RUST TURAKULOV PHD

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www.linkedin.com/in/rust2021 | https://rust.app

Data-driven specialist with a PhD in Molecular Biology, blending expertise in large-scale data analysis, integration, predictive modeling, and interactive dashboard development to transform complex data into actionable insights.

EXPERIENCE

SEP 2023 - CURRENT

SENIOR DEVELOPER, AUSTRALIAN GENOME RESEARCH FACILITY, MELBOURNE, AUSTRALIA

Developed applications for analyzing bacterial profiles and integrating microbial, soil, vegetation, and land usage datasets for the Microbial Landscape project. Designed predictive models for real-time soil bacterial analysis. Built data dashboards for clinical quality control, clinical data ledger and open data registries.

https://rdata.agrf.org.au

NOV 2020 - AUG 2023

LABORATORY INFORMATION SYSTEM DEVELOPER, STAFF SCIENTIST, LABORATORY OF PATHOLOGY, NATIONAL CANCER INSTITUTE, NIH, BETHESDA, USA

Designed Lab Information System (LIS) with the Palantir enterprise system and developed high-throughput data workflows, integrating public domain and in-house clinical datasets for large-scale research. Led tumor classification research, optimized R-Shiny systems, and launched the Methylscape portal, supporting 200+ molecular pathologists in cancer diagnostics.

https://methylscape.ccr.cancer.gov

APR 2019 - NOV 2020

BIOINFORMATICIAN, ANU RSB DIVISION OF ECOLOGY AND EVOLUTION, CANBERRA, AUSTRALIA

Establish cloud systems for high-throughput sequencing analysis, including variant calling, de novo assembly, and phylogenetics. Design and integrate research databases (MySQL) with historical records, automate data quality control reporting, and develop streamlined data management protocols for acquisition, transfer, storage, and tracking.

APR 2016 - APR 2019

DATA SCIENTIST (CONTRACTOR), SMARTDNA LTD, MELBOURNE, VIC

Developed and maintained high-throughput workflows for bacterial analysis of human clinical samples, including an in-house sequence database processing 100+ samples monthly. Designed patented diagnostic methods, automated reporting pipelines, and predictive models for IBS, enhancing clinical decision-making for practitioners, reducing turnaround times, and expanding direct-to-consumer microbiome products.

EDUCATION

ONGOING

HONORARY LECTURER

College of Science & Engineering, Flinders University, Adelaide, SA

2024

BESPOKE TRAINING (ONLINE).

AWS DevOps Engineering and Cloud practitioner

2001

BIOLATERAL PTY., SYDNEY.

Bioinformatics and Programming Courses

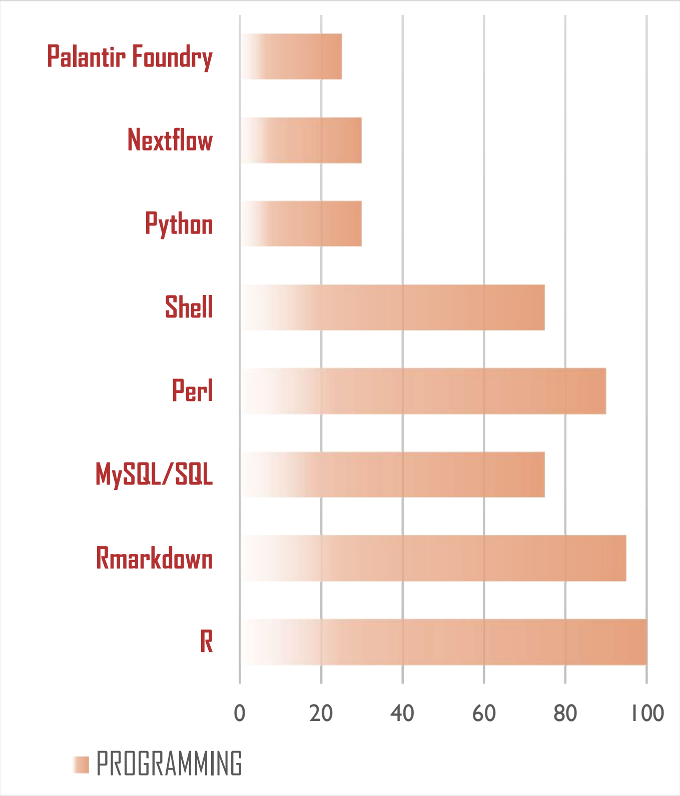
1998

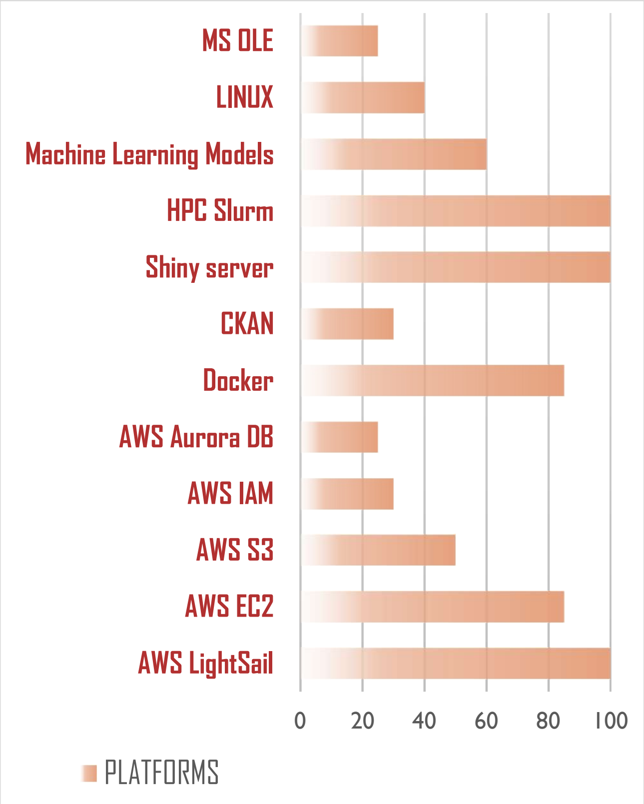
PH.D. IN MOLECULAR BIOLOGY. MOSCOW STATE UNI

Ph.D. Thesis - "Short tandem repeats (STRs) as markers for human hereditary diseases. STRs application in genome fingerprinting."

aws certified
Cloud Practitioner
FOUNDATIONAL

SKILLS





Numbers are based on self-assessment and calibrated by day-to-day usage.

SELECTED PUBLICATIONS

- 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
- Turakulov R, Nontachaiyapoom S, Mitchelson KR, Gresshoff PM, Men AE.Ultrasensitive determination of absolute mRNA amounts at attomole levels ofnearly identical plant genes with high-throughput mass spectrometry (MassARRAY).Plant Cell Physiol. 2007 Sep;48(9):1379-84. doi: 10.1093/pcp/pcm103. Epub 2007Aug 8. PMID: 17686807.
- Turakulov R, Easteal S. Number of SNPS loci needed to detect population structure. Hum Hered. 2003;55(1):37-45. doi: 10.1159/000071808. PMID: 12890924.

REFERENCES

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