

Roman Novikov

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About

Senior Bioinformatician with over 4 years of experience in developing scalable data pipelines for genomic data analysis. Expertise in liquid biopsy research, biomarker discovery, and high-throughput sequencing workflows. Proficient in modern bioinformatics tools and frameworks, including 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, C, Go
Technologies	FastAPI, Docker, Kubernetes, Jenkins, AWS, PostgreSQL, ClickHouse, MongoDB, Tortoise ORM, Apache Kafka, Apache Airflow
Bioinformatics Tools	Picard, BWA, SAMtools, Bedtools, CWL, Nextflow

Experience

Hero.io <i>Data Engineer</i>	<i>October 2024 - Present</i> <i>Dubai, UAE</i>
<ul style="list-style-type: none">Designed and optimized robust ETL pipelines using Apache Airflow, FastAPI and Tortoise ORM for transforming and validating data across multiple sources.Collaborated on automating data scraping and cleansing techniques to ensure high-quality inputs for ML models.	
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.	
<i>Data Analyst</i>	<i>July 2021 - October 2022</i> <i>Waltham, MA</i>
<ul style="list-style-type: none">Developed an analytical system using FastAPI significantly speeding up sample verification processes by 60%.Automated data validation processes for large datasets, increasing processing efficiency by 40% and reducing error rates by 30%.	

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%) 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	<i>September 2022 - June 2024</i> <i>Moscow, Russia</i>
Lomonosov Moscow State University <i>Bachelor's degree in Biology, Major in Bioengineering</i> Grade: 3.83 GPA (Top 5%) Graduate project: Design of a nucleic acid biosensor based on two dCas9 proteins.	<i>Septembre 2017 - June 2021</i> <i>Moscow, Russia</i>

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 high sensitivity and 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., Studitsky, V. M., Shaytan, A. K. (2020). Determining the Binding Constant of LANA Protein Fragment with Nucleosome. *Moscow University Biological Sciences Bulletin*, 75(4), 252–256. [Link](#).