# Gabriel J. Benitez | Bioinformatics Research Scientist

Edinburgh, UK + 44 7960 559416 gabbenitez99@gmail.com gabbenitez

## ABOUT ME

I am a research scientist with strong quantitative analysis skills, complemented by a foundation in biomedical science and molecular biology. I specialise in analysing complex health data and translating findings into clear, evidence-based outputs tailored to diverse stakeholders. With experience in managing multiple projects, mentoring colleagues, publishing presentation material across several conferences, and developing strategies to deliver and anticipate business needs, I am looking to apply my comprehensive skillset at the interface of scientific research and health policy to deliver meaningful change.

Expert in analysing and communicating large-scale, multi-modal data, focusing on complex, sensitive datasets to understand the drivers behind clinical health outcomes. Highly proficient in Python and interactive dashboard development, with experience in project management and stakeholder engagement.

## EXPERIENCE

**Bioinformatician | Wobble Genomics (Startup) | 2024 - Present**

- Worked cross-functionally across bioinformatics, R&D, and Operations teams to produce conference abstracts and posters for dissemination across multiple audiences. Led to poster acceptances at SABCS 2024 and 2025, ESMO 2025, and EDCC 2024.
- Management of 3 concurrent projects, across 3 teams, ensuring high quality and timely deliverables. Findings were presented to board members and external pharma clients, informing key business decisions.
- Development of novel computational tools and pipelines for quality control and statistical analysis of ONT RNA-seq alongside clinical metadata for HER2-variable breast cancer patients.
- Built software for predicting cross-validated cancer burden diagnosis, target identification, and biomarker interpretation from multi-modal datasets for improved patient stratification for targeted ADC therapies.
- Assessment, optimization, and reporting on R&D protocols to improve efficiency and reproducibility of our experimental platforms. Responsible for reducing costs of our sequencing pipeline by over 60%.
- Mentoring and guiding 3 junior members in interacting and contributing to our internal codebase.
- Temporary co-management of the bioinformatics team in the absence of line-manager, supporting the prioritization and delivery of tasks to internal and external stakeholders.

**Bioinformatics Research Scientist | Anthony Nolan Research Institute | 2021 - 2024**

- Designed pipelines and internal software for automated PacBio sequencing, variant calling, and high-throughput analysis of hyper-polymorphic genes in the MHC, supporting data annotation for the improvement of blood-cancer patient outcomes, culminating in a poster presented at EFI 2022.
- Integrated statistical and machine-learning tools to enhance error correction methods and quality control for sequence polishing, and improved variant calling analysis for more informed patient stratification.
- Conducted detailed phylogenetic analysis of over 37,000 HLA alleles in the IPD-IMGT/HLA database and built a *k*-mer variant calling tool, implementing Meta's Facebook AI Similarity Search (FAISS) algorithm.
- Represented the Research division at monthly, company-wide meetings, championing equity and inclusion.
- Hosted the annual summer briefing, motivating and compering an audience of 200+ employees and guests.

**Researcher | MRC Institute of Genetics and Cancer, Chandra and Schumacher Groups. | 2020 - 2021**

- Modelled telomere dynamics in ageing via a DNA methylation-based estimator, applied to the longitudinal, multi-decade Lothian Birth Cohort and Generation Scotland datasets.
- Evaluated the use of biological clocks in the context of predictive healthcare analytics.
- Performed single-cell transcriptomic analysis on senescent cells, validating therapeutic targets for the treatment of age-related diseases. Assessed deconvolution tools within the lab's canonical computational analysis pipeline.

## EDUCATION

**MSc Bioinformatics | University of Edinburgh | 2020 – 2021**

- Graduated with Distinction.
- Represented the course, creating a positive and authentic narrative to prospective students as a student ambassador via the Unibuddy program.

**BSc Biomedical Sciences (Hons.) | University of Edinburgh | 2017 – 2020**

- Awarded a 2:1 classification from year 2 direct entry of a 4-year honours program.
- Volunteered as a BioBuddy, supporting peers and building academic and social communities within the University.

## SKILLS / TECHNOLOGIES

**Analysis**
Data Visualization | Statistical Modelling | Regression Analysis | Time Series | Clustering | Machine Learning
Simulation Modelling | Dimensionality Reduction | Network Analysis | Quality Control | Functional Enrichment

**Communication**
Microsoft Office | Data Storytelling | Publication-Ready Figures | SOP Writing | Peer Reviewing | Feedback
Cross-Departmental Collaboration | Stakeholder Engagement | Documentation | Mentoring | Jira | Confluence

**Biomedical Sciences**
Oncology | Molecular Genetics | Functional Genomics | Systems Biology | Next Generation Sequencing
Epigenetics | Cancer Genomics | Biomarker Discovery | Predictive Analytics | Sensitivity/Specificity Analysis

**Informatics**
Python | numpy | pandas | seaborn | maplotlib | scikit-learn | tensorflow| R | tidyverse | Linux/Bash | Nextflow
Docker | HTML | conda | Git/version control | AWS | GCP | Cloud Computing | Parallelization | Containerization

## SELECTED POSTERS / PRESENTATIONS

Isoform Level RNA Detection Provides More Detailed Profiling of HER2 Expression in Breast Cancer. Poster, San Antonio Breast Cancer Symposium (SABCS), Texas, 2025.

Analytical Performance of a Novel Long-Read RNA Sequencing Assay for Low-Abundance Cancer Transcript Detection from Whole Blood. Poster, European Society for Medical Oncology Congress (ESMO), Berlin, 2025.

Novel Liquid Biopsy Technology Reveals Cancer-Specific Isoforms for Breast Cancer Diagnosis and Therapy. Poster, SABCS, Texas, 2024.

Novel Liquid Biopsy Technology Reveals Hidden RNA Signals in Early-Stage Breast Cancer. Poster, Early Detection of Cancer Conference (EDCC), San Francisco, 2024.

Gnomic Typer: Uncovering Homopolymer and Repeat Region Sequencing Errors via K-mer Based HLA Typing. Presentation, EFI, Geneva, 2024.

Full- Gene Sequence Characterization of HLA-DMA, -DMB, -DOA, and –DOB in a Panel of International HLA and Immunogenetics Workshop Cell Lines. Poster, EFI, Nantes, 2023

Automated Workflow for HLA Analysis of Pacific Biosciences Sequel Data Using Google Cloud Platform. Poster, EFI, Amsterdam, 2022.