

Salvatore Barbagallo

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Professional Summary

Bioinformatics analyst with a background in clinical genomics and 7+ years of laboratory experience supporting NGS-based diagnostics and cell & gene therapy workflows. Experienced in building reproducible analysis pipelines and performing downstream RNA-seq and variant analysis using Python, R, Bash, and SQL. Strong track record in regulated healthcare environments (documentation, consistency, data quality) and experience bridging wet-lab processes with computational workflows.

Skills

Programming & Reproducibility: Python, R, SQL, Bash, Git, Nextflow, Docker

NGS Workflows & Tools: BWA, Bowtie2, STAR, HISAT2, SAMtools, BEDtools, bcftools, Picard, featureCounts, DESeq2, Cutadapt, IGV, MultiQC

Data Analysis & Visualisation: SAS, Tableau, ggplot2, matplotlib, scikit-learn, SciPy

Cloud & Delivery: Google Cloud; Kubernetes Engine foundations; Amazon Web Services (AWS) Cloud Practitioner foundations; Agile, Scrum, Waterfall

Lab Systems & Instrumentation: Illumina Control Software; SPT Labtech Software; BD FACS DIVA; WinPath; QPulse; EPIC; iPassport

Languages: Italian (Native), English (Fluent), Portuguese (Fluent), Spanish (Intermediate)

Projects

RNA-seq Pipeline (Nextflow + Docker)

- Designed and implemented a containerised RNA-seq analysis pipeline using Nextflow and Docker to ensure reproducibility across environments.
- Integrated FastQC, Cutadapt, STAR, featureCounts, and DESeq2 into an automated workflow producing standardised QC and differential expression outputs.
- Enabled one-command execution and reproducible analysis suitable for research and clinical genomics contexts.

M. tuberculosis WGS Variant Analysis Workflow (Galaxy, Linux, bcftools)

- Built and ran a full WGS analysis workflow in Galaxy for *M. tuberculosis* short-read data, including BWA-MEM2 alignment, BAM sorting and duplicate marking, mapping QC, depth analysis, variant calling, filtering, consequence annotation, and final reporting.
- Applied tools including **fasterq-dump**, **Falco**, **fastp**, **Cutadapt**, **BWA-MEM2**, **Picard SortSam/MarkDuplicates**, **Samtools**, **mosdepth**, **bcftools SnpEff**, **SnpSift**, and **IGV** for read-level inspection and variant review.
- Interpreted variants in clinically relevant resistance loci using coverage metrics, variant allele frequencies, annotation outputs, and visual inspection of mapped reads.

NGS Analysis Workflows (RNA-seq & Variant Calling)

(Bowtie2/BWA, SAMtools, BEDtools, VCFtools, (R (Bioconductor/DESeq2), STAR/HISAT2)

- Implemented end-to-end NGS analysis workflows including RNA-seq processing and variant calling using STAR/HISAT2, BWA/Bowtie2, SAMtools, BEDtools and DESeq2.
- Performed quality control, alignment, count generation, differential expression analysis, and basic variant filtering.
- Documented reproducible command-line pipelines and parameter choices for transparency and reusability.

Work Experience

Specialist Biomedical Scientist

University College London Hospitals, Stem Cell Laboratory, *September 2021 - December 2025*

- Analysed CD3+ and CD34+ cell populations via flow cytometry and reported results supporting patient treatment decisions.
- Evaluated Burst-Forming Unit-Erythroid (BFU-E) and Granulocyte-Macrophage Colony-Stimulating Factor (GM-CSF) colonies for stem cell transplant suitability.
- Applied computational skills to streamline stock management and training assessments, reducing inventory errors by 30% and saving 10+ hours weekly.
- Supported 11 clinical trials, handling Advanced Therapy Medicinal Products (including CAR-T cells), and maintained high-quality documentation for regulated workflows.

Laboratory Scientist

CooperGenomics, London, *July 2019 - September 2021*

- Processed embryo and cheek swab samples for PGT-A, PGT-SR, and PGT-M testing.
- Conducted NGS library preparation (manual: 96 samples/run; automated: 192 samples/run) with strict QC adherence for Whole Genome Sequencing.
- Generated 500+ clinical reports per week from NGS data, maintaining consistency through documented checks and templates.
- Maintained and calibrated automated liquid handling systems Mosquito HV and Dragonfly Discovery from SPT Labtech.
- Developed and reviewed SOPs to ensure ISO-compliant laboratory practices.

Education

Master of Science: Bioinformatics

Atlantic Technological University (Remote), *September 2025 - Present (ongoing)*

Master of Science: Cell and Gene Therapy

University College London, *September 2021- September 2023*

Bachelor: Biomedical Science

Siciliae Studium Generale - University of Catania, *September 2014 - October 2017*

Certificates

Google: Data Analytics; Advanced Data Analytics; IT Automation with Python; Project Management; Business Intelligence

Google Cloud: Architecting with Google Kubernetes Engine

Amazon Web Services (AWS): Cloud Practitioner Essentials; Cloud Solutions Architect

Johns Hopkins University: Genomic Data Science Specialization

SAS: SAS Programming 1: Essentials; SAS Programming 2: Data Manipulation Techniques