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Head of the Bioinformatics Group

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Academia

2013 – 2017	Ph.D. (Dr. rer. physiol.), Bioinformatics, Institute of Medical Biostatistics, Epidemiology and Informatics (IMBEI), University Medical Center Mainz, Mainz, Germany
2005 – 2008	Master of Science in Biomedical Engineering, Politecnico di Milano, Milan, Italy
2002 – 2005	Bachelor in Biomedical Engineering, Politecnico di Milano, Milan, Italy.

Career

since 2021	Head of the Bioinformatics Group, Institute of Medical Biostatistics, Epidemiology and Informatics (IMBEI), University Medical Center, Mainz, Germany
since 2017	Joint Head of the Core Facility Bioinformatics BIUM(MZ), University Medical Center, Mainz, Germany
2018– 2020	Postdoctoral Researcher - Division Genomic Statistics and Bioinformatics, Institute of Medical Biostatistics, Epidemiology and Informatics (IMBEI) and Center for Thrombosis and Hemostasis (CTH), University Medical Center Mainz, Mainz, Germany

Awards

2021	Winner of the Best package demo, Bioc2021 conference
2019	Winner of the 1st Shiny Contest with the iSEE package
2016	Best Poster Award, ISCB (International Society for Computational Biology) Student Symposium on Computational Genomics
2015	Best Presentation Award, TransMed Science Day
2001	Pädagogischer Austauschdienst (PAD) scholarship for high-school exchange

Selected Publications

Abassi N, Schwarz L, Filippi E, **Marini F**. DeeDeeExperiment: Building an infrastructure for integrating and managing omics data analysis results in R/Bioconductor. Schwartz R, editor. Bioinformatics [Internet]. 2026 Mar 27;1–4.

Hemberg M*, **Marini F***, Ghazanfar S*, Al Ajami A, Abassi N, Anchang B, et al. Insights, opportunities, and challenges provided by large cell atlases. Genome Biol [Internet]. 2025 Oct 20;26(1):358. *equal contribution

Nedwed AS, Helbich SS, Braband KL, Volkmar M, Delacher M*, **Marini F***. Using combined single-cell gene expression, TCR sequencing and cell surface protein barcoding to characterize and track CD4+ T cell clones from murine tissues. Front Immunol [Internet]. 2023 Oct 12;14(October):1–39. *equal contribution

Braband KL, Nedwed AS, Helbich SS, Simon M, Beumer N, Brors B, **Marini F***, Delacher M*. Using single-cell chromatin accessibility sequencing to characterize CD4+ T cells from murine tissues. Front Immunol [Internet]. 2023 Oct 16;14(October):1–33. *equal contribution

Ludt A, Ustjanzew A, Binder H, Strauch K, **Marini F**. Interactive and Reproducible Workflows for Exploring and Modeling RNA-seq Data with pcaExplorer, ideal, and GeneTonic. Curr Protoc [Internet]. 2022 Apr 25;2(4):1–55.

Marini F, Ludt A, Linke J, Strauch K. GeneTonic: an R/Bioconductor package for streamlining the interpretation of RNA-seq data. BMC Bioinformatics [Internet]. 2021 Dec 23;22(1):610.

Amezquita RA, Lun ATL, Becht E*, Carey VJ*, Carpp LN*, Geistlinger L*, **Marini F*** et al. Orchestrating single-cell analysis with Bioconductor. Nat Methods [Internet]. 2020 Feb 2;17(2):137–45. Available from: http://www.ncbi.nlm.nih.gov/pubmed/31792435 *equal contribution