient boosting, random forests, VAEs, statistical modeling	Methods
HCA, UniParc, KEGG, GTEx, CCLE	Databases
Boston Marathon finisher (2025)	Athletics
English (2023 IELTS 7.5)	Languages