Dany **Mukesha**

Curriculum Vitae

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Education

2023–2026	**Doctor of Philosophy, Bioinformatics**, *Université Côte d'Azur*, Nice, France
2020–2023	**Master's degree, Bioinformatics**, *University of Rome Tor Vergata*, Rome, Italy
2016–2019	**Bachelor's degree, Bioinformatics**, *Sapienza Università di Roma*, Rome, Italy

Experience

March 2022 – Sept. 2023	**Bioinformatician**, *Wayne State University*, Detroit, Michigan, United States Performed computational analysis for gene expression data to evaluate the effects of environmental contaminants, such as plasticizers, on cardiovascular risk and disease.
Dec. 2021 – Jan. 2023	**Software Engineer**, *Accenture SpA*, Rome, Italy Supported the implementation of software solutions for companies to conduct business operations and processes at enterprise-level.
Sept. 2020 – August 2021	**Bioinformatician**, *The University of Manchester*, Manchester, England, UK 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 – Dec. 2021	**TIBCO Developer**, *Catenate Group*, Rome, Italy 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 – Dec. 2020	**Bioinformatician**, *Policlinico Agostino Gemelli IRCCS*, Rome, Italy 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 – Oct. 2019	**Bioinformatician**, *Sapienza Università di Roma*, Rome, Italy 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, 2025 Poster-Online at **AAIC® 2025** International Conference, Toronto, Canada.
Topic: Integrating *APOE* Genotyping and Serum Metabolomics with Machine Learning to Distinguish Alzheimer's Disease and Dementia with Lewy Bodies.

April 1–5, 2025 Poster-Onsite at **AD/PD™ 2025** International Conference, Vienna, Austria.
Topic: Metabolomic Signatures and Machine Learning Models for Distinguishing Alzheimer's Disease and Dementia with Lewy Bodies.

March 5–9, 2024 Poster-Onsite at **AD/PD™ 2024** International Conference, Lisbon, Portugal.
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-Dev.	Java microservices, Spring Boot, REST APIs, Angular, React
DevOps & Tools	Kubernetes, Linux, Bash scripting, network configuration, Git, Docker, Terraform, Jenkins, GitLab/GitHub, LDAP.
Operations	Unix, Cloud, Containers
Programming	C++, Python/R, Java, Bash
Databases	Oracle, PostgreSQL, MySQL
Languages	English, Italian, French