GABRIEL J. BENITEZ

Bioinformatics Research Scientist

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ABOUT ME

My background consists of strong programming skills and a demonstrated training in genetic, molecular, and quantitative research. I bring hands-on experience in software development for high-throughput analysis and evolutionary research of the most polymorphic region of the human genome.

EXPERIENCE

Bioinformatics Research Scientist
2021 – Present

Anthony Nolan Research Institute

- Development, optimisation, and automation of NGS tools and pipelines for sequencing, typing, and analysis of HLA and other polymorphic genes of interest.
- Development of software and novel research to interrogate evolutionary patterns in the MHC.

Co-Camp Leader
2019, 2020

All Special Kids

- Led teams of 15+ staff members and directed day programs for 30+ special needs campers, acted as a diplomatic point of liaison for external communications.

Medical Engineering Intern
2016

CERN

- Explored applications of particle physics in medical diagnosis & treatment of cancer via hadron therapy, LHC engineering of field quality, & beam instrumentation.

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.

International Baccalaureate
2015 –2017

Institut International de Lancy

- Achieved 40 points (out of 45, top 10% worldwide).

SKILLS & TECHNOLOGIES

Python R Nextflow Linux/Shell HTML Git

NGS Pipelines scRNAseq Docker PacBio Jupyter

Scikit-Learn Statistics Visualisation Automation HPC

PROJECTS

Pipeline Development
2021 – Present

Anthony Nolan Research Institute

- Development of workflows and software for high-throughput, long-read PacBio sequencing and cloud-based analysis using Nextflow, Google Cloud Platform and Docker containerisation.
- Development and integration of statistical and machine-learning tools to enhance sequence error-correction methods and quality control for variant calling analysis.

Genomic Analysis
2021 – Present

Anthony Nolan Research Institute

- *K*-mer based phylogenetic and functional analysis of over 37,000 HLA alleles in the IPD-IMGT/HLA database.
- Designing *k*-mer based typing software for homopolymer error-informed variant calling.

Computational Modelling
2021

MRC Institute of Genetics & Cancer

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

Differential Expression Analysis
2020

MRC Institute of Genetics & Cancer

- scRNAseq analysis of etoposide-induced senescent fibroblast subpopulations.

CONFERENCES / POSTERS

Tierney, M.T., Turner, T.R., Benitez, G.J., Barker, D., Mayor, N.P., Marsh, S.G. (2023, May)
Full-Gene Sequence Characterisation of HLA -DMA, -DMB, -DOA, and -DOB in a Panel of International HLA and Immunogenetics Workshop Cell Lines.

Cambridge, C.A., Benitez, G.J., Dishington, J., Georgiou, X., Mayor, N.P., Marsh, S.G. (2023, May)
Comparing Accuracy of HLA Typing from DNA Extracted from Blood and Buccal Samples for Patients in Remission from Malignant Haematological Disease and Healthy Donors.

Nadeem, D., Benitez, G.J., Leen, G., Turner, T.R., Mayor, N.P., Robinson, J., & Marsh, S.G. (2022, May)
Automated Workflow for HLA analysis of Pacific Biosciences Sequel Data Using Google Cloud Platform.

Cambridge, C.A., Turner, T.R., Lucas, J.A., Benitez, G.J., Leen, G., Nadeem, D., & Marsh, S.G. (2022, May)
Advantages of Pacbio's Barcoded Adapter Strategy for Single Molecule Real-Time (SMRT) Sequencing of the Classical HLA Class II Genes on the Sequel Instrument.