



# ANDREA POLETTI

Bioinformatician and  
Data Science Specialist

## CONTACT

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## PERSONAL INFO

DATE OF BIRTH: 4 Oct 1991

NATIONALITY: Italian

**Personal Summary:** Bioinformatician with 7 years of experience, specializing in data-driven solutions and large-scale genomic data analysis for healthcare and biotech applications. Expertise in programming (Python and R), statistical data analysis and developing scalable pipelines/algorithms for multi-omics data integration, enabling actionable insights and optimizing workflows. Proficient in handling big-data generated by modern technologies (WGS, RNA-seq, single-cell sequencing) using machine-learning, computational workflows and cloud systems. Passionate about leveraging data science and bioinformatics to drive innovation and enhance decision-making processes, ultimately improving patient outcomes and accelerating the development of precision medicine applications.

## KEY PROFESSIONAL ROLES



### **Bioinformatician Research Fellow – University of Bologna Bologna, Italy – from Feb 2018 to Present**

- Designed end-to-end bioinformatics/clinical data workflows, effectively addressing complex challenges and delivering tailored technical solutions. E.g. conceptualized and validated a novel targeted sequencing panel for diagnostics, combining cost-efficiency and practical application for clinical routine.
- Designed and implemented scalable data analysis pipelines, reducing processing time by 50% and enhancing reproducibility across projects. Applied machine learning models to multi-omics datasets, improving predictions for patient outcomes.
- Led cross-functional international collaborations with clinicians and data scientists to translate genomic data into clinical insights for healthcare applications.



### **Visiting Researcher – Dana-Farber Cancer Institute / Broad Institute of Harvard and MIT Boston, Massachusetts, US – from Mar 2022 to Jan 2023**

- Collaborated with globally recognized experts in cancer genomics and bioinformatics, integrating cutting-edge genomics research into actionable solutions.
- Developed bioinformatic tools to analyze and harmonize complex genomic data, enabling precise tracking of copy number alterations in cancer evolution.
- Designed scalable methodologies for single-cell genomic data analysis, enhancing data reproducibility and cross-institutional collaboration.



### **Visiting Scientist – Francis Crick Institute London, UK – from Jan 2019 to Apr 2019**

- Developed custom R-based pipelines for ultra-deep NGS analysis, improving the detection of low VAF mutations.
- Conducted machine-learning analyses on genomic data to uncover patterns of clonal evolution, contributing to the refinement of prognostic tools.

## LANGUAGE SKILLS

Language	Italian	English
Listening	Native	B2
Reading	Native	C1
Speaking	Native	B2
Writing	Native	C1

Levels: A1 and A2: Basic user,  
B1 and B2: Independent user,  
C1 and C2: Proficient user.

## WEBSITE

<https://github.com/andrea-poletti-unibo>



## EDUCATION



### PhD in Biomedical Sciences (2019 - 2023) University of Bologna, Italy

- Focus on cancer genomics and bioinformatics, with expertise in developing computational methods for NGS data analysis and clonal evolution tracking.
- Dissertation: TiMMing: developing a bioinformatic suite of tools to harmonize and track the origin of Copy Number Alterations in the evolutive history of Multiple Myeloma. Results published in *Nature Genetics*.



### Master's Degree in Health Biology (2015 - 2017) University of Bologna, Italy Grade: 110/110 cum Laude

- Specialized in human health and genomics, with hands-on experience in molecular biology and bioinformatics.
- Thesis: Development of bioinformatics approaches for Multiple Myeloma genomic data interpretation.



### Postgraduate Master's Degree in Machine Learning and Big Data in Precision Medicine and Biomedical Research (2024 - Present, expected in 2025) University of Padua, Italy

- Advanced training in machine learning and deep-learning techniques, big data integration, and applications in precision medicine and biomedical research.

## TECHNICAL SKILLS

### Programming and Data Manipulation

- Python, R, Bash, SQL – R packages development
- Data wrangling, visualization, and manipulation (tidyverse, matplotlib, ggplot2, Plotly, etc.)
- Dashboards and data storytelling (Shiny apps)

### NGS and Multi-omics Data Analysis

- Creation of optimized solutions for NGS data analysis (WGS, RNA-seq, targeted-seq, Bioconductor workflows)
- Single-cell and multi-omics data integration.

### Machine Learning and AI

- Development of predictive models for clinical applications (scikit-learn, caret, deepsurv, TidyModels)
- Application of deep-learning techniques to large-scale genomic datasets (Keras, TensorFlow)

### Pipeline Development and Automation

- Workflow management tools: Snakemake, Nextflow
- Containerization: Docker, Singularity
- Version control: Git, GitHub, GitLab

### High-Performance Computing (HPC) and Cloud Computing

- Experience in parallel computing on HPC clusters
- Cloud platforms: AWS, GCP

## RESEARCH PROFILES LINKS

### ORCID:

0000-0002-0753-1248

<https://orcid.org/0000-0002-0753-1248>

### Scopus ID:

57429675100

<https://www.scopus.com/authid/detail.uri?authorId=57429675100>

### Google Scholar page

<https://scholar.google.com/citations?user=7iZHItEAAAJ>

### ResearchGate

<https://www.researchgate.net/profile/Andrea-Poletti>

## INVOLVMENT IN FUNDED RESEARCH PROJECTS

- **“SYNTHIA: Synthetic Data Generation Framework for Integrated Validation of Use Cases and AI Healthcare Applications”**, 2024-2029. Code: 101172872-SYNTHIA-HORIZON-JU-IHI-2023-05. IHI Grant through EU Funding.
- **“GenoMed4ALL: Genomics and Personalized Medicine for all through Artificial Intelligence in Haematological Diseases”**, 2021-2025. Code: 101017549. EU Horizon 2020. DOI: <https://doi.org/10.3030/101017549>
- **“StreamMing: the dynamics of Multiple Myeloma minimal residual disease in the peripheral blood stream”**, 2018-2024. AIRC Investigator Grant. code: AIRC-IG-22059, PI: Michele Cavo.
- **“AIMMer: A machine-learning approach to connect Multiple Myeloma complexity to early disease recurrence”**, 2023-2026. PNRR M6/C2 CALL 2023, Code: PNRR-TR1-2023-12378246, PI: Elena Zamagni.



## PUBLICATIONS

Author of 13 peer-reviewed publications and 43 oral and poster communications accepted at international conferences (source: Scopus / Google Scholar).

### FIRST-AUTHOR RESEARCH PAPERS

- **Alberge J.B., Dutta A. and Poletti A (co-first)**, et al. “Genomic landscape of multiple myeloma and of its precursor conditions, and its clinical implications”. Accepted for publication in **Nature Genetics**.
- **Terragna C. and Poletti A. (co-first)**, et al. “Multi-dimensional scaling techniques unveiled gain  $1q$  and loss  $13q$  co-occurrence in Multiple Myeloma patients with specific genomic, transcriptional and adverse clinical features”. **Nature Communications**, 15(1), 1551, 2024. DOI: [10.1038/s41467-024-45000-z](https://doi.org/10.1038/s41467-024-45000-z)
- **Mazzocchi G. and Poletti A. (co-first)**, et al. “BoBafit: A copy number clustering tool designed to refit and recalibrate the baseline region of tumors’ profiles”. **Computational and Structural Biotechnology Journal**, 20, 3718-3728, 2022. DOI: [10.1016/j.csbj.2022.06.062](https://doi.org/10.1016/j.csbj.2022.06.062)



## AWARDS AND RECOGNITIONS

- **IMS Career Development Award – International Myeloma Society, 2022**  
Awarded a \$75,000 grant to support career development. Recognized as a promising early-career researcher in plasma cell dyscrasias research.
- **ASH Abstract Achievement Award – American Society of Hematology, 2022**  
Awarded for outstanding abstract on copy number signature extraction in Multiple Myeloma.
- **IMS Young Investigator Award – International Myeloma Society, 2023**  
Honored for exemplary research and bioinformatics tool development for tracking cancer genomic evolution.
- **IRCCS Sant’Orsola Best Presentation Award – IRCCS Policlinico di Sant’Orsola Research Retreat, 2024**  
Recognized for the presentation “TiMMing: A Bioinformatics Toolkit to Trace the Origin and Clinical Significance of Copy Number Alterations in Multiple Myeloma”.
- **Finalist of the “Under40 in Hematology” 2024 event**  
Selected among top young researchers in Italy for innovative contributions in hematology. The event promotes and rewards outstanding scientific production, methodology, scientific impact, and applicability.