

LOLITA ALEKSEEVA

Bioinformatician

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Summary

Results-driven Bioinformatician with over 5 years of expertise in NGS data analysis, specializing in ctDNA, WES, and RNA-Seq. Proficient in developing automated bioinformatics pipelines, and leading cancer and microbiome research initiatives. Skilled in computational biology, ML, and tool development, with a proven track record of delivering impactful insights for oncology and personalized medicine.

Experience

Senior Bioinformatician

April 2024 – Sep. 2024

BostonGene

Waltham, MA, USA · Remote

- Led collaborative **Liquid Biopsy** projects, specializing in ctDNA data analysis for patients with solid tumors and lymphomas, improving diagnostic precision and patient care strategies.
- Developed **automated bioinformatics analysis systems** for large cohorts, reducing validation errors and expediting turnaround times.
- Implemented **validation workflows** for somatic and germline mutation analysis, ensuring high accuracy and regulatory compliance.

Bioinformatician

August 2022 – April 2024

BostonGene

Waltham, MA, USA · Remote

- Integrated and optimized pipelines for **indel and SNP detection**, improving sensitivity in ctDNA and WES data analysis. Authored comprehensive **SOPs and user manuals** for ctDNA-based pipelines.
- Contributed to the **CLIA certification** of liquid biopsy products through robust validation and testing frameworks.

Bioinformatician, Data Analyst

Sep. 2021 – August 2022

BostonGene

Waltham, MA, USA · Remote

- Conducted **microbiome analyses** for over 1,000 colorectal and pancreatic cancer cases from TCGA, CPTAC, and proprietary datasets. Identified key correlations between survival status, gene expressions, and microbiome presence, leading to the development of novel prognostic biomarkers based on bacterial genera.
- Enhanced machine learning models for **bacterial classification** and built a specialized pipeline for **bacterial transcript detection** in RNA-seq data.

Junior Research Scientist

Sep. 2017 – August 2020

Federal Research Centre “Fundamentals of Biotechnology” of the Russian Academy of Sciences

Moscow, Russia · On-site

- Investigated the **taxonomy, phylogeny, and evolution** of magnetotactic bacteria in environmental samples using **metagenomic workflows** (NGS data, taxonomic classification systems) and large-scale **sequence database retrieval** (NCBI, JGI/IMG).
- Applied **molecular techniques** and **big-data handling** with bioinformatics tools to profile microbial communities.

Core Skills

Programming & Data Management: Python, R, Bash, SQL (PostgreSQL); Git (GitHub, GitLab, Bitbucket); AWS, Docker, Kubernetes; Nextflow, CWL

Bioinformatics & Data Analysis: NGS (WES, RNA-Seq, WGS, cfDNA), Metagenomics; Single-Cell RNA-Seq, Microbiome analysis, Taxonomy & Phylogenetics, Mutation Calling; Machine Learning (ML), Statistics, Pipeline Development; Sequence Databases (NCBI, JGI/IMG, Ensembl, GEO), Cancer Repositories (TCGA, CPTAC)

Molecular & Microbiology Techniques: DNA Extraction, PCR, Gel Electrophoresis, Fluorescence In Situ Hybridization (FISH), Transmission Electron Microscopy (TEM), Ultramicrotomography, Microbial Cultivation, Bacterial Strain Isolation

Education

Bioinformatics Certification

Sep. 2019 – Dec. 2020

Bioinformatics Institute (<https://bioinf.me/en>)

Moscow, Russia

MSc in Microbiology

Sep. 2018 – May 2020

Lomonosov Moscow State University (#94 in QS World University Rankings 2025)

Moscow, Russia

Selected Projects & Publications

- George, Ben, et al. "Transcriptomic-Based Microenvironment Classification Reveals Precision Medicine Strategies for PDAC." *Gastroenterology* (2024) DOI: 10.1053/j.gastro.2024.01.028.
- Uzun M., Alekseeva L., et al. "Unravelling the diversity of magnetotactic bacteria through analysis of open genomic databases", *Scientific Data* (2020) DOI: 10.1038/s41597-020-00593-0.
- For more publications, visit 🌐 <https://orcid.org/0000-0002-8224-7298>