


UNIVERSITÀ DEGLI STUDI DI MILANO


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Giovanni Fiorito CURRICULUM VITAE

PERSONAL INFORMATIONS

Giovanni Fiorito

 Via Filadelfia n.139, 10137 Torino – Italy.

 +39-340-5255785.

 giovanni.fiorito85@gmail.com

Sex M | Date of birth 25 / 01 / 1985 | Nationality Italian.

EDUCATION AND TRAINING

From 2013 to 2016

PhD in Complex Systems for Life Sciences

University of Torino – Italy

Thesis title: *Genomic and epigenomic variability across the Italian population and impact on complex diseases.*

Supervisor: Prof. Giuseppe Matullo (University of Torino).

Thesis short description: **GWAS and EWAS methods in epidemiological cohort studies and population genetics.**

From 2009 to 2011

Master's degree in Applied Mathematics

University of Torino – Italy

Thesis title: *On the homomorphism between formal neural nets and automata theory - An application in robotics.*

Supervisor: Prof. Roberto Moreno-Diaz (University of Las Palmas de Gran Canaria) and Prof. Maria Teresa Giraudo (University of Torino).

Thesis short description: *Development and implementation of an efficient **Machine Learning** algorithm to teach a robot 'how to solve a labyrinth'.*

From 2005 to 2008

First Level Degree in Mathematics

University of Torino – Italy

Thesis: *On the first passage time problem for diffusion processes.*

Supervisor: Prof. Cristina Zucca (University of Torino)

RESEARCH ACTIVITIES

From October 2019 -
current position

Researcher Rtd-A (MED/01), Laboratory of Biostatistics, Department of Biomedical Sciences, University of Sassari, Italy.

- Research activities:
 - Impact of **lifestyle** behaviours (diet, physical activity, smoking, alcohol consumption) on biomarkers of **epigenetic aging** and cancer risk.
 - **Microbiome** and **Metaproteome** biomarkers in colorectal cancer (**CRC**) prognosis.
 - **MiRNAs** expression as diagnostic and prognostic **biomarkers** in **CRC** and **prostate cancer**.
- **Teaching** activity for first level degree, master's degree, and PhD students.
- **Supervisor** for master's degree and PhD students.

From March 2019 to
September 2019

Research Analyst at 'Cancer Risk Factors and life-style epidemiology' group headed by Dr. Domenico Palli, Istituto per lo Studio, la Prevenzione e la Rete Oncologica – ISPRO, Firenze, Italy.

- **DNA-methylation** data **analyses** within the EPIC Italy cohort and DAMA intervention study (AIRC grants to Domenico Palli).

From September 2017 to
March 2019

Post-doc researcher at the Italian Institute for Genomic Medicine (**IIGM**), 'Molecular epidemiology and exposomics' unit (headed by Prof. Paolo Vineis, Torino, Italy).

- Evaluation, comparison and **development** of algorithms and **analytical methods** for the analysis of **omics data** in molecular epidemiology and clinical trials.
- **DNA-methylation** data analyses within the H2020 European project 'LIFEPATH'.
- **Tutor** for **PhD** and master-degree **students**.

From March 2016 to
September 2017

Post-doc researcher at the University of Torino, Department of Medical Science, and collaboration with the Italian Institute for Genomic Medicine (**IIGM**), 'Molecular epidemiology and exposomics' unit (headed by Prof. Paolo Vineis, Torino, Italy).

- Identification of **epigenetic biomarkers** in **age-related diseases**.

- Methods for the **integration of omics data** with multiple exposure measures, within the H2020 European project '**EXPOsOMICS**'.
- **Tutor** for **PhD** and master-degree **students**.

From January 2012 to February 2016

Research fellow at the Human Genetics Foundation (HuGeF), '**Genomic variability and translational research**' unit (headed by Prof. Giuseppe Matullo), Torino, Italy.

- Mathematical models in **population genetics**.
- **EWAS** and **GWAS** association studies: malignant pleural **mesothelioma** and **cardiovascular** diseases.
- Collaboration with the Scientific Investigation Unit (RIS, Parma) for the **identification of geographical origin** and age from **DNA of unknown origin**.

OTHER RESEARCH ACTIVITIES

- Part of the '**Machine Learning and Deep Learning**' working group within the Società Italiana di Statistica Medica (SISMEC).
- **Stakeholder** for the **H2020 European Project SYNCHROS**: 'synchronising cohorts and population surveys in Europe and worldwide'.
- **Reviewer** for several scientific journals.
- **Editor** for the scientific journals '*Genes*', '*Biology*', '*Diagnostics*', '*International Journal of Environmental Research and Public Health*' and '*Frontiers in Cardiovascular Medicine*'.
- 'Lifepath' (<https://www.lifepathproject.eu/>) H2020 European project participant.
- 'EXPOsOMICS' (<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6192011/>) H2020 European project participant.
- 56 scientific publications on peer-review journals, **H-index (Scopus) = 25**.
- Two book Chapters
 - Vodicka, P. et al. Chapter 37: Micronucleus Assay for Assessing Chromosomal Damage in Medical Workers Exposed to Anaesthetic Gases, from Vodicka, P. et al. The Micronucleus Assay in Toxicology (2019).
 - **Fiorito, G.** et al. Chapter 2: Lessons from Knowledge on the Correlates of the Age of Onset of Physical Illness, from De Girolamo, G. et al. Age of Onset of Mental Disorders (2018).

Link to publications in PubMed:

<https://www.ncbi.nlm.nih.gov/pubmed/?term=Fiorito+Giovanni+%5Bauthor%5D>.

RESEARCH INTERESTS

I have a background in applied mathematics, and I have always been part of multi-disciplinary research groups together with biologists, epidemiologists, and physicians.

I am interested in the study, evaluation, comparison, and development of mathematical and **statistical methods** for the **analysis of multi-omic datasets** in **epidemiological studies** (**cohort**, **case-control**, and **intervention studies**), and **clinical research** with the aim to identify novel **diagnostic** and **prognostic biomarkers**. In the last few years of my research career, I focused on ageing-related epigenetic modifications (**epigenetic clocks** and **epigenetic drift**) and their association with age-related diseases, specifically cancer.

MAIN EXPERTISES

- Mathematical-statistical models and bio-informatics methods for the analysis of **omics data**: **clustering analyses** for patient stratification, **machine learning** based methods for variable selection, integration of epigenetic data produced with different technologies and 'noise reduction'.
- Advanced analytical techniques: **Neural Networks** and **Deep Learning**.
- Mediation analysis, causal inference, meta-analysis, network analysis, pathway/enrichment analysis, Mendelian randomization.
- Study design, sample collection and power analyses in molecular epidemiology.
- Pre-processing **pipelines implementation** for NGS data (genomic and epigenomic).
- Excellent knowledge of programming languages **R**, **PYTHON** and **UNIX** environment.
- Excellent teamwork ability and ability to communicate statistical concepts.

EXPERIENCES ABROAD

- From March 2021 (ongoing collaboration): 'Visiting Researcher' at the Department of Medical Gerontology, **Trinity College – Dublin**, Ireland.
- From January 2020 to January 2021: 'Visiting Researcher' at the **Imperial College London - School of public health**, Environmental epidemiology group, St Mary's Campus Norfolk Place W2 1PG, London, UK.
- From January to June 2014: 'Visiting Student' at the **Stanford University**, Morrison Institute for Population and Resources Studies, **Palo Alto, California – USA**, for the development of population genetics algorithms.
- From September 2009 to September 2010: 'Erasmus' project at the University of **Las Palmas de Gran Canaria (Spain)**.

TEACHING

- **Course owner** 'An introduction to statistical analyses of genomic and epigenomic dataset with R' **PhD course in 'Life Sciences and Biotechnologies'**, University of Sassari (academic years 2019-20 and 2020-21), 3 CFU, s.s.d. MED/01.
- **Course owner** 'Mathematics' degree in Biological Sciences, University of Sassari (academic year 2020-21), 6 CFU s.s.d MAT/05.
- **Exercises and Tutoring** 'Statistics' degree in Biological Sciences, University of Sassari (academic year 2020-21), 2 CFU s.s.d. MED/01.
- **Exercises and Tutoring** 'Laboratory of Statistics' degree in Biotechnology, University of Sassari (academic year 2020-21), 2 CFU s.s.d. MED/01.
- Member of the **examination board**: Courses of 'Mathematics', 'Statistics' and 'Laboratory of Statistics' for the degrees in Biotechnology and Biological Sciences, University of Sassari (academic years 2019-20 and 2020-21).

FOREIGN LANGUAGES

- English
 - UNDERSTANDING excellent
 - SPEAKING excellent
 - READING excellent
- Spanish
 - UNDERSTANDING excellent
 - SPEAKING excellent
 - READING excellent

COURSES and CONFERENCES

- **Oral presentation** at the Web Conference 'The pandemic phenomenon: models and multi-disciplinary aspects' - '*Mathematical models in genetics and epigenetics research*', **Accademia dei Lincei**, 15 January 2021.
- **Oral presentation** at the annual meeting of the '**Società Italiana di Statistica Medica (SISMEC)**' - '*Education inequalities in longevity: a multi-cohort study on the role of epigenetic clocks*', on-line meeting, 12 November 2020.
- **Oral presentation** at the 2020 **NIA Biomarker Network Meeting on Functional Genomics: RNA & Epigenetics in Population Health Research** - '*Associations of 4 epigenetic clocks with measures of functional health, cognitive performance, and all-cause mortality*', on-line meeting, 21-22 April 2020.
- **Oral presentation** at the **European Congress of Epidemiology (ECE)** - '*Low socioeconomic status and unhealthy lifestyle habits are associated with a premature occurrence of stochastic epigenetic mutations*', 4 - 6 July 2018, Lyon, France.
- Poster presentation at the 'Healthy ageing: from molecules to organisms' conference, 31 January - 2 February 2018, Cambridge, UK.

- **Oral presentation** at the National conference of **Società Italiana di Genetica Umana** (SIGU) – ‘*Genomic and epigenomic variability in the Italian population and incidence on complex diseases risk*’, 21 - 24 October 2015, Rimini, Italy.
- Poster presentation at the American Society of Human Genetics (ASHG) annual meeting in 2013 (Boston, Massachusetts, U.S.A.) and 2014 (San Diego, California, U.S.A).
- **Oral presentation** at the **European Society of Human Genetics** (ESHG) annual meeting – ‘*Genomic and epigenomic variability in the Italian population and incidence on complex diseases risk*’ in 2013 (Paris, France).
- Attendant at the ‘*Epigenetics and aging: Biological clocks in health and disease*’ conference, Royal Society of Medicine, June 14th, 2021.
- Attendant at the ‘*Epigenetics – the full picture 2021*’ conference, May 12th - 16th, 2021.
- Attendant at the course ‘Genetic Analysis of population-based association studies’ in 2013, Wellcome Genome Campus - Cambridge, UK.
- Attendant at the course ‘Stat-XP Exposome Advanced – Statistical models and machine learning techniques for OMICs profiling and integration in exposome research’ in 2014, Imperial College London, London, UK.

Publications

1. Fiorito, G. et al. DNA methylation-based biomarkers of aging were slowed down in a two-year diet and physical activity intervention trial: the DAMA study. *Aging Cell* (2021).
2. Idda, M.L. et al. Sex-biased expression of pharmacogenes across human tissues. *Biomolecules* (2021).
3. Fiorito, G. et al. The mediating role of epigenetic clocks underlying educational inequalities in mortality: a multi-cohort study. Preprint on medRxiv (2021), <https://medrxiv.org/cgi/content/short/2021.07.01.21259023v1>.
4. Karabregovic, I. et al. Epigenome-wide association meta-analysis of DNA methylation with coffee and tea consumption, *Nature Communications* (2021).
5. Caini, S. et al. Pre-diagnostic DNA methylation patterns in women developing breast cancer differ according to mammographic breast density: a case-only study in the EPIC-Florence cohort. *Breast Cancer Research and Treatment* (2021).
6. Tanca, A. et al. Comparative Evaluation of MaxQuant and Proteome Discoverer MS1-based Protein Quantification Tools. *Journal of Proteome Research* (2021).
7. Rocha, V. Life-course socioeconomic disadvantage and lung function: a multicohort study of 70 496 individuals, *European Resp. Journal* (2021).
8. McCrory, C. et al. GrimAge outperforms other epigenetic clocks in the prediction of age-related clinical phenotypes and all-cause mortality. *Journals Gerontol. Ser. A* (2020).
9. Yusipov, I. et al. Age-related DNA methylation changes are sex-specific: a comprehensive assessment. *Aging* (Albany. NY). 12, 24057–24080 (2020).
10. Pisano, A. et al. The inhibitory role of mir-486-5p on csc phenotype has diagnostic and prognostic potential in colorectal cancer. *Cancers* (Basel). 12, 1–24 (2020).
11. Gagliardi, A. et al. Stochastic Epigenetic Mutations Are Associated with Risk of Breast Cancer, Lung Cancer, and Mature B-cell Neoplasms. *Cancer Epidemiol. Biomarkers Prev.* (2020).
12. Dagnino, S. et al. Agnostic Cys34-albumin adductomics and DNA methylation: Implication of N-acetylcysteine in lung carcinogenesis years before diagnosis. *Int. J. Cancer* 146, 3294–3303 (2020).

13. Robinson, O. et al. Determinants of accelerated metabolomic and epigenetic aging in a UK cohort. *Aging Cell* 19, (2020).
14. McCrory, C. et al. Epigenetic clocks and allostatic load reveal potential sex-specific drivers of biological aging. *Journals Gerontol. - Ser. A Biol. Sci. Med. Sci.* (2020).
15. Vineis, P. et al. Health inequalities: Embodied evidence across biological layers. *Soc. Sci. Med.* 246, (2020).
16. Fasanelli, F. et al. DNA methylation, colon cancer and Mediterranean diet: results from the EPIC-Italy cohort. *Epigenetics* 14, (2019).
17. Agha, G. et al. Blood Leukocyte DNA Methylation Predicts Risk of Future Myocardial Infarction and Coronary Heart Disease. *Circulation* 140, 645–657 (2019).
18. McCrory, C. et al. How does socio-economic position (SEP) get biologically embedded? A comparison of allostatic load and the epigenetic clock(s). *Psychoneuroendocrinology* 104, 64–73 (2019).
19. McCrory, C. et al. Maternal educational inequalities in measured body mass index trajectories in three European countries. *Paediatr. Perinat. Epidemiol.* 33, 226–237 (2019).
20. Fiorito, G. et al. Socioeconomic position, lifestyle habits and biomarkers of epigenetic aging: A multi-cohort analysis. *Aging (Albany, NY)*. 11, 2045–2070 (2019).
21. Azzolina, D. et al. Machine learning in clinical and epidemiological research: Isn't it time for biostatisticians to work on it? *Epidemiology Biostatistics and Public Health* (2019).
22. Schmidt, A. F. et al. Phenome-wide association analysis of LDL-cholesterol lowering genetic variants in PCSK9. *BMC Cardiovasc. Disord.* 19, (2019).
23. Campanella, G. et al. Epigenome-wide association study of adiposity and future risk of obesity-related diseases. *Int. J. Obes.* 42, 2022–2035 (2018).
24. Jeong, A. et al. Perturbation of metabolic pathways mediates the association of air pollutants with asthma and cardiovascular diseases. *Environ. Int.* 119, (2018).
25. Castagné, R. et al. Allostatic load and subsequent all-cause mortality: which biological markers drive the relationship? Findings from a UK birth cohort. *Eur. J. Epidemiol.* 33, (2018).
26. Fiorito, G. et al. Oxidative stress and inflammation mediate the effect of air pollution on cardio- and cerebrovascular disease: A prospective study in nonsmokers. *Environ. Mol. Mutagen.* 59, 234–246 (2018).
27. Dugué, P.-A. et al. Association of DNA Methylation-Based Biological Age with Health Risk Factors and Overall and Cause-Specific Mortality. *Am. J. Epidemiol.* 187, 529–538 (2018).
28. van Baak, T. E. et al. Epigenetic supersimilarity of monozygotic twin pairs. *Genome Biol.* 19, (2018).
29. D'Amico, F. et al. FOXP3, ICOS and ICOSL gene polymorphisms in systemic sclerosis: FOXP3 rs2294020 is associated with disease progression in a female Italian population. *Immunobiology* 223, (2018).
30. Fiorito, G. et al. Social adversity and epigenetic aging: A multi-cohort study on socioeconomic differences in peripheral blood DNA methylation. *Sci. Rep.* 7, (2017).
31. Karlsson Linnér, R. et al. An epigenome-wide association study meta-analysis of educational attainment. *Mol. Psychiatry* 22, 1680–1690 (2017).
32. Marcon, F. et al. Telomerase activity, telomere length and hTERT DNA methylation in peripheral blood mononuclear cells from monozygotic twins with discordant smoking habits. *Environ. Mol. Mutagen.* 58, (2017).
33. Schmidt, A. F. et al. PCSK9 genetic variants and risk of type 2 diabetes: a mendelian randomisation study. *Lancet Diabetes Endocrinol.* 5, (2017).
34. Wahl, S. et al. Epigenome-wide association study of body mass index, and the adverse outcomes of adiposity. *Nature* 541, 81–86 (2017).
35. Ligthart, S. et al. DNA methylation signatures of chronic low-grade inflammation are associated with complex diseases. *Genome Biol.* 17, (2016).

36. Turinetti, V. et al. H2AX phosphorylation level in peripheral blood mononuclear cells as an event-free survival predictor for bladder cancer. *Mol. Carcinog.* 55, 1833–1842 (2016).
37. Marzi, C. et al. Epigenetic signatures at AQP3 and SOCS3 engage in low-grade inflammation across different tissues. *PLoS One* 11, (2016).
38. Vodicka, P. et al. DNA and chromosomal damage in medical workers exposed to anaesthetic gases assessed by the lymphocyte cytokinesis-block micronucleus (CBMN) assay. A critical review. *Mutat. Res. - Rev. Mutat. Res.* 770, 26–34 (2016).
39. Sazzini, M. et al. Complex interplay between neutral and adaptive evolution shaped differential genomic background and disease susceptibility along the Italian peninsula. *Sci. Rep.* 6, (2016).
40. Fiorito, G. et al. The Italian genome reflects the history of Europe and the Mediterranean basin. *Eur. J. Hum. Genet.* 24, (2016).
41. Zanolli, L. et al. Association between Beta¹-Adrenergic Receptor Polymorphism and Risk of ICD Shock in Heart Failure Patients. *PACE - Pacing Clin. Electrophysiol.* 39, (2016).
42. Guarrera, S. et al. Gene-specific DNA methylation profiles and LINE-1 hypomethylation are associated with myocardial infarction risk. *Clin. Epigenetics* 7, (2015).
43. Singmann, P. et al. Characterization of whole-genome autosomal differences of DNA methylation between men and women. *Epigenetics and Chromatin* 8, (2015).
44. Figueroa, J. D. et al. Identification of a novel susceptibility locus at 13q34 and refinement of the 20p12.2 region as a multi-signal locus associated with bladder cancer risk in individuals of european ancestry. *Hum. Mol. Genet.* 25, (2015).
45. Tunesi, S. et al. Gene-asbestos interaction in malignant pleural mesothelioma susceptibility. *Carcinogenesis* 36, (2015).
46. Cordero, F. et al. 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, 1144–1153 (2015).
47. Khadjavi, A. et al. Early diagnosis of bladder cancer through the detection of urinary tyrosine-phosphorylated proteins. *Br. J. Cancer* 113, 469–475 (2015).
48. Allione, A. et al. Novel epigenetic changes unveiled by monozygotic twins discordant for smoking habits. *PLoS One* 10, (2015).
49. Campanella, G. et al. Epigenetic signatures of internal migration in Italy. *Int. J. Epidemiol.* 44, 1442–1449 (2015).
50. Di Gaetano, C. et al. Sardinians genetic background explained by runs of homozygosity and genomic regions under positive selection. *PLoS One* 9, (2014).
51. Fiorito, G. et al. B-vitamins intake, DNA-methylation of One Carbon Metabolism and homocysteine pathway genes and myocardial infarction risk: The EPICOR study. *Nutr. Metab. Cardiovasc. Dis.* 24, 483–488 (2014).
52. Russo, A. et al. Shorter leukocyte telomere length is independently associated with poor survival in patients with bladder cancer. *Cancer Epidemiol. Biomarkers Prev.* 23, 2439–2446 (2014).
53. Hoggart, C. J. et al. Novel approach identifies SNPs in SLC2A10 and KCNK9 with evidence for parent-of-origin effect on body mass index. *PLoS Genet.* 10, 1–12 (2014).
54. Matullo, G. et al. Genetic Variants Associated with Increased Risk of Malignant Pleural Mesothelioma: A Genome-Wide Association Study. *PLoS One* 8, (2013).
55. Cadby, G. et al. A genome-wide association study for malignant mesothelioma risk. *Lung Cancer* 82, (2013).
56. Di Gaetano, C. et al. An Overview of the Genetic Structure within the Italian Population from Genome-Wide Data. *PLoS One* 7, (2012).

Chapters in books

1. Fiorito, G., Sacerdote, C. & Vineis, P. Lessons from knowledge on the correlates of the age of onset of physical illness. in Age of Onset of Mental Disorders: Etiopathogenetic and Treatment Implications (2018).
2. Vodicka, P. et al. CHAPTER 37: Micronucleus Assay for Assessing Chromosomal Damage in Medical Workers Exposed to Anaesthetic Gases. Issues in Toxicology vols 2019-Janua (2019).

Il sottoscritto Giovanni Fiorito, consapevole che le dichiarazioni false comportano l'applicazione delle sanzioni penali previste dall'Articolo 76 del D.P.R. 445/2000, dichiara che le informazioni riportate nel seguente curriculum vitae, redatto in formato europeo corrispondono a verità. Le dichiarazioni rese nel presente curriculum sono da ritenersi rilasciate ai sensi degli artt. 46 e 47 del D.P.R. 445/2000.

The undersigned Giovanni Fiorito, aware that false declarations lead to the application of the criminal sanctions provided in Article 76 of D.P.R. 445/2000, declares that the information contained in the following curriculum vitae, drawn up in European format, corresponds to the truth. All the declarations in this curriculum must be interpreted according with art. 46 and 47 of the D.P.R. 445/2000.

21/09/2021

Giovanni Fiorito