

# Marianyela Petrizzelli

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Date of birth: March 22, 1990

Nationality: Italian

Languages: Italian and Spanish mother tongues; professional English and French

## PROGRAMMING SKILLS

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★★★★★ R: I performed **all** statistical analysis, methods, and algorithms throughout my career in R language.

★★★★☆ Python: I **taught** python at IUT d'Orsay. I use it for data management and when no R package is available.

★★★★☆ MATLAB: I use it to solve **optimization** problems (more efficient with respect to R and Python).

## EXPERIENCE

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### Research experience

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#### Postdoctoral Researcher

September 2019 – Present

Computational Systems Biology of Cancer Group

Employer and affiliation: Institut Curie, PSL Research University, INSERM U900, Computational Biology, MINES ParisTech, F-75006 Paris, France.

- 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/ipcrg/tree/master/scripts/data-driven\\_relational\\_graphs](https://github.com/iPC-project-H2020/ipcrg/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.
- I **collaborated** with biologists, computational biologists, engineers, and physicists within the H2020-ICT-2018-2 project individualized Pediatric Cure project (<https://ipc-project.eu/>) to **design algorithms** that address Cancer specific questions.
- I **produced a data catalog** containing links to omics datasets linked to Ewing sarcoma (<https://sysbio-curie.github.io/EwSOmicsAtlas/index.html>).

#### Research intern

January 2015 - April 2015

Employer: Institut National de Recherche Agronomique – GQE – Le Moulon

Second-year master research internship in population genetics.

- 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.

### Teaching experience

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#### Junior lecturer and assistant professor

September 2019 – Present

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

- I was responsible of the evaluation of my students
- I planned learning activities and complete records
- I managed class activities to enhance learning

## EDUCATION

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### Doctor of Philosophy in Life-Science

October 2015 - July 2019

*Initiative doctoral d'excellence - IDI - Paris Saclay*

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

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*

- I lead this **interdisciplinary project** at the interface between mathematics, statistics, and biology. It involved modeling and analysis of **complex biological data**.
- I performed **multivariate analysis** and **clustering** considering the cross design on which the data was measured.
- I constructed a unique **statistical method** and performed clustering analysis to disentangle hybrid vigor and inbreeding depression.
- I performed all the analysis in **R**.

### Msc. Physics of Complex Systems (European Double Master Degree)

September 2013 – July 2015

The course was organized in four semesters: 1° semester in Trieste at *SISSA* and *ICTP*. 2° semester in Torino at *Politecnico di Torino* University. 3° semester in Paris at a consortium involving Universities *Pierre et Marie Curie*, *Paris Diderot*, *Paris Sud* and the *Ecole Normale Supérieure*. 4° semester was devoted to a research stage and to the European multidisciplinary *Spring College* in Trieste at *ICTP* (<http://indico.ictp.it/event/a14244/>)

Master Thesis: "Multilocus probabilities in the presence of genetic recombination".

Affiliation: *Institut National de Recherche Agronomique - laboratory Génétique Quantitative et Evolution*. Supervisor: Olivier Martin

### Bsc. Mathematics

September 2009 – March 2013

*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

*Lyceum "Girolamo Fracastoro"*

Majors: Mathematics and Physics

## AWARDS

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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, [shraiman@kitp.ucsb.edu](mailto:shraiman@kitp.ucsb.edu)

## LIST OF PUBLICATIONS

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- . Petrizzelli M., de Vienne D. and 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.
- . Jebreen K.\*, Petrizzelli M.\*, and Martin O. C. (2019) *Probabilities of multi-locus genotypes in SIB recombinant inbred lines*. *Front. Genet.* 10:833. doi: 10.3389/fgene.2019.00833.
- . Petrizzelli M., Merlevede J., Zinovyev A. (2021) *Systems Biology Analysis for Ewing Sarcoma*. Springer Ewing Sarcoma: Methods and Protocols.
- . Petrizzelli M., de Vienne D., Nidelet T. and 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
- . Nuñez-Carpintero I., Petrizzelli M., Zinovyev A., Cirillo D., Valencia A. (2021) *The multilayer community structure of medulloblastoma*. *iScience*, 24 (4). doi: 10.1016/j.isci.2021.102365.