

Giulio Ferrero - Curriculum Vitae

Name and Surname: Giulio Ferrero

Nationality: Italian

Affiliation: University of Turin

Institution: Department of Clinical and Biological Sciences

Address: Gonzole region, 10 - 10043, Orbassano - TO

Country: Italy

Email: giulio.ferrero@unito.it

Brief presentation

Dr. Ferrero is a researcher at the Department of Clinical and Biological Sciences of the University of Turin. The achievement of the Master's Degree in Cellular and Molecular Biology and of the Doctorate in Complex Systems for Life Sciences (University of Turin) allowed Dr. Ferrero to acquire a solid interdisciplinary background allowing him to effectively develop computational techniques for the integrative analysis clinical and lifestyle data with genomic, epigenomic, transcriptomic, and metagenomic data in the context of basic and applied research projects. In these contexts, Dr. Ferrero investigated the functional activity of noncoding RNAs, in particular microRNA (miRNAs), circular RNA (circRNAs) and long noncoding RNA (lncRNAs) in complex diseases and their candidate role as molecular biomarkers that can be monitored in the human biofluids. For these investigations, in 2019, Dr. Ferrero was awarded a Fellowship from the Italian Cancer Research Association (AIRC) for the project "Host-gut microbiome small RNA cross-talk: an innovative source of biomarkers for an accurate colorectal cancer detection".

Dr. Ferrero main research topic is the molecular activity of extracellular RNAs detectable in human biofluids, their role in complex non-communicable diseases (particularly of the gastrointestinal tract) and their modulations in relationship to host microbiome and individual exposure to environmental factors, including pollution, lifestyle, and dietary habits. These aspects are investigated through the development of bioinformatic and systems biology techniques for the integrative analysis of omics data.

Main expertise

Dr. Ferrero consolidated his expertise in the implementation of bioinformatic and systems biology strategies for the analysis of omic data, particularly RNA-Seq, small RNA-Seq, shotgun metagenomic sequencing, ChIP-Seq, whole-exome and whole-genome sequencing. He has a corroborated knowledge of different programming languages for data analysis, including R and Python. He is able to manage all steps of omic data analysis, from raw data processing to downstream analyses.

He is able to implement bioinformatic pipelines in the frame of computational reproducibility criteria as those achievable using Docker-based containerization framework. He developed methods for the integrative analysis of omic data (RefGen, NormChIP) as well as pipelines for the analysis of small RNA (Docker4Seq) and circRNAs (Docker4Circ). His bioinformatic approaches adhere to the FAIR (Findable, Accessible, Interoperable, Reusable) principles of bioinformatic data analysis.

He knows different statistical and data science methods for the design and analysis of cohort-based studies. His particular interest on the analysis of heterogenous omic data allowed him to improve his understanding of statistical and machine learning methods to extract biomedical insights from the integrative analysis of omic data. These include analysis frameworks like the tidyverse, mixOmic, and scikit-learn.

Formation

- 25/01/2016 **PhD in Complex Systems for Life Sciences**
 Institution: University of Turin
 Thesis title: *"Functional characterization of the human noncoding genome by integrative analysis of High-Throughput data."*
 Supervisors: Prof. Francesca Cordero (Dept. of Computer Science) and
 Prof. Michele De Bortoli (Dept. of Clinical and Biological Sciences)
- 17/10/2012 **Master's Degree in Cellular and Molecular Biology**
 Institution: University of Turin
 Thesis title: *"A new data processing pipeline for the bioinformatic analysis of transcription factor genomic binding events."*
 Supervisors: Prof. Francesca Cordero (Dept. of Computer Science) and
 Prof. Michele De Bortoli (Dept. of Clinical and Biological Sciences)
 Grade: 110/110 cum laude

Research experience

- | | |
|--------------|---|
| 2022-
now | Associated Researcher at the Department of Clinical and Biological Sciences, University of Turin. Project: <i>"Identification of molecular biomarkers of chronic exposure to environmental pollution"</i> . |
| 2021 | Research Fellow ("Assegno di Ricerca") at the Department of Clinical and Biological Sciences, University of Turin. Project: <i>"Setting bioinformatics pipelines for omics data integration in human diseases"</i> . |
| 2020 | Research Fellow ("Assegno di Ricerca") at the Department of Clinical and Biological Sciences, University of Turin. Project: <i>"Setting bioinformatics pipelines for omics data integration in human diseases"</i> . |
| 2019 | Research Fellow ("Borsa di Ricerca") at the Department of Computer Science, University of Turin. Funded by FIRC-AIRC . Project: <i>"Host-gut microbiome small RNA cross-talk: an innovative source of biomarkers for an accurate colorectal cancer detection"</i> . |
| 2018 | Research Fellow ("Borsa di Ricerca") at the Department of Computer Science, University of Turin. Project: <i>"Definition of new pipelines to analyze transcriptome data for the identification of diagnostic and prognostic tumor biomarkers"</i> . |
| 2017 | Research Fellow ("Assegno di Ricerca") at the Department of Computer Science, University of Turin. Project: <i>"Development of algorithms for the identification of biomarkers in cancer"</i> . |
| 2017 | Research Fellow ("Borsa di Ricerca") at the Department of Computer Science, University of Turin. Project: <i>"Development of algorithms for the integration of heterogeneous biological and clinical data"</i> . |
| 2016 | Research Fellow ("Borsa di Ricerca") at the Department of Clinical and Biological Sciences, University of Turin. Project: <i>"Integrative bioinformatic analysis of genomic, epigenomic, and transcriptomic data"</i> . |

2016 | **Research Fellow** ("Borsa di Ricerca") at the Department of Computer Science. University of Turin. Project: "*Development of algorithms for the integration of heterogeneous biological and clinical data*".

Research grants / Fellowships as Principal Investigator

2022-
now | **CRT Bando Erogazioni Ordinarie 2022**. Funded by **CRT Foundation**. Project: "*Identification of faecal biomarkers of chronic exposure to environmental pollutants*". Budget: 25,000 Euro

2019 | **FIRC-AIRC Fellowship**. Funded by **FIRC-AIRC**. Project: "*Host-gut microbiome small RNA cross-talk: an innovative source of biomarkers for an accurate colorectal cancer detection*".

Research activities and scientific publications

Research topics

- Non-coding RNAs
- Host-microbiota interactions
- Molecular biomarkers of complex diseases in human biofluids
- Integrative Bioinformatics and Systems Biology
- Functional Genomics

Participation in national and international research groups

Dr. Ferrero is an active member of three research groups. In particular:

- since 2010, Dr. Ferrero has actively contributed to the research and computational analyses of the Genomic Regulation group of Prof. Michele De Bortoli, of the Department of Clinical and Biological Sciences, University of Turin. This continuous collaboration is supported by >10 publications in international journals and the involvement in the bioinformatics unit of a research project for the Italian Association of Cancer Research (AIRC), which was concluded in December 2018.

- since 2011, Dr. Ferrero has been an active member of the "quantitative biology" (q-Bio) group of Prof. Francesca Cordero and Prof. Marco Beccuti of the Department of Computer Science, University of Turin. In this group, Dr. Ferrero deals with the bioinformatic and integrative analysis of genomic data. The work within this group is supported by nine publications in international journals and participation as a bioinformatic unit in research projects. In 2019, in this group, Dr. Ferrero was the principal investigator of the research project funded with a research fellowship by the Italian Cancer Research Association (AIRC) for the investigation of human and microbial biomarkers of host-microbiota interactions for the early diagnosis of colorectal cancer.

- since 2014, Dr. Ferrero collaborates with the research group of Dr. Alessio G. Naccarati at the Italian Institute for Genomic Medicine (IIGM). This collaboration is supported by 20 publications in international journals, particularly for research projects related to the identification of RNA biomarkers in body biofluids for the early diagnosis of complex diseases, lifestyle habits, and environmental pollutants. The collaboration is ongoing in the context of the AIRC project entitled "Fecal non-coding RNA markers for a precision medicine approach: how they reflect colorectal cancer onset and progression" and the European Union's Horizon 2020 project ONCOBIOME.

National and international collaboration network

In the following are reported the main national and international collaborators of Dr Ferrero.

National

- Dept. of Clinical and Biological Sciences, University of Turin, Orbassano - Prof. Michele De Bortoli, Prof. Santina Cutrupi, Dr. Ymera Pignochino
- Dept. of Computer Science, University of Turin, Turin - Prof. Francesca Cordero, Prof. Marco Beccuti, and Prof. Marco Aldinucci
- Italian Institute for Genomic Medicine (IIGM), Candiolo - Dr. Alessio Naccarati and Dr. Barbara Pardini.
- Center for Integrative Biology (CIBIO), University of Trento, Trento - Prof. Nicola Segata.
- FIRC Institute of Molecular Oncology, Milan - Dr. Manuela Gariboldi.
- Dept. of Molecular Biotechnology and Health Sciences, University of Turin, Turin - Prof. Raffaele Calogero, Prof. Tiziana Vaisitti, Prof. Francesco Novelli
- Epidemiology and Screening Unit-CPO, University Hospital Città della Salute e della Scienza, Turin - Dr. Carlo Senore. - Dept. of Translational Medicine (DIMET), Università del Piemonte Orientale, Novara, Italy - Dr. Francesca Orso. - Dept. of Oncology, University of Turin, Candiolo - Dr. Chiara Riganti.
- Pathology Unit - FPO - IRCCS, Candiolo - Prof.ssa Tiziana Venesio.

International

- Dept. of Molecular Biology of Cancer, Institute of Experimental Medicine, Prague, Czech Republic - Dr. Pavel Vodicka.
- Institute for Clinical and Experimental Medicine (IKEM), Prague, Czech Republic - Prof. Monika Cahova.
- RECETOX, Faculty of Science, Masaryk University, Brno, Czech Republic - Dr. Eva Budinska
- School of Medicine, Boston University, Boston, USA - Prof. Valentina Perissi.
- Radboudumc, Nijmegen, The Netherlands - Dr. Annemarie Boleij.
- Dept.- of Research, Cancer Registry of Norway, Oslo, Norway - Dr. Trine B Rounge.
- University Hospital of Friedrich-Alexander-University Erlangen-Nürnberg, Erlangen, Germany. Dr. Regine Schneider-Stock.

Scientific publications

Dr. Ferrero has published 41 articles (14 as first, co-first and one as co-senior author) in peer-reviewed journals, 2 papers in proceedings in congresses and 1 book chapter. The scientific publications of Dr. Ferrero have a total of 1,194 citations and H-index equal to 16 (source Scopus at 15 Apr 2024).

41. Pomposo, I. O., Ferrero, G.*, Belfiore, A., Pardini, B., Tarallo, S., Ciniselli, C. M., Noci, S., Daveri, E., Signoroni, S., Cattaneo, L., et al. (2024). Modulation of faecal miRNAs highlights the preventive effects of a mediterranean low-inflammatory dietary intervention. *Clinical Nutrition*, pages [*Co-first author]
40. Gómez-Matas, J., Duran-Sanchon, S., Lozano, J. J., Ferrero, G., Tarallo, S., Pardini, B., Naccarati, A., Castells, A., and Gironella, M. (2024). SnoRNA profiling in colorectal cancer and assessment of non-invasive biomarker capacity by ddpcr in fecal samples. *iScience*
39. Ferrero, G., Festa, R., Follia, L., Lettieri, G., Tarallo, S., Notari, T., Giarra, A., Marinaro, C., Pardini, B., Marano, A., et al. (2024). Small noncoding RNAs and sperm nuclear basic proteins reflect the environmental impact on germ cells. *Molecular Medicine*, 30(1):12
38. Pastorino, G. A., Sheraj, I., Huebner, K., Ferrero, G., Kunze, P., Hartmann, A., Hampel, C., Husnugil, H. H., Maiuthed, A., Gebhart, F., et al. (2024). A partial epithelial-mesenchymal transition signature for highly aggressive colorectal cancer cells that survive under nutrient restriction. *The Journal of Pathology*

37. Birkeland, E., Ferrero, G.*, Pardini, B., Umu, S. U., Tarallo, S., Bulfamante, S., Hoff, G., Senore, C., Rounge, T. B., and Naccarati, A. (2023). Profiling small rnas in fecal immunochemical tests: is it possible? *Molecular Cancer*, 22(1):161, [*Co-first author]
36. Pardini, B., Ferrero, G.*, Tarallo, S., Gallo, G., Francavilla, A., Licheri, N., Trompetto, M., Clerico, G., Senore, C., Peyre, S., et al. (2023). A fecal miRNA signature by small RNA sequencing accurately distinguishes colorectal cancers: results from a multicentric study. *Gastroenterology*, 165(3):S82–599, [*Co-first author]
35. Francavilla, A., Ferrero, G.*, Pardini, B., Tarallo, S., Zanatto, L., Caviglia, G. P., Sieri, S., Grioni, S., Francescato, G., Stalla, F., et al. (2023). Gluten-free diet affects fecal small non-coding RNA profiles and microbiome composition in celiac disease supporting a host-gut microbiota crosstalk. *Gut Microbes*, 15(1):2172955, [*Co-first author]
34. Picchio, V., Ferrero, G.*, Cozzolino, C., Pardini, B., Floris, E., Tarallo, S., Dhori, X., Nocella, C., Lofredo, L., Biondi-Zoccai, G., et al. (2023). Effect of traditional or heat-not-burn cigarette smoking on circulating mirnas in healthy subjects. *European Journal of Clinical Investigation*, pages e14140, [*Co-first author]
33. Boretto, C., Actis, C., Faris, P., Cordero, F., Beccuti, M., Ferrero, G., Muzio, G., Moccia, F., and Autelli, R. (2023). Tamoxifen activates transcription factor eb and triggers protective autophagy in breast cancer cells by inducing lysosomal calcium release: A gateway to the onset of endocrine resistance. *International Journal of Molecular Sciences*, 25(1):458
32. Tarallo, S., Ferrero, G.*, De Filippis, F., Francavilla, A., Pasolli, E., Panero, V., Cordero, F., Segata, N., Grioni, S., Pensa, R. G., et al. (2022). Stool microRNA profiles reflect different dietary and gut microbiome patterns in healthy individuals. *Gut*, 71(7):1302–1314, [*Co-first author]
31. Gagliardi, A., Francescato, G., Ferrero, G., Birolo, G., Tarallo, S., Francavilla, A., Piaggesechi, G., Di Battista, C., Gallo, G., Realis Luc, A., et al. (2022). The 8q24 region hosts miRNAs altered in biospecimens of colorectal and bladder cancer patients. *Cancer Medicine*, pages 1–15
30. Berrino, E., Annaratone, L., Bellomo, S. E., Ferrero, G., Gagliardi, A., Bragoni, A., Grassini, D., Guarnera, S., Parlato, C., Casorzo, L., et al. (2022). Integrative genomic and transcriptomic analyses illuminate the ontology of HER2-low breast carcinomas. *Genome Medicine*, 14(1):98
29. Elhasnaoui, J., Ferrero, G., Miano, V., Franchitti, L., Tarulli, I., Coscujuela Tarrero, L., Cutrupi, S., and De Bortoli, M. (2022). A regulatory axis between epithelial splicing regulatory proteins and estrogen receptor α modulates the alternative transcriptome of luminal breast cancer. *International Journal of Molecular Sciences*, 23(14):7835
28. Moisoiu, T., Dragomir, M. P., Iancu, S. D., Schallenberg, S., Birolo, G., Ferrero, G., Burghelea, D., Stefanu, A., Cozan, R. G., Licarete, E., et al. (2022). Combined miRNA and SERS urine liquid biopsy for the point-of-care diagnosis and molecular stratification of bladder cancer. *Molecular Medicine*, 28(1):1–13
27. Merlini, A., Centomo, M. L., Ferrero, G., Chiabotto, G., Miglio, U., Berrino, E., Giordano, G., Brusco, S., Pisacane, A., Maldi, E., et al. (2022). DNA damage response and repair genes in advanced bone and soft tissue sarcomas: An 8-gene signature as a candidate predictive biomarker of response to trabectedin and olaparib combination. *Frontiers in Oncology*, 12:844250
26. Francavilla, A., Gagliardi, A., Piaggesechi G., Tarallo, S., Cordero, F., Pensa, R. G., Impeduglia, A., Caviglia, G. P., Ribaldone, D. G., Gallo, G., Grioni, S., Ferrero, G.*, Pardini, B., and Naccarati, A. (2021). Faecal miRNA profiles associated with age, sex, BMI, and lifestyle habits in healthy individuals. *Scientific Reports*, 11(20645):[*Co-last author]

25. Giordano, G., Merlini, A., Ferrero, G., Mesiano, G., Fiorino, E., Brusco, S., Centomo, M. L., Leuci, V., D'Ambrosio, L., Aglietta, M., et al. (2021). EphA2 expression in bone sarcomas: Bioinformatic analyses and preclinical characterization in patient-derived models of osteosarcoma, Ewing's sarcoma and chondrosarcoma. *Cells*, 10(11):2893
24. Elhasnaoui, J., Ferrero, G., Miano, V., Cutrupi, S., and De Bortoli, M. (2021). The estrogen receptor α signaling pathway controls alternative splicing in the absence of ligands in breast cancer cells. *Cancers*, 13(24):6261
23. Ferrero, G., Licheri, N., Coscujuela Tarrero, L., De Intinis, C., Miano, V., Calogero, R. A., Cordero, F., De Bortoli, M., and Beccuti, M. (2020). Docker4Circ: A framework for the reproducible characterization of circRNAs from RNA-Seq data. *International Journal of Molecular Sciences*, 21(1):293
22. Elhasnaoui, J., Miano, V., Ferrero, G., Doria, E., Leon, A. E., Fabricio, A. S., Annaratone, L., Castellano, I., Sapino, A., and De Bortoli, M. (2020). DSCAM-AS1-driven proliferation of breast cancer cells involves regulation of alternative exon splicing and 3'-end usage. *Cancers*, 12(6):1453
21. Ferrero, G., Carpi, S., Polini, B., Pardini, B., Grioni, S., Impeduglia, A., Nieri, P., Tarallo, S., and Naccarati, A. (2021a). Intake of natural compounds and circulating microRNA expression levels: their relationship investigated in healthy subjects with different dietary habits. *Frontiers in Pharmacology*, 11:2214
20. Godel, M., Morena, D., Ananthanarayanan, P., Buondonno, I., Ferrero, G., Hattinger, C. M., Di Nicolantonio, F., Serra, M., Taulli, R., Cordero, F., et al. (2020). Small nucleolar RNAs determine resistance to doxorubicin in human osteosarcoma. *International Journal of Molecular Sciences*, 21(12):4500
19. Mandili, G., Curcio, C., Bulfamante, S., Follia, L., Ferrero, G., Mazza, E., Principe, M., Cordero, F., Satolli, M. A., Spadi, R., et al. (2020a). In pancreatic cancer, chemotherapy increases antitumor responses to tumor-associated antigens and potentiates DNA vaccination. *Journal for ImmunoTherapy of Cancer*, 8(2):e001071
18. Mandili, G., Follia, L., Ferrero, G., Katayama, H., Hong, W., Momin, A. A., Capello, M., Giordano, D., Spadi, R., Satolli, M. A., et al. (2020b). Immune-complexome analysis identifies immunoglobulin-bound biomarkers that predict the response to chemotherapy of pancreatic cancer patients. *Cancers*, 12(3):746
17. Thomas, A. M., Manghi, P., Asnicar, F., Pasolli, E., Armanini, F., Zolfo, M., Beghini, F., Manara, S., Karcher, N., Pozzi, C., Gandini, S., Serrano, D., Tarallo, S., Francavilla, A., Gallo, G., Trompetto, M., Ferrero, G., Mizutani, S., Shiroma, H., Shiba, S., Shibata, T., Yachida, S., Yamada, T., Wirbel, J., Schrotz-King, P., Ulrich, C. M., Brenner, H., Arumugam, M., Bork, P., Zeller, G., Cordero, F., Dias-Neto, E., Setubal, J. C., Tett, A., Pardini, B., Rescigno, M., Waldron, L., Naccarati, A., and Segata, N. (2019). Metagenomic analysis of colorectal cancer datasets identifies cross-cohort microbial diagnostic signatures and a link with choline degradation. *Nature Medicine*, 25:334–339
16. Tarallo, S., Ferrero, G.*, Gallo, G., Francavilla, A., Clerico, G., Realis Luc, A., Manghi, P., Thomas, A. M., Vineis, P., Segata, N., Pardini, B., Naccarati, A., and Cordero, F. (2019). Altered fecal small RNA profiles in colorectal cancer reflect gut microbiome composition in stool samples. *mSystems*, 4(5):e00289–19. [*Co-first author]
15. Follia, L., Ferrero, G.*, Mandili, G., Beccuti, M., Giordano, D., Spadi, R., Satolli, M. A., Evangelista, A., Katayama, H., Hong, W., Momin, A. A., Capello, M., Hanash, M. S., Novelli, F., and Cordero, F. (2019). Integrative analysis of novel metabolic subtypes in pancreatic cancer fosters new prognostic biomarkers. *Frontiers in Oncology*, 9:115. [*Co-first author]

14. Iannello, A., Rolla, S., Maglione, A., Ferrero, G., Bardina, V., Inaudi, I., De Mercanti, S., Novelli, F., D'Antuono, L., Cardaropoli, S., Todros, T., Turrini, M. V., Cordioli, C., Puorro, G., Marsili, A., Lanzillo, R., Morra, V. B., Cordero, F., De Bortoli, M., Durelli, L., Visconti, A., Cutrupi, S., and Clerico, M. (2018). Pregnancy epigenetic signature in T helper 17 and T regulatory cells in multiple sclerosis. *Frontiers in Immunology*, 9:3075
13. Ferrero, G., Cordero, F., Tarallo, S., Arigoni, M., Riccardo, F., Gallo, G., Ronco, G., Allasia, M., Kulkarni, N., Matullo, G., Vineis, P., Calogero, R. A., Pardini, B., and Naccarati, A. (2018). Small non-coding RNA profiling in human biofluids and surrogate tissues from healthy individuals: Description of the diverse and most represented species. *Oncotarget*, 9(3):3097
12. Kulkarni, N., Alessandri, L., Panero, R., Arigoni, M., Olivero, M., Ferrero, G., Cordero, F., Beccuti, M., and Calogero, R. A. (2018). Reproducible Bioinformatics Project: A community for reproducible bioinformatics analysis pipelines. *BMC Bioinformatics*, 19(Suppl10):211–219
11. Tarrero, L. C., Ferrero, G., Miano, V., De Intinis, C., Ricci, L., Arigoni, M., Riccardo, F., Annaratone, L., Castellano, I., Calogero, R. A., Beccuti, M., Cordero, F., and De Bortoli, M. (2018). Luminal breast cancer-specific circular RNAs uncovered by a novel tool for data analysis. *Oncotarget*, 9(18):14580
10. Miano, V., Ferrero, G.*, Rosti, V., Manitta, E., Elhasnaoui, J., Basile, G., and De Bortoli, M. (2018). Luminal lncRNAs regulation by ER α -controlled enhancers in a ligand-independent manner in breast cancer cells. *International journal of molecular sciences*, 19(2):593. [*Co-first author]
9. Miglio, U., Berrino, E., Panero, M., Ferrero, G., Coscujuela, L., Miano, V., Dell'Aglio, C., Sarotto, I., Annaratone, L., Marchiò, C., Comoglio, P., De Bortoli, M., Pasini, B., Venesio, T., and Sapino, A. (2018). The expression of LINE1-MET chimeric transcript identifies a subgroup of aggressive breast cancers. *International Journal of Cancer*, pages 1–11
8. Ferrero, G., Miano, V., Beccuti, M., Balbo, G., De Bortoli, M., and Cordero, F. (2017). Dissecting the genomic activity of a transcriptional regulator by the integrative analysis of omics data. *Scientific reports*, 7(1):8564
7. Miano, V., Ferrero, G., Reineri, S., Caizzi, L., Annaratone, L., Ricci, L., Cutrupi, S., Castellano, I., Cordero, F., and De Bortoli, M. (2016). Luminal long non-coding RNAs regulated by estrogen receptor alpha in a ligand-independent manner show functional roles in breast cancer. *Oncotarget*, 7(3):3201
6. Rosso, M. C., Badino, P., Ferrero, G., Costa, R., Cordero, F., and Steidler, S. (2016). Biologic data of cynomolgus monkeys maintained under laboratory conditions. *PloS One*, 11(6):e0157003
5. Guglielmo, M., Reineri, S., Iannello, A., Ferrero, G., Vanzan, L., Miano, V., Ricci, L., Tamagno, E., De Bortoli, M., and Cutrupi, S. (2016). E2 regulates epigenetic signature on neuroglobin enhancer-promoter in neuronal cells. *Frontiers in cellular neuroscience*, 10:147
4. Cordero, F., Ferrero, G., Polidoro, S., Fiorito, G., Campanella, G., Sacerdote, C., Mattiello, A., Masala, G., Agnoli, C., Frasca, G., Panico, S., Palli, D., Krogh, V., Tumino, R., Vineis, P., and Naccarati, A. (2015). Differentially methylated microRNAs in prediagnostic samples of subjects who developed breast cancer in the European Prospective Investigation into Nutrition and Cancer (EPIC-Italy) cohort. *Carcinogenesis*, 36(10):1144–1153
3. Caizzi, L., Ferrero, G., Cutrupi, S., Cordero, F., Ballaré, C., Miano, V., Reineri, S., Ricci, L., Friard, O., Testori, A., Cora, D., Caselle, M., Di Croce, L., and De Bortoli, M. (2014). Genome-wide activity of unliganded estrogen receptor- α in breast cancer cells. *Proceedings of the National Academy of Sciences*, page 201315445

2. Cutrupi, S., Ferrero, G., Reineri, S., Cordero, F., and De Bortoli, M. (2014). Genomic lens on neuroglobin transcription. *IUBMB life*, 66(1):46–51
1. Misale, C., Ferrero, G., Torquati, M., and Aldinucci, M. (2014). Sequence alignment tools: one parallel pattern to rule them all? *BioMed research international*, 2014

Book chapters

1. Ferrero, G., Licheri, N., De Bortoli, M., Calogero, R. A., Beccuti, M., and Cordero, F. (2021b). Computational analysis of circRNA expression data. *Methods in Molecular Biology (Clifton, NJ)*, 2284:181–192

Publications on proceedings of scientific conferences

1. Piaggieschi G.B., Licheri N., Romano G., Pernice S., Follia L., and Ferrero G. MethylFASTQ: a tool simulating bisulfite sequencing data. (2019) PDP2019. Pavia, Italy 13-15 Febr 2019.
2. Follia L., Tordini F., Romano G., Pernice S., Piaggieschi G.B. and Ferrero G. ParallNormal: an efficient variant calling pipeline for unmatched sequencing data. (2018) PDP2018. Cambridge, England 21-23 March 2018.

Awards and recognitions for research activities

2016	SIBBM Travel Grants for participation in international conferences. BITS Travel Grants.
2015	BITS Travel Grants for participation in international conferences.
2015	BITS Travel Grants.
2013	Award for the best Master's thesis in Cellular and Molecular Biology (A.A. 2011-2012). Title: "A new data processing pipeline for the bioinformatic analysis of transcription factor genomic binding events".

Activities in scientific conferences

Dr. Ferrero personally participated in 21 international scientific international conferences, contributing with 5 oral presentations and 16 posters. In addition, Dr. Ferrero also co-authored more than 50 contributions in international conferences.

Oral presentations

5. Ferrero G., Pardini B., Tarallo S., Gallo G., Francavilla A., Licheri N., Senore C., Vymetalkova V., Vodickova L., Vodicka P., Segata N., Cordero F., Naccarati A. Integrative omic analysis of faecal samples shows novel miRNA-mediated host-microbiota interactions in colorectal cancer. (2022). Final TRANSCOLONCAN Meeting 2022. 1-3 Jun. Barcelona, Spain.
4. Ferrero G., Tarallo S., Francavilla A., De Filippis F., Clerico G., Pasolli E., Panero V., Segata N., Gironi S., Pensa R., Ercolini D., Cordero F., Pardini B., Naccarati A. An integrated analysis on stool microRNA and microbial content in subjects with different dietary regimes. (2021). BITS 2021. 1-2 Jul. Online.
3. Ferrero G., Tarallo S., Francavilla A., Gallo G., Clerico G., Manghi P., Thomas A., Segata N., Pardini B., Naccarati A., Cordero F. Gut microbiome composition and small RNA spectra in human stool for colorectal cancer detection. (2018). BITS 2018. 27-29 Jun. Turin, Italy.

2. Ferrero G., Miano V., Balbo G., De Bortoli M., Beccuti M., Cordero F. An integrative strategy to functional analysis of the noncoding genome. (2015). EMBL | STANFORD CONFERENCE: "Personalised Health". 16-19 Nov. Heidelberg, Germany.
1. Ferrero G., Miano V., Balbo G., De Bortoli M., Beccuti M., Cordero F. Integrative strategy for omics data: ERα cistrome and epigenome case-study. (2014). NETTAB 2014, "From structural bioinformatics to integrative systems biology", 15-17 Oct. Turin, Italy.

Poster sessions

16. Ferrero G., Pardini B., Tarallo S., Zwinsova B., Vodickova L., Vodicka P., Segata N., Cordero F., Budinska E., Naccarati A. Integrative omic analysis of faecal samples shows novel miRNA-mediated host-microbiota interactions in colorectal cancer. (2023). EACR 2023 Congress - Innovative Cancer Science. 12-15 Jun. Turin, Italy.
15. Tarallo S., Ferrero G., Francavilla A., Gallo G., Clerico G., Manghi P., Thomas A., Segat N., Cordero F., Pardini B., Naccarati A. Small RNA profiles in human stool reflect gut microbiome composition and together provide high accuracy to detect colorectal cancer. (2019). SIBBM Frontiers in Molecular biology, Nucleic acid immunity: from cellular mechanisms to new technologies. 11-13 Jun. Bologna, Italy.
14. Tarallo S., Ferrero G., Francavilla A., Gallo G., Clerico G., Manghi P., Thomas A., Segata N., Cordero F., Pardini B., Naccarati A. Gut microbiome composition and small RNA spectra in human stool for colorectal cancer detection. (2018). EMBO | EMBL Symposium: The Human Microbiome. 16-19 Sept. Heidelberg, Germany.
13. Follia L., Ferrero G., Mandili G., Beccuti B., Katayama H., Hong W., Momin A.M., Capello M., Hanash S.M., Novelli F., Cordero F. An integrative transcriptomic analysis of glycolytic genes reveals different metabolic subtypes in pancreatic cancer. (2018). BITS 2018. 27-29 Jun. Turin, Italy.
12. Coscujuela T.L., Ferrero G., Miano V., Ricci L., De Intinis C., Arigoni M., Riccardo F., Calogero R.A., Beccuti M., Cordero F. De Bortoli M. CircRNA characterisation in MCF-7 breast cancer cell line. (2017) ISMB/ECCB 2017. 21-25 Jul. Prague, Czech Republic.
11. Coscujuela T.L., Ferrero G., Miano V., Ricci L., De Intinis C., Arigoni M., Riccardo F., Calogero R.A., Beccuti M., Cordero F. and De Bortoli M. CircRNA characterisation in MCF-7 breast cancer cell line. (2017) ISFMS 2017. 21-23 Jun. Basel, Switzerland.
10. Follia L., Ferrero G., Totis N., Riganti C., Novelli F., Balbo G., Beccuti M., Cordero F. Inspecting Energy Releasing Pathways by combination of genomics data and mechanistic approach. (2016). EMBO Conference: From Functional Genomics to Systems Biology. 12-15 Nov. Hiedelberg, Germany.
9. Ferrero G., Beccuti M., Balbo G., Holstein P., Cordero F. Detecting critical nodes in the analysis of cancer integrative networks. (2016). BITS 2016. 15-17 Jun. Salerno, Italy.
8. Ferrero G., Tordini F., Holstein P., Miano V., Coscujuela L., Ricci L., Aldinucci M., Beccuti M., De Bortoli M, Cordero F. Identification of critical enhancers by network modeling of long-range chromatin interactions. (2016). SIBBM Frontiers in Molecular biology, From Single Cell Analysis to Precision Medicine. 16-18 Jun. Naple, Italy.
7. Ferrero G., Miano V., Balbo G., De Bortoli M., Beccuti M., Cordero F. An integrative strategy to functional analysis of the noncoding genome. (2015). EMBL | STANFORD CONFERENCE: "Personalised Health". 16-19 Nov Heidelberg, Germany.

6. Ferrero G., Miano V., Balbo G., De Bortoli M., Beccuti M., Cordero F. Integrative strategies for omics data: ER α cistrome and epigenome case-study. (2015). SIBBM Frontiers in Molecular biology, "From Genomes to Functions". 1-3 Jul. Turin, Italy.
5. Ferrero G., Ricci L., Miano V., Arigoni M., Riccardo F., Annaratone L., Calogero R., Balbo G., De Bortoli M., Beccuti M., Cordero F. Analysis of circular RNAs regulated by Estrogen Receptor α . (2015). BITS 2015. 3-5 May. Milan, Italy.
4. Ferrero G., Miano V., Balbo G., De Bortoli M., Beccuti M., Cordero F. Integrative strategy to elucidate the multiple layers of the transcriptional regulation. (2014). EMBO Conference Series "From functional genomics to systems biology", 8-11 Nov. Heidelberg, Germany.
3. Ferrero G., Miano V., Balbo G., De Bortoli M., Beccuti M., Cordero F. Exploration of hormone-independent Estrogen Receptor α activity by integrative and comparative approaches. (2014). SIBBM Frontiers in Molecular biology, "Arenas in Molecular Biology: from basic mechanisms to personalized medicine", 11-13 Jun. Trento, Italy.
2. Ferrero G., Caizzi L., Miano V., Balbo G., De Bortoli M., Beccuti M., Cordero F. Exploration of hormone-independent Estrogen Receptor α activity by integrative and comparative approaches. (2014). BITS annual meeting 2014. 26-28 Feb. Rome, Italy.
1. Ferrero G., Miano V., Beccuti M., Balbo G., Cordero F., De Bortoli M. Biological and technical variables on lncRNA quantification by RNA-Seq experiments. (2013). SIBBM Frontiers in Molecular biology, "Revisiting the Central Dogma: Emerging New Concepts in Replication, Transcription and Translation". 5-7 Jun. Pavia, Italy.

Participation in the organization of scientific conferences

2019	CIBB 2019: Computational Intelligence methods for Bioinformatics and Biostatistics - PC member in MODELING AND SIMULATION METHODS FOR COMPUTATIONAL BIOLOGY AND SYSTEMS MEDICINE.
2018	BITS Meeting 2018 - PC member. Euro-Par 2018 - PC member in WORKSHOP ON ADVANCES IN HIGH-PERFORMANCE BIOINFORMATICS, SYSTEMS BIOLOGY (MED-HPC 2018). PDP2018 - PC member of Advances in High-Performance Bioinformatics and Biomedicine.

Teaching, Tutoring, and Public Engagement activities

Teacher

2023-2024	- "Informatics (INT0639B)" course of the Bachelor Degree in Biotechnology (L-2), University of Turin - 60 teaching hrs. - 'Bioinformatic module of "Advanced Molecular Biology (SVB0041)" course of the Master Degree of Molecular and Cellular Biology (LM-6), University of Turin - 24 hrs.
2022-2023	- "Informatics (INT0639B)" course of the Bachelor Degree in Biotechnology (L-2), University of Turin - 60 teaching hrs. - 'Bioinformatic module of "Advanced Molecular Biology (SVB0041)" course of the Master Degree of Molecular and Cellular Biology (LM-6), University of Turin - 24 hrs.

2021-2022	- "Informatics (INT0639B)" course of the Bachelor Degree in Biotechnology (L-2), University of Turin - 60 teaching hrs. - 'Bioinformatic module of "Advanced Molecular Biology (SVB0041)" course of the Master Degree of Molecular and Cellular Biology (LM-6), University of Turin - 24 hrs.
2020-2021	- "Informatics (INT0639B)" course of the Bachelor Degree in Biotechnology (L-2), University of Turin - 60 teaching hrs.
2019-2020	- "Informatics (INT0639B)" course of the Bachelor Degree in Biotechnology (L-2), University of Turin - 60 teaching hrs.
2018-2019	- "Informatics (INT0639B)" course of the Bachelor Degree in Biotechnology (L-2), University of Turin - 60 teaching hrs.

Teaching assistant

2020-2021	- Bioinformatic module of "Advanced Molecular Biology (SVB0041)" course of the Master Degree of Molecular and Cellular Biology (LM-6), University of Turin - 15 hrs.
2019-2020	- Bioinformatic module of "Advanced Molecular Biology (SVB0041)" course of the Master Degree of Molecular and Cellular Biology (LM-6), University of Turin - 15 hrs.
2018-2019	- Bioinformatic module of "Advanced Molecular Biology (SVB0041)" course of the Master Degree of Molecular and Cellular Biology (LM-6), University of Turin - 15 hrs.
2017-2018	- Bioinformatic module of "Advanced Molecular Biology (SVB0041)" course of the Master Degree of Molecular and Cellular Biology (LM-6), University of Turin - 15 hrs. - R programming module of the course "Experimental data analysis (MFN1306)" of the Bachelor Degree of Biology (L-13), University of Turin - 18 hrs.
2016-2017	- Bioinformatic module of "Advanced Molecular Biology (SVB0041)" course of the Master Degree of Molecular and Cellular Biology (LM-6), University of Turin - 15 hrs. - R programming module of the course "Experimental data analysis (MFN1306)" of the Bachelor Degree of Biology (L-13), University of Turin - 18 hrs.
2015-2016	- Bioinformatic module of "Advanced Molecular Biology (SVB0041)" course of the Master Degree of Molecular and Cellular Biology (LM-6), University of Turin - 15 hrs. - R programming module of the course "Experimental data analysis (MFN1306)" of the Bachelor Degree of Biology (L-13), University of Turin - 18 hrs.
2014-2015	- Bioinformatic module of "Advanced Molecular Biology (SVB0041)" course of the Master Degree of Molecular and Cellular Biology (LM-6), University of Turin - 15 hrs.
2013-2014	- Bioinformatic module of "Advanced Molecular Biology (SVB0041)" course of the Master Degree of Molecular and Cellular Biology (LM-6), University of Turin - 15 hrs.

Tutored PhD Students

2023- now	- Dr. Alessandro Camandona - PhD Program in Complex Systems for Quantitative Biomedicine, University of Turin.
2021- now	- Dr. Lorenzo Franchitti - PhD Program in Complex Systems for Quantitative Biomedicine, University of Turin.
2019- 2021	- Dr. Jamal Elhasnaoui - PhD Program in Complex Systems for Quantitative Biomedicine, University of Turin.
2019- 2021	- Dr. Laura Follia - PhD Program in Molecular Medicine, University of Turin.

Tutored Master Degree Students

2023- now	- Dr. Paola De Lisa - Master Degree in Molecular Biotechnology, University of Turin. - Dr Lorenzo Garnero - Master Degree in Cellular and Molecular Biology, University of Turin. - Dr Ahmad Khalife El Rawas - Master Degree in Cellular and Molecular Biology, University of Turin.
2022- 2023	- Dr. Alessandro Camandona - Master Degree in Cellular and Molecular Biology, University of Turin. - Dr. Marco Ricercato - Master Degree in Cellular and Molecular Biology, University of Turin. - Dr. Giulia Benedetto - Master Degree in Cellular and Molecular Biology, University of Turin.
2020- 2021	- Dr. Lorenzo Franchitti - Master Degree in Cellular and Molecular Biology, University of Turin.
2018- 2019	- Dr. Gianluca Dalmaso - Master Degree in Computer Science, University of Turin.

Public Engagement

2022	- Oral and poster presentation at Clinical and Biological Science Department Day 2022. Orbassano, Italy
	- Participation to the "Just The Woman I Am 2022" event. Turin, Italy
2020	- Interview for the "Sharper - SHARing Researchers' Passion for Evolving Responsibilities. Notte Europea delle Ricercatrici e dei Ricercatori 2020" event. Turin, Italy
2019	- Participation to the "Sharper - SHARing Researchers' Passion for Evolving Responsibilities. Notte Europea delle Ricercatrici e dei Ricercatori 2019" event. Turin, Italy - Short article and interview for "FRIDA La ricerca si racconta su frida - 2019".
	- Participation to the "Just The Woman I Am 2019" event. Turin, Italy
2013	- Participation to the "Notte Europea dei Ricercatori 2013" event. Turin, Italy

Non-academic scientific activities

Experience in companies

2019- 2021	Bioinformatic consultant at Bactell inc (US), a startup specialized in the prediction of microbial antibiotic resistance through the computational analysis of DNA sequencing data.
---------------	---

Certified professional development

2023	"Corso ECM: Lo Studio EPIC Torino, tra Passato Presente e Futuro" from the University of Turin, Italy.
2022	"IRIDI - Start 6" from the University of Turin, Italy.
2019	"Machine Learning A-Z: Hands-On Python & R In Data Science" through da Udemy. "Whole genome sequencing of bacterial genomes - tools and applications." from the Technical University of Denmark (TDU) through Coursera.

- “Metagenomics applied to surveillance of pathogens and antimicrobial resistance.” from the Technical University of Denmark (TDU) through Coursera.
 “Introduction to Machine Learning” through DataCamp.
 “Data visualization with ggplot2” through DataCamp.
 “Reporting with R Markdown” through DataCamp.
- 2017 “Python for Genomic Data Science” from the Johns Hopkins University through Coursera.
- 2016 “Bioinformatic Methods II” from the University of Toronto through Coursera.
- 2015 “Big Data Science with the BD2K-LINCS Data Coordination and Integration Center” from the Icahn School of Medicine at Mount Sinai through Coursera.
 “Case Study: ChIP-seq data analysis” from the Harvard University through edX.
 “Data Analysis and Statistical Inference” from the Duke University through Coursera.
 “Bioinformatic Methods I” from the University of Toronto through Coursera.
 “Statistics and R for the Life Sciences” from the Harvard University through edX.
 “Data Mining with Weka” from the University of Waikato.
 “Genomic and Precision Medicine” from the University of California, San Francisco through Coursera.
 “Network Analysis in Systems Biology” from the Icahn School of Medicine at Mount Sinai through Coursera.
- 2014 “R Programming” from the Johns Hopkins Bloomberg School of Public Health through Coursera.
 “An Introduction to Interactive Programming in Python” from Rice University through Coursera.
 “Intro to Computer Science” through Udacity.
- 2013 “Csama 2013: computational statistics for genome biology (11th edition)” at Bressanone, Italy.

Membership in scientific associations

Italian Society in Biophysics and Molecular Biology (SIBBM).
 The Bioinformatics Italian Society (BITS).
 The Italian Cancer Society (SIC).

Turin, April 15, 2024

