

# Salvatore Barbagallo

Bioinformatics Analyst | NGS & Computational Genomics  
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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 focus on data quality, workflow automation, and translating biological questions into computational solutions within regulated healthcare environments.

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## Skills

**Programming & Reproducibility:** Python, R, SQL, Bash; Git/GitHub; Biopython, Bioconductor

**Bioinformatics & Genomics:** RNA-seq analysis, Variant Calling, Sequence Alignment, Genome Assembly, Quality Control (FastQC, MultiQC)

**NGS Tools & Pipelines:** STAR, HISAT2, Bowtie2, BWA, SAMtools, BEDtools, featureCounts, DESeq2, Cutadapt, Nextflow, Docker

**Data Analysis & Visualisation:** SAS, Statistical modelling; model evaluation basics; Tableau; ggplot2; matplotlib; seaborn; SciPy; scikit-learn; XGBoost

**Cloud & Delivery:** Google Cloud; Kubernetes Engine foundations; Amazon Web Services (AWS) Cloud Practitioner foundations;

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

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## 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

### 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

### Computational Genomics & Sequence Data Processing

*(Python (Biopython), SQL, Bash)*

- Retrieved and processed biological sequence data and metadata using Python

(Biopython), SQL, and Bash

- Structured datasets for downstream analysis and automation within Linux-based environments

## Work Experience

### Specialist Biomedical Scientist

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

- Processed and cryopreserved peripheral blood stem cells, bone marrow collections, DLI, and CD34+ enrichments for transplant procedures.
- 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.
- Analysed CD3+ and CD34+ cell populations via flow cytometry and reported results supporting patient treatment decisions.

### 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.

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## 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

**IBM:** Data Engineering Professional Certificate (in progress)

**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

**Wellcome Connecting Science Learning and Training:** Bioinformatics for Biologists: An Introduction to Linux, Bash Scripting, and R; Analysing and Interpreting Genomics Datasets