

Dany Mukesha

Curriculum Vitae

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Education

- Sept. 2023 – **Doctor of Philosophy, Bioinformatics**, Université Côte d'Azur, Nice, France
Exp:July 2026
- March 2020 – **Master's degree, Bioinformatics**, University of Rome Tor Vergata, Rome, Italy
July 2023
- Nov. 2016 – **Bachelor's degree, Bioinformatics**, Sapienza Università di Roma, Rome, Italy
Oct. 2019

Experience

- March 2022 – **Bioinformatician**, Wayne State University, Detroit, Michigan, United States
- Sept. 2023 Performed computational analysis for gene expression data to evaluate the effects of environmental contaminants, such as plasticizers, on cardiovascular risk and disease.
- Dec. 2021 – **Software Engineer**, Accenture SpA, Rome, Italy
- Jan. 2023 Supported the implementation of software solutions for companies to conduct business operations and processes at enterprise-level.
- Sept. 2020 – **Bioinformatician**, The University of Manchester, Manchester, England, UK
- August 2021 Integrated epigenetic data and GWAS results to identify causal variants, genes, and cell types in Rheumatoid Arthritis (RA). Updated credible SNPs list through analysis of unrelated samples, assuming linkage disequilibrium between marker alleles and disease susceptibility alleles, improving RA genetic risk mapping.
- Jan. 2021 – **TIBCO Developer**, Catenate Group, Rome, Italy
- Dec. 2021 Developed and maintained TIBCO applications, including setting up Mashery API with security protocols. Created BusinessWorks processes for UAT and monitored TIBCO EAI applications for billing and inventory synchronization.
- July 2020 – **Bioinformatician**, Policlinico Agostino Gemelli IRCCS, Rome, Italy
- Dec. 2020 Performed transcriptomic analysis of ependymoma tumor samples, identifying Hub genes and key pathways through gene co-expression network analysis. Findings published in the International Journal of Molecular Sciences.
- Jan. 2019 – **Bioinformatician**, Sapienza Università di Roma, Rome, Italy
- Oct. 2019 Conducted genomic analysis of Burkholderia cepacia complex (BCC) isolates to identify genetic mutations and classify phylogenetic subgroups, revealing distinct virulence factors and antibiotic resistance profiles associated with each subgroup.

Publications

- [Mukesha, 2024] Mukesha, D. Scalable and interpretable genetic algorithm framework for high-throughput genomic data. 2024. doi:10.5281/zenodo.15801072.
- [Mukesha et al., 2025] Mukesha, D., Sarter, M., Dubray, M., et al. Targeted serum metabolomic

profiling and machine learning approach in alzheimer's disease using the alzheimer's disease diagnostics clinical study (addia) cohort. *medRxiv*, 2025. doi:10.1101/2025.04.01.25325021.

Software Contributions

- 2025 **BioGA**: Bioinformatics Genetic Algorithm R package (v0.99.16).
<https://bioconductor.org/packages/BioGA/>

Other Publications

- 2021 Servidei T, Meco D, Martini M, et al. *The BET Inhibitor OTX015 Exhibits In Vitro and In Vivo Antitumor Activity in Pediatric Ependymoma Stem Cell Models*. *Int J Mol Sci.* 2021;22(4):1877. <https://doi.org/10.3390/ijms22041877>
Contribution: Performed correlation network analysis of large, high-dimensional datasets.

Conferences and Awards

- July 27-30, Poster-Online at **AAIC® 2025** International Conference, Toronto, Canada.
2025 Topic: Integrating APOE Genotyping and Serum Metabolomics with Machine Learning to Distinguish Alzheimer's Disease and Dementia with Lewy Bodies.
- April 1–5, Poster-Onsite at **AD/PD™ 2025** International Conference, Vienna, Austria.
2025 Topic: Metabolomic Signatures and Machine Learning Models for Distinguishing Alzheimer's Disease and Dementia with Lewy Bodies.
- March 5–9, Poster-Onsite at **AD/PD™ 2024** International Conference, Lisbon, Portugal.
2024 Topic: Updated panel of genetic variants associated with multiple forms of neurodegenerative diseases.
- 2023–2026 **PhD Scholarship funded by European Union (EU) program** (France):
Marie Skłodowska-Curie Actions (MSCA) Doctoral Network.
- 2016–2022 **LazioDisco Scholarship of Merit** (Italy):
Awarded for academic excellence during Bachelor's (2016–2019) and Master's (2020–2022) studies.

Skills

Bioinformatics Genomics, transcriptomics, GWAS, gene co-expression network analysis

Statistics/ML Regression (Linear, Logistic, Mixed), Clustering (K-means, HCA), Neural Networks, Gaussian processes, Feature and Model Selection, PCA/ICA, LDA, KNN, RF, Bagging, Bayesian methods, CV, Meta-analysis, Text mining.

Software- Java microservices, Spring Boot, REST APIs, Angular, React, Kubernetes, Linux,
DevOps. Bash scripting, network configuration, Git, Docker, Terraform, Jenkins, GitLab/GitHub, LDAP.

Operations Unix, Cloud, Containers

Programming C++, Python/R, Java, Bash, Nextflow (Workflow manager), Slurm/PBS (HPC clusters)

Languages English, Italian, French

Databases Oracle, PostgreSQL, MySQL