RUST TURAKULOV PhD

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I am molecular biologist with advanced training in bioinformatics and genomics. My specialities are genomics, sequencing analysis, workflow automation, data wrangling, quality assurance and visualization. My programming languages are Perl, R, SQL, Shell, Python all based on solid Linux system administration skills and cloud systems configuration. I had developed and coded graphical dashboards and quality control metrics for production analytics used in biotech companies: AGRF, SmartDNA and pathology lab: NIH/NCI Laboratory Of Pathology. I also have massive academic research experience in DNA sequencing applications in population and genomics studies. I am interested in Bioinformatics role oriented on genetics research and technical support for academic or biotechnology industry where my biological and programming experience would be the most valuable.

PROFESSIONAL SKILLS

Bioinformatics:	NextGen Sequencing Data analysis: Variant Calling, RNAseq and DNAseq pipelines, 16S rDNA.
Programming:	Perl, R, R/Shiny, R markdown, mySQL, Python, shell, MS OLE, MS Windows powershell.
Platforms:	PC/Windows, LINUX, High Performance Computers Cluster (NCI/PAWSEY/QCIF/Biowulf), VM VirtualBox, Docker, Cloud VM, AWS, AWS S3, AWS textract, AWS EC2, AWS lightsail, CKAN/

EMPLOYMENT HISTORY

2023 – current **Senior developer Australian Genome Research facility (AGRF), Melbourne, Australia**
- ❖ Applications development for soil bacterial profiles and in-house data assets.
- ❖ Large bacterial datasets and metadata integrations.
- ❖ Predictive modelling and classification of soil bacterial profiles.

2020 – 2023 **Bioinformatician / LIS developer, Laboratory Of Pathology, NCI , NIH, Bethesda USA**
- ❖ Methylation analysis and cancer classification based on Illumina methylation data.
- ❖ Historical data harmonization and preparing structural input for Palantir database.
- ❖ RNAseq, MethylationArray and Clinical Sequencing panel report customization.
- ❖ Tumor classifier containerization and workflow optimization.
- ❖ Research of accumulated historical data for Cancer patients and associated metadata.

2019 – 2020 **Bioinformatician / ANU RSB Division of Ecology and Evolution (E&E), Centre For Biodiversity Analysis. Canberra, Australia.**
- ❖ Developing, optimization and maintenance of cloud systems for high-throughput analysis of sequencing data (variant calling, de novo, phylogenetic)
- ❖ Research database (mySQL) development and integration with historical records
- ❖ Data quality control metrics extraction and automatic reporting system
- ❖ Research and analysis for the custom and adhoc projects
- ❖ Development and optimization of data flow and data management protocol: acquiring, transfer, generation, storage, removal and tracking system

2016 – 2019 **Bioinformatician / Data Scientist, smartDNA Pty Ltd, Melbourne, Australia.**
- ❖ Computational technology development for bacteria identification
- ❖ Automatic reporting system and company products development (smartGUTTM test, smartHITTM database, IBS GutDetectorTM, Spectrum DetectorTM)
- ❖ In-house bacterial sequences database maintenance and versioning documentation
- ❖ Statistical analysis and experiment design for internal and third parties projects with report writing and follow-ups discursions
- ❖ Patent developing and patent application lodgement assistance

2004 – 2016 **Senior Scientist / Bioinformatician, Australian Genome Research Facility (AGRF), The Walter and Eliza Hall Institute, Melbourne, Australia.**
- ❖ Developing and maintenance of core production analysis pipelines: whole-genome and exome sequencing variant calling
- ❖ Quality control metrics developing and LIMS integration
- ❖ Statistical analysis for various in-house and clients experiments
- ❖ Routine bioinformatics paid service and collaboration support
- ❖ Developing and validation new products and technologies

2001 – 2003 **Postdoctoral fellow, Center for Bioinformation Science (CBiS), Australian National University, Canberra, Australia**
- ❖ Research project with data mining from the public domain
- ❖ Establishing local MySQL database and applications development
- ❖ Statistical analysis and methods comparisons for data clustering
- ❖ Writing research paper and grant proposals

1999 – 2001 **Postdoctoral fellow, Martyn Smith's lab, School of Public Health, University of California at Berkeley, USA**
- ❖ Developing laboratory and statistical methods for cancer detection
- ❖ Reports and publications preparation

EDUCATION AND ACADEMIC DEGREES

2024	DevOps Engineering on AWS / AWS Cloud Practitioner (certified)
2001	Bioinformatics and Programming Courses, Biolateral Pty., Sydney.
1998	Ph.D. in Molecular Biology. Ph.D. Thesis - "Short tandem repeats (STRs) as markers for human hereditary diseases. STRs application in genome fingerprinting."
1995 – 1998	Post-graduate study, Molecular Biology & Biochemistry, Moscow State University, Russia
1990 – 1995	Under-graduate study, Department of Biophysics, Biological Faculty, Moscow State University, Russia

PROJECTS AND EXPERIENCE

:: 2001 – 2003 ::

As postdoctoral fellow at the Centre for Bioinformatics Science (CBiS), Australian National University, Canberra I was running research project focusing on unsupervised and supervised clustering algorithms for genetic profile classification. This work was based on open public dataset downloaded directly from public domain or with utilization of my own website scrapper. Acquired data was reshaped and deposited into local mySQL database. I used Perl::ODBC module to make ETL (extract, transform, load) operations. Some of the research results of this work were published in Human Heredity Journal (Turakulov R, Easteal S. Number of SNPs loci needed to detect population structure. Hum Hered. 2003;55(1):37-45. PubMed PMID: 12890924). That was my first experience with Perl and SQL coding and then I was up keeping my skills sharp.

:: 2004 – 2016 ::

After Canberra I joined Australian Genome Research Facility which is non for profit organization and one of the major service providers for genomics research in Australia. I did lot of experiment designs statistical testing and client support with data transfer and analysis on routine and custom projects. Eventually I found myself writing Perl coded variant calling pipeline for high performance cluster machine (16 nodes with 16-32CPUs each). I also did lot of data integration and provided linkage between Laboratory Information System (In-house sample tracking database) and analysis pipeline which I was in charge. I wrote lot of documentations for clients and internal, projects participated in various accreditation processes, did many presentations for company trainings and provided teaching on company organized workshops. As a measurable results of that job were high number returned clients (over 70%), incorporation of graphical quality controls metrics into LIMS system, several publications in research journals, establishing from scratch or adding improvements to many company services: 16S quality control monitoring system, MLST testing lab protocol and analysis script, BVDV test, GoldenGate assay, GBS pipeline (still in use), R code for automation of microarray data analysis.

:: 2016 – 2019 ::

In 2016 I joined small start-up company smartDNA where I was working as contractor to establish and operating in-house Perl coded pipeline for 16S sequence analysis and human microbiome database (smartHIT^{TM}). This is fully automated data analysis workflow which takes the raw data and process through multiple transformation stages. The individual data (patient file) was merging with information from the matching reference group from Australian population set. After that program starts prediction/classification with randomForest model and finally producing PDF report which is delivered to the client (medical practitioner). For this analysis workflow I used Perl, R (various libraries), PDF::API2 module and various Linux bash command. I also had other side projects running on backgrounds like maintaining inhouse sequences database or scripts for other reports. For example script to transform spreadsheet data with multiple clients (Excel file) to individual report files with static and customized text in word document or PDF format. Another side of the job was development a patented method for human medical condition based on bacterial profile (Method of diagnosing a dysbiosis. Patent date: May 29, 2019. AU Patent number: au 2019203763).

:: 2019 – 2020 ::

Just one year before COVID era I started as a Bioinformatician at Moritz lab at ANU RSB Division of Ecology and Evolution (E&E), Centre For Biodiversity Analysis I was responsible for developing analytical pipelines for sequencing data on various in-house servers and clusters including Australian Supercomputer Facility, PAWSEY and NECTAR cloud machines. I developed containerized GATK best practice variant pipeline for non-model organisms and then also build phylogenetic pipeline for exone capture data both used by different groups across Australia and were deposited on public resource:
https://hub.docker.com/r/trust1

:: 2020 – 2023 ::

In late of 2020 I joined Laboratory Of Pathology at National Cancer Institute at NIH in USA, this job is focused on historical data harmonization generated over the years and integration of reports and results with Palantir enterprise system as well as interaction with other groups supporting alternative platforms like R-Shiny and specialized in-house systems and analytical workflows. Particularly normalization and dimensionality reduction methylation data pipeline on NIH HPC cluster (Biowulf). Research wise position is oriented on brain, haematological and other type of tumours classifications. I am working on testing different machine learning algorithms, dataset optimization, and exploratory analysis of new clusters formed by methylation profiling.
I had developed and maintaining entire backend of Methylation analysis portal for the Laboratory Of Pathology publicly available on this link:
https://methylscape.ccr.cancer.gov/
This backend includes quality controls implementations, data management and metadata maintenance for the in-house collection of over 60,000 samples. Each sample has multiple clinical records, multiple records for genomics tests (DNA/RNA) accompanied with analysis product files, reports and metrics linked on the methylscape portal, LIMS, Clinical database, backup systems.

:: 2023 -- current::

In September 2023 I have returned back to AGRF in Melbourne and started at the role for Senior Applications developer with focus on bioinformatics analysis of large soil bacterial datasets and interactive user graphical interface in shiny applications. I am also working integration of various laboratory records (excels, PDFs, run databases) with quality control metrics generated by multiple bioinformatics production pipelines in integrated QC platform based on MariaDB, Shiny server and AWS textract. Also working on developing new and maintaining existing services withing organization.

PUBLICATIONS

1. Hoang DT, Shulman ED, Turakulov R, Abdullaev Z, Singh O, Campagnolo EM, Lalchungnunga H, Stone EA, Nasrallah MP, Ruppin E, Aldape K. Prediction of DNA methylation-based tumor types from histopathology in central nervous system tumors with deep learning. Nature Med. 2024 May 17. doi: 0.1038/s41591-024-02995-8. PMID: 38760587
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3. Schreck KC, Strowd RE, Nabors LB, Ellingson BM, Chang M, Tan SK, Abdullaev Z, Turakulov R, Aldape K, Danda N, Desideri S, Fisher J, Iacoboni M, Surakus T, Rudek MA, Bettegowda C, Grossman SA, Ye X. Response Rate and Molecular Correlates to Encorafenib and Binimetinib in BRAF-V600E Mutant High-Grade Glioma. Clin Cancer Res. 2024 May 15;30(10):2048-2056. doi: 10.1158/1078-0432.CCR-23-3241. PMID: 38446982
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5. Miettinen M, Abdullaev Z, Turakulov R, Quezado M, Contreras AL, Curcio CA, Rys J, Chlopek M, Lasota J, Aldape KD. Assessment of The Utility of The Sarcoma DNA Methylation Classifier In Surgical Pathology. Am J Surg Pathol. 2024 Jan 1;48(1):112-122. doi: 10.1097/PAS.0000000000002138.
6. Potter S, Moritz C, Piggott MP, Bragg JG, Afonso Silva AC, Bi K, McDonald-Spicer C, Turakulov R, Eldridge MDB. Museum Skins Enable Identification of Introgression Associated with Cytonuclear Discordance. Syst Biol. 2024 Sep 5;73(3):579-593. doi: 10.1093/sysbio/syae016. PMID: 38577768
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