Maria Luisa **Ratto**

Researcher

About me

My interest in genetics brought me into biotechnology, then, during my university years, I fell in love with bioinformatics. I spent all my practicals hours training first in bulk RNAseq experiments and then with single cell RNAseq.

Personal

Maria Luisa Ratto
nationality: Italian
1998

Areas of specialization

RNAseq · DNAseq · Single cell · Omics · Functional screens

Interests

I enjoy facing complex biological problems with the powerful tools of computational biology, especially when integrating different technologies. I most of all like working in close contact with the biological questions at hand.

Extra

I spend my free time in nerdy activities. I love playing RPGs such as Dungeon and Dragons.

Contacts

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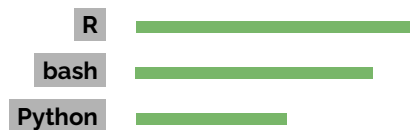📞 +39 3889866861

in Maria Luisa Ratto
MariaLuisaRatto
ResearchGate

Degrees

2020	**Biotechnology** BACHELOR · University of Turin 🏛 106/110	
2022	**Molecular Biotechnology** MASTER DEGREE · University of Turin 🏛 110/110 *Cum Laude*	

Programming

R ████████████████
bash ███████████████
Python ██████████

Languages

Italian	C2	mother tongue
English	C1	● ● ● ○
German	A1	● ○ ○ ○

Curriculum

2022–2025 — **Complex Systems for Quantitative Biomedicine**
PHD STUDENT · University of Turin, Turin, IT 📍
Data scientist in Calogero Lab and Bertero Lab.
My project focuses on dissecting data for the optimization of iPS2-seq (iPS-optimized inducible Postranscriptional Silencing in pool deconvoluted by single cell sequencing) method and developing a tailored pipeline for specific and user-friendly analysis of these results.

2025 — **GeneCore**
VISITING FELLOW · EMBL, Heidelberg, DE 📍
Data scientist in the Genomics Core Facility.
I worked on long reads DNAseq data of ALT+ primary tumors, investigating the role of telomeres maintenance and intrachromosomal telomeric repeats.

Publications

2025 Balmas, E., Ratto, M.L., Snijders, K.E. et al. *Single cell transcriptional perturbome in pluripotent stem cell models*, Molecular Systems Biology. DOI: 10.1038/s44320-025-00172-8

2024 Arigoni, M. and Ratto, M.L. et al., *A single cell RNAseq benchmark experiment embedding "controlled" cancer heterogeneity*, Scientific Data. DOI: 10.1038/s41597-024-03002-y

2024 Alessandri, S. et al., *CREDO: a friendly Customizable, REproducible, DOcker file generator for bioinformatics applications*, BMC Bioinformatics. DOI: 10.1186/s12859-024-05695-9

2023 Balmas, E. et al., *Manipulating and studying gene function in human pluripotent stem cell models*, Febs Letters. DOI: 10.1002/1873-3468.14709

2021 Alessandri, L. et al. *Sparsely Connected Autoencoders: A Multi-Purpose Tool for Single Cell omics Analysis*, International Journal of Molecular Sciences. DOI: 10.3390/ijms222312755

Skills

Computational	Scripting · Containerization · Git · Packaging (R) · Reproducibility · Documentation · Machine learning · Statistical analysis · Visualization · High-throughput data processing · Seurat · Monocle3
Transferable	Effective communication · Presentations · Critical thinking · Problem-solving · Teamwork · Independent work · Organization · Bridging disciplines

Certificates

2023 Trainer at EMBL Course: Whole transcriptome data analysis

2023 Trainer at IFOM, Istituto Fondazione Oncologia Molecolare: Whole transcriptome data analysis

2024 Poster at BITS - Bioinformatics Italian Society Annual Meeting

2024 Poster at ISSCR Annual Meeting - International Society for Stem Cell Research

2025 Trainer at EMBL Course: Analysis and integration of transcriptome and proteome data