GABRIEL J. BENITEZ

Bioinformatics Research Scientist

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ABOUT ME

My background consists of strong programming skills, complemented by a foundation in molecular biology and quantitative research. I bring hands-on experience in software development for high-throughput genomic analysis, focussed on the most polymorphic region of the human genome.

EXPERIENCE

Bioinformatics Research Scientist
2021 – Present

Anthony Nolan Research Institute

- Developed pipelines for NGS sequencing, QC, variant calling and interpretation for analysis of genes in the MHC.
- Performed k-mer based analysis of evolutionary dynamics in the MHC and built a *k*-mer based typing tool.
- Created visualisations and communicated research to internal, non-scientific staff, as well as external clients.

Researcher
2020, 2021

MRC Institute of Genetics and Cancer

- Evaluated a DNA methylation-based estimator as proxy for telomere attrition in human models of ageing.
- Profiled transcriptomic subpopulations in senescent cells to validate therapeutic targets for the treatment of age-related diseases.

Medical Engineering Intern
2016

CERN

- Explored applications of particle physics in medical diagnosis and treatment of cancer, via hadron therapy.

EDUCATION

MSc Bioinformatics
2020 –2021

University of Edinburgh

- Graduated with distinction.

BSc Biomedical Sciences (Hons.)
2017 - 2020

University of Edinburgh

- Awarded a 2:1 classification from year 2 direct entry of a 4-year honours program.

SKILLS / TECHNOLOGIES

Python R Nextflow/DSL2 Linux/Shell HTML Git

pandas scipy scikit-learn tensorflow PCA t-SNE

NGS Pipelines scRNA-seq Statistics Visualisation

Jupyter Docker Google Cloud Platform PacBio

PROJECTS

Pipeline Development
2021 – Present

Anthony Nolan Research Institute

- Designed internal workflows and software for automated, high-throughput, long-read PacBio sequencing and analysis, using Nextflow, Google Cloud Platform, Docker.
- Established statistical and machine-learning tools to enhance error correction methods and quality control for variant calling analysis and sequence polishing.

Genomic Analysis
2021 – Present

Anthony Nolan Research Institute

- Implemented *k*-mer based phylogenetic analysis of over 37,000 alleles in the IPD-IMGT/HLA database, identifying sets of progenitor alleles.
- Formulated *k*-mer based typing software for homopolymer error-informed variant calling, using Meta's Facebook AI Similarity Search (FAISS) algorithm.

Computational Modelling
2021

MRC Institute of Genetics and Cancer

- Computational modelling of telomere dynamics, applied to the Lothian Birth Cohort and Generation Scotland datasets, as foundation for predictive healthcare tools of ageing populations. Chandra and Schumacher groups.

Differential Expression Analysis
2020

MRC Institute of Genetics and Cancer

- scRNAseq and enrichment analysis of etoposide-induced senescent fibroblast subpopulations. Chandra group.

SELECTED TALKS / POSTERS

Gnomic Typer: Uncovering Homopolymer and Repeat Region Sequencing Errors via k-mer Based HLA Typing. Oral Presentation, 37th EFI Conference, Geneva, 2024.

Full-Gene Sequence Characterisation of HLA-DMA, -DMB, -DOA, and -DOB in a Panel of International HLA and Immunogenetics Workshop Cell Lines. Poster, 36th EFI Conference, Nantes, 2023.

Comparing Accuracy of HLA Typing from DNA Extracted from Blood and Buccal Samples for Patients in Remission from Malignant Haematological Disease and Healthy Donors. Poster, 36th EFI Conference, Nantes, 2023.

Automated Workflow for HLA analysis of Pacific Biosciences Sequel Data Using Google Cloud Platform. Poster, 35th EFI Conference, Amsterdam, 2022.