Roman Novikov

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About

Senior Bioinformatician 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.

Experience

Cancer Research UK National Biomarker Centre *August 2025 - Present*
Senior Bioinformatician *Manchester, UK*

- Developing computational methods for early detection of non-small cell lung cancer (NSCLC).
- Building and validating machine learning classifiers for biomarker discovery and clinical application.
- Integrating and analysing multi-omics data (methylomics, fragmentomics, CNAs, proteomics, cfDNA features).

Hero.io *October 2024 - May 2025*
Data Engineer *Dubai, UAE*

- 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 *July 2021 - October 2024*
Software Engineer *Waltham, MA*

- 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.
- 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 *September 2022 - June 2024*
Master's degree in Applied Mathematics and Physics *Moscow, Russia*
Major in Computational Bioinformatics
Professional qualification in Data Science
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

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.

Skills

Languages	Python, R, Bash/Shell scripting
Bioinformatics	NGS analysis, variant calling, genomic data processing, alignment tools (BWA, Bowtie2), variant analysis (GATK, VarScan), scRNA-seq analysis
Technologies	FastAPI, Pydantic, Docker, AWS (S3, AWS Glue), PostgreSQL, ClickHouse, MongoDB, SQLAlchemy, Tortoise ORM, Apache Kafka, Apache Airflow, Nextflow, CWL, Snakemake
Machine Learning and Data Science	Scikit-learn, TensorFlow, PyTorch, tidyverse, tidymodels, Bioconductor, DESeq2, scanpy
Visualization	ggplot2, matplotlib, seaborn, plotly

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.