

Marianyela Petrizzelli

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Date of Birth: March 22, 1990

Nationality: Italian

Languages: Italian and Spanish (native), English and French (professional proficiency)

Computer Skills

- **Operating Systems:** macOS, Windows
- **Programming Languages:** R, Python, MATLAB, LaTeX, Bash
- **Programming Environments:** RStudio, Visual Studio Code
- **Notebooks:** RMarkdown, Jupyter

Experience

Principal Data Scientist – AI for Precision Medicine

January 2023 – Present

Sanofi, Digital R&D, R&D Data and Computational Science

- Developed Shiny/Streamlit applications for exploration of complex single-cell results (e.g., ligand-receptor interactions, gene regulatory networks, differentially expressed genes, gene ontologies, patient stratification).
- Trained foundation single-cell large language models (scLLMs) with publicly and/or internally available single-cell datasets to build disease-associated scLLMs.
- Applied cutting-edge ML and AI techniques for the analysis of large complex (multimodal) omics datasets.
- Proposed and supervised a master's-level internship on a Computational Systems Biology project.
- Leveraged collaborations both internally and externally to accelerate biomarker discovery.
- Adopted the Agile way of working.

Postdoctoral Researcher

September 2019 – January 2023

Institut Curie, Computational Systems Biology of Cancer Group

PI: Andrei Zinovyev

- Performed advanced statistical analysis of large complex omics datasets.
- Developed methods for multi-level data representation (multi-level networks) and integration.
- Designed pipelines to analyze interaction networks of statistical associations among features (genes) and similarity networks among observations (patients).
- Created pipelines that integrate machine learning and optimization techniques to model cell metabolism.
- Produced a data catalog containing links to Ewing sarcoma omics datasets.
- Collaborated with biologists, computational biologists, engineers, and physicists within the H2020-ICT-2018-2 individualized Pediatric Cure project to design algorithms that address cancer-specific questions.

Junior Lecturer and Assistant Professor

September 2019 – September 2022

Université Paris Descartes

Courses: Mathematics, Statistics, and Probability; 153 teaching hours

Temporary Assistant Professor (A.T.E.R)

October 2018 – August 2019

Université Paris Descartes

Courses: Mathematics, Statistics, and Probability; 172 teaching hours

Junior Lecturer

Université Paris Sud

Courses: *Mathematics, Python, Data Analysis*; 128 teaching hours

October 2016 – September 2018

Research Intern

Université Paris-Saclay, INRAE, Génétique Quantitative et Evolution - Le Moulon

PI: *Olivier Martin*

January 2015 – April 2015

- Developed a general model to calculate probabilities of multi-locus genotypes in sibling mating scenarios.
- Built the associated algorithm in R for practical applications in data imputation.

Education

Doctor of Philosophy in Life Sciences

Université Paris-Saclay

Thesis: *“Mathematical Modeling and Integration of Complex Biological Data: Analysis of the Heterosis Phenomenon in Yeast”*

Supervisors: *Christine Dillmann, Dominique de Vienne*

October 2015 – July 2019

M.Sc. in Physics of Complex Systems (International Track)

Politecnico of Turin

Thesis: *“Multilocus Probabilities in the Presence of Genetic Recombination”*

Supervisor: *Olivier Martin*

September 2013 – July 2015

B.Sc. in Mathematics

University of Trento

Thesis: *“On the Preisach Model for Hysteresis: From the Deterministic Case to the Stochastic One”*

Supervisor: *Fabio Bagagiolo*

September 2009 – March 2013

High School Diploma in Science

Lyceum “Girolamo Fracastoro”

Majors: *Mathematics and Physics*

September 2004 – July 2009

Awards & Distinctions

Acknowledged in 2 international reviews:

- Fiévet, J. B., Nidelet, T., Dillmann, C., & de Vienne, D. (2018). Heterosis Is a Systemic Property Emerging From Non-linear Genotype-Phenotype Relationships: Evidence From in Vitro Genetics and Computer Simulations. *Frontiers in Genetics*, 9, 159. DOI:10.3389/fgene.2018.00159
- Raffoux, X., Bourge, M., Dumas, F., Martin, O. C., & Falque, M. (2018). Role of Cis, Trans, and Inbreeding Effects on Meiotic Recombination in *Saccharomyces cerevisiae*. *Genetics*, 210(4), 1213–1226. DOI:10.1534/genetics.118.301644

Selected as Graduate Fellow for Fall 2017 from a competitive pool of applicants to spend 6 months at the Kavli Institute of Theoretical Physics (KITP), University of California, Santa Barbara. Worked on a collaborative project at the interface between physics and biology under the mentorship of Boris Shariaman.

List of Publications

Journal Articles

- Núñez-Carpintero, I., Petrizzelli, M., Zinovyev, A., Cirillo, D., & Valencia, A. (2021). The multilayer community structure of medulloblastoma. *iScience*, 24(4), 102365. DOI:10.1016/j.isci.2021.102365
- Petrizzelli, M., de Vienne, D., Nidelet, T., Noûs, C., & Dillmann, C. (2021). Data integration uncovers the metabolic bases of phenotypic variation in yeast. *PLoS Computational Biology*, 17(7), e1009157. DOI:10.1371/journal.pcbi.1009157

- Jebreen, K., Petrizzelli, M., & Martin, O. C. (2019). Probabilities of Multilocus Genotypes in SIB Recombinant Inbred Lines. *Frontiers in Genetics*, 10, 833. DOI:10.3389/fgene.2019.00833
- Petrizzelli, M., de Vienne, D., & Dillmann, C. (2019). Decoupling the Variances of Heterosis and Inbreeding Effects Is Evidenced in Yeast's Life-History and Proteomic Traits. *Genetics*, 211(2), 741–756. DOI:10.1534/genetics.118.301635

Preprint

- Petrizzelli, M., Coton, C., & de Vienne, D. (2023). Formalizing the law of diminishing returns in metabolic networks using an electrical analogy. *Preprint*. DOI:10.21203/rs.3.rs-3580603/v1

Book Chapter

- Petrizzelli, M., Merlevede, J., & Zinovyev, A. (2021). Systems Biology Analysis for Ewing Sarcoma. In *Methods in Molecular Biology (Clifton, N.J.)*, 2226, 303–333. DOI:10.1007/978-1-0716-1020-6_23

Thesis

- Petrizzelli, M. (2019). Mathematical Modelling and Integration of Complex Biological Data: Analysis of the Heterosis Phenomenon in Yeast. *Université Paris Saclay*. [Link](#)

Project Deliverables

- Petrizzelli, M., Zinovyev, A., Failli, M., & di Bernado, D. (2022). Metabolic Models. DOI:10.5281/zenodo.6669810
- Cirillo, D., Núñez-Carpintero, I., Capella-Gutiérrez, S., Merlevede, J., Petrizzelli, M., & Zinovyev, A. (2022). Consensus Multi-omics Subtypes of Pediatric Cancers. DOI:10.5281/zenodo.6669753
- Zinovyev, A., Merlevede, J., Petrizzelli, M., & Cirillo, D. (2022). Topological Analysis of Multi-omics and Multi-cancer Molecular Networks Resulting in the Definition of Molecular Mechanisms. DOI:10.5281/zenodo.6669709
- Manica, M., Cadow, J., Petrizzelli, M., Zinovyev, A., & Cirillo, D. (2021). Building of Cancer Type-Specific Multi-layered Molecular and Patient Similarity Networks. DOI:10.5281/zenodo.6546365