

Alejandro Bernabéu Duréndez

BIOINFORMATICS SOFTWARE DEVELOPER | APPLIED BIOINFORMATICS, PYTHON & NGS WORKFLOWS

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Based in Spain | Open to fully remote roles | English: Advanced (C1)

PROFESSIONAL PROFILE

Bioinformatics software developer with an MSc in Computational Biology and a BSc in Biotechnology, combining applied bioinformatics with production software engineering. At ISCIII/CIBER I develop and troubleshoot NGS workflows and Python tools used in genomic surveillance, working with Nextflow/nf-core, Linux/HPC, SLURM, containers, metadata validation and relational databases. I also contribute upstream to community bioinformatics pipelines. I enjoy turning complex biological analyses into reliable, reproducible software that researchers can use and trust.

TECHNICAL SKILLS

Applied bioinformatics & NGS: viral and bacterial genomics, sequence assembly, NGS/genomic analysis, FASTQ/CRAM/VCF, metadata QC and validation

Programming & analysis: Python, Bash, SQL, pandas, NumPy, JSON/JSON Schema, Nextflow DSL, REST APIs, Django/DRF, CLI development

Scientific workflows: Nextflow/nf-core, nf-test, Linux, HPC/SLURM, Docker/Podman, Git/GitHub, GitHub Actions, automated testing, reproducible workflows

Data & software: PostgreSQL, MySQL/MariaDB, data ingestion, reporting, API integration, performance troubleshooting

Computational biology: AlphaFold2/3, PyRosetta, structural analysis, model confidence metrics, comparison with experimental evidence

PROFESSIONAL EXPERIENCE

Bioinformatics Analyst | Genomic Workflows & Scientific Software

Instituto de Salud Carlos III (ISCIII) / CIBER | Madrid, Spain | October 2024 - Present

RELECOV project; CIBER appointment since July 2025.

Production NGS workflows & open source | Python, Nextflow/nf-core & HPC

- Develop, run and troubleshoot production sequencing workflows for public-health surveillance, including viral and bacterial analyses with nf-core/viralrecon, nf-core/bacass, IRMA, Linux/HPC and SLURM.
- Contribute upstream to nf-core/bacass with merged work on MEGAHIT short-read assembly, assembly-type/assembler compatibility validation, pipeline metadata and nf-test/test-dataset coverage.
- Develop Python tooling for sequencing-data ingestion, metadata transformation, schema-based validation, reporting and result handling; investigate failed analyses, unexpected outputs and data-quality issues before downstream use.

Scientific software & genomic platforms | RELECOV-Platform / relecov-tools

- Develop and maintain Python software used by public-health laboratories to collect, validate, process and report genomic surveillance data, including reusable command-line tools and integrations with internal laboratory services.
- Work across REST APIs, relational data models, variant/sample ingestion and metadata validation; improve reliability and performance through bulk operations, transactions, lookup caches, composite indexes and server-side processing.
- Collaborate with bioinformaticians, laboratory teams and software engineers to translate biological and operational requirements into maintainable, reproducible software changes.

PROFESSIONAL EXPERIENCE (CONTINUED)

Biomedical data services | MePRAM OMOP API

- Developed the initial Python/Django REST API exposing aggregated clinical data for research dashboards, with filtering, pagination and demographic stratification; structured the backend into service, serializer and routing layers with OpenAPI documentation and automated tests.

Secure genomic research infrastructure | LocalEGA / FEGA

- Contribute to deploying and operating secure genomic-data infrastructure using Linux, rootless Podman, PostgreSQL, RabbitMQ, NFS and SSH/SFTP; work on storage, permissions, service connectivity and operational troubleshooting.
- Developed safe file-retention tooling with archival verification, dry-run mode, audit logs and database tracking, and prepared operational documentation for validation, backups and troubleshooting.

EARLIER EXPERIENCE

Computational Biology Intern | Protein Structure Modelling

Centro de Investigaciones Biológicas Margarita Salas (CSIC) | Madrid, Spain | January 2024 - June 2024

Developed Python workflows for molecular modelling and structural analysis using AlphaFold2, AlphaFold3 and PyRosetta. Prepared inputs, simulated mutations and evaluated predicted structures and interactions using confidence metrics, structural comparisons and experimental evidence.

Python Developer Intern | Genomic Data Analysis

Instituto de Biología Molecular y Celular de Plantas (IBMCP) | Valencia, Spain | January 2022 - July 2023

Built Python command-line tools to process genomic datasets with pandas and NumPy, including filtering, feature selection and structured exports. Implemented information-theory metrics and statistical analysis scripts for biological datasets.

SCIENTIFIC SOFTWARE & OPEN SOURCE

nf-core workflows | bacass & viralrecon

Public contributions to community bioinformatics pipelines covering workflow logic, validation, automated tests, module integration and documentation. Merged nf-core/bacass contributions include MEGAHIT integration and assembly/assembler compatibility validation. Participant and co-organizer in nf-core hackathons in 2025 and 2026.

Production bioinformatics tooling | relecov-tools & buisciii-tools

Maintain Python tools that connect sequencing workflows, metadata validation, databases, file transfer and reporting in recurring production environments. Contribute through shared repositories, code review, testing and incremental releases.

EDUCATION & TRAINING

Master's Degree in Computational Biology | Universidad Politécnica de Madrid

Bachelor's Degree in Biotechnology | Universitat Politècnica de València

Artificial Intelligence, Samsung Innovation Campus | 2023