DR. LUCAS MALDONADO (PhD)

Researcher and Bioinformatics Scientist | NGS & Multi-Omics Specialist

Specialised in bioinformatics strategies, NGS and data-driven research. Scientific innovation for the organizational growth.

SUMMARY

I am a Professor and Bioinformatics Scientist with 15+ years of experience applying Next-Generation Sequencing (NGS) across medicine, biotechnology, pharmaceuticals, agriculture, and biodiversity, bringing a profound understanding of the field that facilitates innovation and enables seamless integration of bioinformatics techniques.

During my career, I have played pivotal roles that combine leadership, hands-on bioinformatics analysis, and wet lab work, with experience spanning both academic and private sectors. My work has focused on developing innovative bioinformatics solutions while building and leading teams, creating advanced computational pipelines, designing NGS wet labs, and implementing HPC infrastructure.

I have spearheaded numerous projects advancing our understanding of complex biological systems, contributing to human health and biotechnological innovation, with outcomes including high-impact publications and proprietary intellectual property for industrial applications.

My expertise encompasses different bioinformatic areas:

- **Transcriptomics**: Bulk and single-cell transcriptomics for differential expression, phenotypic and functional characterization, cell type identification, biomarker discovery, and gene annotation.
- **Genomics & Precision Medicine:** Variant discovery (hereditary diseases, rare diseases, cancer) and genome assembly/characterization across species.
- **Metagenomics & Metatranscriptomics**: Ecosystem and microbiota diversity assessment through taxonomic classification and functional profiling, including human microbiota studies.
- **Bioinformatics Pipeline Development:** Scalable, automated pipelines for multi-omics data processing.

Beyond leadership roles, I remain actively involved in developing tools and software to streamline multi-omics analysis, enabling reproducible, high-performance processing of complex biological datasets. My work bridges fundamental research with practical applications, driven by a focus on scalable, robust solutions that integrate:

- Strategic thinking and meticulous attention to detail
- Agile methodologies for impactful results (Scrum - Kanban)
- Responsibility and enthusiasm for collaborative innovation

My extensive wet lab and in silico expertise, combined with leadership experience, allows me to deliver high-value contributions in any professional setting.

Leadership & Innovation

I have experience managing and leading multidisciplinary teams dedicated to developing advanced computational pipelines for genomic, transcriptomic, and proteomic analyses, as well as creating tailored bioinformatics software solutions. Key contributions include:

- Establishing a cutting-edge bioinformatics infrastructure (HPC) to support high-throughput sequencing data analysis, including large-scale datasets from single-cell RNA-seq, genomics, and proteomics.
- Building and mentoring specialized bioinformatics teams across diverse domains, including transcriptomics, multi-omics, and NGS-based precision medicine.
- Designing and implementing scalable sequencing analysis strategies for research, clinical, and biotechnological applications

Resume of Technical & Computational Skills

I am an expert in **bioinformatics technologies** for analyzing multiplatform NGS outputs (both short- and long-read data), applying advanced analytical techniques across diverse life science domains.

- Proficient in programming and scripting with R, Python, Bash and Perl, with extensive experience working in HPC and cloud environments. Skilled in workflow management systems (Nextflow, Snakemake, CWL), version control (Git, GitHub/GitLab), and containerization technologies (Docker, Singularity, Conda).
- Genomic Data Science expertise includes: Variant analysis: Germline/somatic mutation detection (GATK). Structural variation: CNV/SV calling. Clinical bioinformatics: Survival analysis, risk stratification. Genome assembly: Reference-based alignment (BWA, STAR, minimap2), De novo assembly (SPAdes, Flye, Canu). Metagenomics and diversity profiling: Microbiome analysis (QIIME2, MetaPhlAn), taxonomic/functional profiling (Kraken2, HUMAnN2, Kaiju, PICRUSt2).
- Transcriptomics Data Science proficiency includes: bulk and single-cell RNA-seq analysis using Cell Ranger, Seurat, Monocle3, Scanpy, DESeq2, EdgeR, limma, and the scverse ecosystem; biomarker

FIND ME ONLINE

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LinkedIn Profile
GitHub Profile
My portfolio web site
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EXPERIENCE

BIOINFORMATICS MANAGER
Stamm Vegh Corporation - Aug 2021 - Present

- I lead the design and implementation of advanced bioinformatics pipelines and algorithms, oversee the sequencing facility, and provide guidance to a skilled team.
- Develop strategic plans for the bioinformatics team.
- Established and direct a specialized division with departments, integrating bioinformatics techniques into operations
- Oversee the bioinformatics aspects of NGS projects from inception to completion.
- Provide innovation and increased operational efficiency in bioinformatics developments

LEADER OF BIOINFORMATICS DEPARTMENT
Stamm Vegh Corporation - Aug 2021 - Present

- I lead the design and implementation of pipelines and algorithms while overseeing staff in data analysis
- Ensure projects are delivered on time, within scope, and within budget and serve as a Scientific R&D advisor.
- Develop and implement bioinformatics pipelines and workflows and tools for NGS data analysis.
- Interpret and present results to scientific and non-scientific audiences.
- Design and apply novel computational methods/bioinformatics algorithms to aid in the analysis and interpretation of genetic data

UNIVERSITY PROFESSOR
UADE University - Jul 2020 - Present

- I organize international postgraduate courses and design workshops in bioinformatics, focusing on Linux operating systems.
- I lead practical workshops and courses for students and professionals employing engaging teaching methods.
- I supervise students and provide mentorship to technical trainees.

SCIENTIFIC R&D ADVISOR | BIOINFORMATICS & NGS SPECIALIST
Free Lance - Independent Bioinformatics Consultant - Jul 2015 - Present

- I provide expert guidance in Scientific R&D, specializing in NGS experiments and bioinformatics analysis.
- I advise public and private institutions on optimizing protocols, quality control, and interpreting omics data.
- I provide experimental protocols and interpretation of intricate omics datasets applied for translational biomedicine.

POST-DOCTORATE BIOINFORMATICS AND GENOMICS
CONICET – University of Buenos Aires, Argentina - 2019-2021

- Led bioinformatics and genomics projects on infectious diseases.
- Analysed genomic and transcriptomic data to uncover disease mechanisms.
- Collaborated on interdisciplinary teams to develop innovative approaches.
- Published research findings in peer-reviewed journals.

POST-DOCTORATE, BIOINFORMATICS AND GENOMICS
University of Edinburgh", United Kingdom. 2017-2019

- Led R&I projects on infectious diseases and biodiversity, utilizing bioinformatics and genomics.
- Conducted sequencing to discover novel species and study biodiversity.
- Published research findings in peer-reviewed journals.

discovery and trajectory analysis; spatial transcriptomics (Visium, Xenium); and epigenomics (ChIP-seq, ATAC-seq).
- Proteomics experience covers mass spectrometry data analysis using MaxQuant, FragPipe, and DIA-NN for protein profiling and differential abundance estimation.
- Advanced analytical capabilities include: statistical modeling and machine learning (Scikit-learn, TensorFlow); network biology (WGCNA, Cytoscape, NetworkX).

Domain expertise spans precision medicine and oncology, rare disease genomics, microbiome therapeutics, and agricultural biotechnology, with strong knowledge of key biological databases and resources, real-world data (RWD) and evidence (RWE) frameworks.

EDUCATION

- Ph. D in Biological Sciences specialised in Bioinformatics – Doctorate in Philosophy

University of Buenos Aires, CONICET, Argentina
Major: Bioinformatics, Genomics, and Infectious Diseases

- Master, Biotechnology and Molecular Biology

National University of La Plata, Argentina
Major: Biotechnology and Molecular Biology

- Bachelor, Biotechnology and Molecular Biology

National University of La Plata, Argentina
Major: Biotechnology

LANGUAGES

Spanish
Native

English
Proficiency

Portuguese
Advance

ACHIEVEMENTS

Pioneering Leadership at STAMM Corporation:
- Created and led the Bioinformatics Division, driving cutting-edge pipeline implementation and team growth.
- Spearheaded sequencing facility design, ensuring advanced genomic analysis capabilities.

Trusted Scientific Advisor and Extensive R&D Portfolio:
- Provided invaluable expertise to public and private institutions, shaping NGS experiments and bioinformatics pipelines, while significantly increasing time response in wet lab settings.
- Facilitated groundbreaking research on diverse genomic complexities, offering strategic guidance, particularly in translational medicine and biotechnology, resulting in increased yield and insights.

Establishment and Management of Bioinformatic Nodes:
- Created bioinformatic nodes, optimizing computational analysis and providing solutions.
- Ensured seamless operations crucial for scientific advancement.

Internationally Acclaimed Author:
- Published 19 groundbreaking scientific articles, advancing understanding in genomics and biomedicine.

Successful Project Leadership:
- Led projects to success, integrating software development with bioinformatics for biological insights and technological solutions.

STRENGTHS

- Leadership and Project Management
- Strategic Thinker, Innovation and R&D criteria
- Expertise in Bioinformatics and Biology
- Interdisciplinary Expertise
- Resilient Under Pressure
- Responsibility, Precision and Accuracy
- Effective Team Communicator
- Trusted and Empathetic Leader

R&D SCIENTIST
National Institute of Agricultural Technology - Buenos Aires, Argentina - 2011 - 2013

- Research to provide valuable contributions to plague controls.
- Designed experiments with rigorous controls to ensure the validity and reliability of findings.
- Interpreted data analysis results to draw inferences and conclusions.
- Worked as a member of an integrated project team in a highly collaborative work environment.

R&D SCIENTIST
Barenbrug-Palaversich Company - Buenos Aires - 2009 - 2011

- Spearheaded cross-functional projects, ensuring timely completion while maintaining high-quality standards.
- Conducted Microbiology techniques applied to the improvement of soybean inoculants.
- Utilized Genetic engineering to modify organisms as a method for the improvement of crop yield.

PUBLICATIONS

PubMed (19)
- NCBI Profile
- Scopus Profile

WIPO
- WO2024059658

SKILLS

Programming Languages, Tools And Technologies
Python | R | Shell Script | Perl | BASH | Linux Systems | Docker | Snakemake | Nextflow | VIM | fastapi | Git & Version Control | Jupyter Notebooks | RMarkdown | Regular Expressions | Markdown & LaTeX for Docs | Jupyter | conda | Conda/Virtualenv | Poetry | RStudio | Visual Studio Code | Software Development | Django | Flask | R Shiny | Amazon AWS | AWS, GCP, Azure | Cloud Computing | Virtualization (VirtualBox, VMWare)

Bioinformatics skills

Core areas and omics disciplines
Genomics | Transcriptomics | Single Cell | Spatial RNASeq | Proteomics | Metabolomics | ChIP Seq/ATAC Seq | Epigenomics | Multiomics Analysis | Metagenomics | Comparative Genomics | Ancient DNA | Lipidomics | Glycomics | Structural Bioinformatics

Bioinformatics technologies
NGS | De novo Assembly | CRISPR-Cas | Database Management | Genome Annotation | Genome Browsers | Variant Calling | Genetic Variants analysis | Haplotype Analysis | eQTL Analysis | RNA-Seq Analysis | Gene Fusion Detection | CNV Analysis | Metabolic Pathway Analysis | Long Read Technologies | Expression Profile Analysis | Differential Expression Analysis | Functional Enrichment Analysis | Biodiversity and Abundance Analysis | ncRNA and microRNA Analysis | microRNA Target Prediction | Pattern Analysis

Analytical methods
Statistical Analysis | Machine Learning | Data Visualization | Systems Biology | Phylogenetics | Clustering Analysis | Dimensionality Reduction

Genomic data analysis
GWAS/Burden Tests | Statistical Modeling | Read Mapping | Sequence Alignment | Functional Enrichment | De Novo and Reference Based Assembly | Copy Number Variation (CNV) Detection | Mutational Signature Analysis

Transcriptomics data analysis
Bulk RNA-Seq Analysis | Single-Cell & Spatial Transcriptomics | Quality Control & Preprocessing | Transcript Quantification | Gene Expression Profiling | Differential Gene Expression (DGE) | Functional Enrichment | Alternative Splicing & Isoform Analysis | Cell Type Identification & Clustering | Trajectory Inference | pseudotime, cell fate | Biomarker Discovery | Epitranscriptomics | RNA Modification Profiling | Long-Read Transcriptomics | Full-Length Isoform Detection | Fusion Gene & Novel Transcript Discovery | Small RNA & Non-Coding RNA | Multi-Omics Integration | RNA + Chromatin (ATAC-seq) | RNA + Proteomics | Cross-Species Comparative Transcriptomics | Dynamic Transcriptomics | Time-Series Analysis | Perturbation Modeling

Diversity and profiling
Alpha and Beta Diversity Analysis | Shannon Index, Bray–Curtis dissimilarity | Functional Profiling | Ordination Methods | Taxonomic Profiling | Strain Level Profiling & Variant Detection | Assembly & Binning | Visualization & Statistical Analysis | Integrated Pipelines | Reference Databases

Statistical advanced methods and modeling
Multi-omics Factor Analysis (MOFA) | Canonical Correlation Analysis (CCA) | Similarity Network Fusion (SNF) | Feature Selection / Importance Ranking | Predictive Modeling | Autoencoders / Deep Learning Models | Zero-Inflated Models | Bayesian Hierarchical Models | False Discovery Rate Control | Multivariate Analysis | Hidden Markov Models (HMMs)