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Marianyela Petrizzelli

Date of birth: March 22, 1990
Nationality: Italian
Languages: Italian and Spanish mother tongues; professional English and French

COMPUTER SKILLS

Operating systems	macOS, Windows
Programming languages	R, Python, MATLAB, Latex, Bash
Programming environments	Rstudio, Visual Studio
Notebook	Rmarkdown

EXPERIENCE

Principal Data Scientist – Bioinformatics – AI for precision medicine

January 2023 – Present

Sanofi

Affiliation: *Sanofi R&D Data and Data Science, Artificial Intelligence & Deep Analytics, Omics Data Science, 1, Av Pierre Brossolette 91385, Chilly-Mazarin, France*

Manager: **Franck Augé**

- I developed a pipeline consisting of independent but complementary approaches to perform a mechanistic study of drugs mechanism of action.
- I apply ML and AI techniques for the analysis of large complex omics datasets.
- I develop a shiny app to visualize complex datasets and results.

Postdoctoral Researcher

September 2019 – January 2023

Computational Systems Biology of Cancer Group

Affiliation: *Institut Curie, PSL Research University, INSERM U900, Computational Biology, MINES ParisTech, F-75006 Paris, France.*

PI: **Andrei Zinovyev**.

I performed advance statistical analysis of large complex omics datasets.

- I developed methods for multi-level data representation (multi-level networks) and integration (e.g., https://github.com/iPC-project-H2020/ipcrp/tree/master/scripts/data-driven_relational_graphs).
- I designed pipelines to analyze interaction networks of statistical associations among features (genes) and similarity networks among observations (patients) (e.g., <https://github.com/iPC-project-H2020/wp4-deliverables/tree/main/D4.1/BMNPPSN>).
- I created pipelines that integrates machine learning and optimization techniques to model cell metabolism (<https://github.com/iPC-project-H2020/wp8-metabolic-modeling>).
- I produced a data catalog containing links to omics datasets linked to Ewing sarcoma (<https://sysbio-curie.github.io/EwSOmicsAtlas/>).
- I collaborated with biologists, computational biologists, engineers, and physicists within the H2020-ICT-2018-2 project individualized Pediatric Cure project to design algorithms that address cancer specific questions.

Junior lecturer and assistant professor

September 2019 – September 2022

Employer: *Université Paris Descartes*

Courses: *Mathematics, Statistics and Probability*. Number of teaching hours: 153.

Temporary assistant professor (A.T.E.R)

October 2018 – August 2019

Employer: *Université Paris Descartes*

Courses: *Mathematics, Statistics and Probability*. Number of teaching hours: 172.

Junior lecturer

October 2016 – September 2018

Employer: *Université Paris Sud*

Courses: *Mathematics, Python, Data Analysis*. Number of teaching hours: 128

Research intern

January 2015 – April 2015

Affiliation: *Génétique Quantitative et Evolution–Le Moulon, Institut National de la Recherche Agronomique, Université Paris-Saclay, Université Paris-Sud, Centre National de la Recherche Scientifique, AgroParisTech, 91190 Gif-sur-Yvette, France.*

PI: **Olivier Martin**.

Second-year master research internship in population genetics. I developed a general model able to calculate the probabilities of multi-locus genotypes in brother and sister mating.

- I constructed the associated algorithm in R.
- I showed a practical application of the model for data imputation.

EDUCATION

Doctor of Philosophy in Life-Science

October 2015

– July 2019

Initiative doctoral d'excellence - IDI – Paris-Saclay

Institution: *Université Paris-Saclay*.

Thesis: *“Mathematical modelling and integration of complex biological data: analysis of the heterosis phenomenon in yeast”*.

Supervisors: **Christine Dillmann** and **Dominique de Vienne**.

- I lead this interdisciplinary project at the interface between mathematics, statistics, and biology. It involved modeling and analysis of complex biological data.
- I apply cutting-edge ML/AI techniques to disentangle hybrid vigor and inbreeding depression.

Msc. Physics of Complex Systems (International track)

September 2013 – July 2015

Institution: *Politecnico di Torino*.

Master Thesis: *“Multilocus probabilities in the presence of genetic recombination”*.

Supervisor: **Olivier Martin**

Bsc. Mathematics

September 2009 –

March 2013

Institution: *University of Trento*.

Bachelor Thesis: *“On the Preisach model for hysteresis: from the deterministic case to the stochastic one”*.

Supervisor: **Fabio Bagagiolo**

Hsd. Science

September 2004 – July 2009

Institution: *Lyceum “Girolamo Fracastoro”*

Majors: Mathematics and Physics

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.

<https://doi.org/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. <https://doi.org/10.1534/genetics.118.301644>

Selected as one KITP Graduate Fellow for the fall 2017, out of the 7 applicants received at a time, to spend 6 months at the Kavli Institute of Theoretical Physics, University of Santa Barbara, to work on a collaborative project at the interface between physics and biology, based on academic success. Faculty mentor: **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. <https://doi.org/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. <https://doi.org/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. <https://doi.org/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. <https://doi.org/10.1534/genetics.118.301635>

Book chapter

- . **Petrizzelli, M.**, Merlevede, J., & Zinovyev, A. (2021). Systems Biology Analysis for Ewing Sarcoma. *Methods in molecular biology (Clifton, N.J.)*, 2226, 303–333. https://doi.org/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. <https://tel.archives-ouvertes.fr/tel-02290961>

Project deliverables

- . **Petrizzelli, M.**, Zinovyev, A., Failli, M., & di Bernado, D. (2022). Metabolic models. <https://doi.org/10.5281/zenodo.6669810>
- . Cirillo, D., Núñez-Carpintero, I., Capella-Gutiérrez, S., Merlevede, J., **Petrizzelli, M.**, & Zinovyev, A. (2022). Consensus multi-omics subtypes of paediatric cancers. <https://doi.org/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. <https://doi.org/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. <https://doi.org/10.5281/zenodo.6546365>