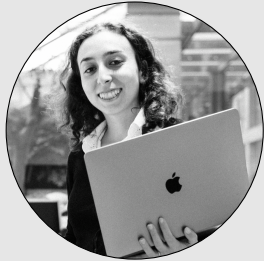


Maria Luisa Ratto

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
• Oncology

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. I find cancer to be the most interesting disease.

Extra

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

Contacts

✉ marialuisa.ratto@unito.it
☎ +39 3889866861

[Maria Luisa Ratto](#)

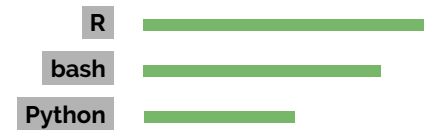
[MariaLuisaRatto](#)

[ResearchGate](#)

DEGREES

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

PROGRAMMING



LANGUAGES

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

CURRICULUM

- 11/2022-10/2025 **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.
- 01/2025-06/2025 **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

- 2024** Arigoni, M. and Ratto, M.L. et al., *A single cell RNAseq benchmark experiment embedding "controlled" cancer heterogeneity*, Sci Data 11, 159. 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 25, 110. DOI: [10.1186/s12859-024-05695-9](#)
- 2024** Balmas, E. and Ratto, M.L. et al., *Single Cell Transcriptional Perturbome in Pluripotent Stem Cell Models*, preprint available at [SSRN](#) and now accepted for publication at Molecular Systems Biology.
- 2023** Balmas, E. et al., *Manipulating and studying gene function in human pluripotent stem cell models*, Febs Letters, Volume597, Issue18, 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 (IJMS), 22(23):12755, 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