

Roman Novikov

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About

Bioinformatics Engineer with over 4 years of experience in developing scalable data pipelines and robust workflows for genomic data analysis, with specific expertise in liquid biopsy research, biomarker discovery, and high-throughput sequencing. Proficient in modern bioinformatics tools and frameworks, including Nextflow, CWL, Docker, and AWS, with a proven ability to optimize workflows for the development of cancer biomarkers. Strong interdisciplinary collaboration skills with a focus on translating computational science into impactful clinical outcomes.

Skills

Languages	Python, R, Bash, JavaScript
Technologies	FastAPI, Pydantic, Docker, AWS (S3, AWS Glue), PostgreSQL, ClickHouse, MongoDB, SQLAlchemy, Tortoise ORM, Apache Kafka, Apache Airflow
Machine Learning	Scikit-learn, TensorFlow, PyTorch
Bioinformatics	Nextflow, CWL, Picard, WGS, WES

Experience

Hero.io <i>Data Engineer</i>	<i>October 2024 - May 2025</i> <i>Dubai, UAE</i>
<ul style="list-style-type: none">Collaborated with three cross-functional teams to develop and implement data models, ensuring data integrity and consistency across the organization.Designed and optimized robust ETL pipelines using Apache Airflow, FastAPI, Tortoise ORM and SQLAlchemy for transforming and validating data across multiple sources.Worked on automating data scraping and cleansing techniques to ensure high-quality inputs for ML models and analytics, resulting in a 25% reduction in data processing time.	
BostonGene <i>Software Engineer</i>	<i>October 2022 - October 2024</i> <i>Waltham, MA</i>
<ul style="list-style-type: none">Automated the validation of raw NGS data from liquid biopsy samples using Python and AWS, improving processing efficiency by 40% and reducing error rates by 30%.Developed and maintained standardized bioinformatics pipelines with CWL, and Docker, leading to a 30% faster integration of new features.Streamlined workflows in LIMS systems, enhancing interdepartmental collaboration and data accuracy.	
BostonGene <i>Data Analyst</i>	<i>July 2021 - October 2022</i> <i>Waltham, MA</i>
<ul style="list-style-type: none">Developed a FastAPI-based analytical system for flow cytometry sample metadata verification, speeding up the process by 60%.	

Education

Moscow Institute of Physics and Technology <i>Master's degree in Applied Mathematics and Physics</i> <i>Major in Computational Bioinformatics</i> <i>Professional qualification in Data Science</i> Grade: 3.90 GPA (Top 2%)	<i>September 2022 - June 2024</i> <i>Moscow, Russia</i>
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Graduate project: Comprehensive analysis of quality control data for liquid biopsy samples based on cell-free DNA using NGS.

Awards: Scholarship of Vladimir Potanin Foundation

Lomonosov Moscow State University

Septembre 2017 - June 2021

Bachelor's degree in Biology, Major in Bioengineering

Moscow, Russia

Grade: 3.83 GPA (Top 5%)

Graduate project: Design of a nucleic acid biosensor based on two dCas9 proteins.

Projects

iGEM Projects (2019 and 2020)

March 2019 - November 2020

Moscow, Russia

Led computational modeling efforts in two award-winning CRISPR/Cas biosensor projects for the international iGEM competition. Developed biosensors for hepatitis C and Lyme disease detection, achieving > 98% sensitivity and > 99% specificity. Successfully presented results in Boston.

Publications

Shaytan, A. K., **Novikov, R. V.**, Vinnikov, R. S., et al. (2022). From DNA-Protein Interactions to the Genetic Circuit Design Using CRISPR-dCas Systems. *Frontiers in Molecular Biosciences*, 9, 1070526. [Link](#).

Novikov, R. V., Gribkova, A. K., Kacher, J. G., et al. (2021). Design of Nucleic Acid Biosensors Based on CRISPR/Cas Systems and Reporter Split Proteins. *Moscow University Biological Sciences Bulletin*, 76(2), 52–58. [Link](#).

Novikov, R. V., Bondarenko, E. A., Malyuchenko, N. V., Feofanov, A. V., et al. (2020). Determining the Binding Constant of LANA Protein Fragment with Nucleosome. *Moscow University Biological Sciences Bulletin*, 75(4), 252–256. [Link](#).