

## STEFANO DI GIOVENALE

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### EDUCATION

**University of Rome "La Sapienza", Rome, Italy** **PhD student in Data Science** **Oct. 2021 – Present**

*Winner of a three years PhD fellowship financed by the National Cancer Institute "Regina Elena".*

**Project aim:** *Developing a computational method to dissect accessibility profiles from longitudinal datasets.*

**University of Rome Tor Vergata, Rome, Italy** **MSc Bioinformatics (Summa cum Laude)** **2019 – 2021**

**Degree Thesis:** *Worked on Epigenetics of pediatric type-B ALL, investigated the differences in chromatin accessibility in type-B ALL cancer evolution, crossed the data from multiple next-generation sequencing data.*

**University of Rome Tor Vergata, Rome, Italy** **BSc Biotechnology (Summa cum Laude)** **2016 – 2019**

**Degree Thesis** *Researched interaction between cellular alteration and IC50 from different chemotherapy in cellular line based on Francesco Iorio publication "A Landscape of Pharmacogenomic Interactions in Cancer"*

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### PROFESSIONAL EXPERIENCE

**Medical University of Vienna, Vienna, Austria** **PhD visiting** **Feb 2023 – Aug 2023**

*Visiting PhD student at the Barozzi's Lab*

- Developed a co-accessibility network to investigate the alteration in chromatin accessibility during cancer evolution in bulk and single cell sequencing
- Performed single cell multiomics analysis

**National Cancer Institute "Regina Elena", Rome, Italy** **Off-Cycle trainee** **Sep 2020 – June 2021**

*Leading Cancer research institute and Bioinformatics facility in Lazio*

- Developed and tested bash pipeline to standardize new approach in ATACseq analysis and peaks classification
- Analysed ATACseq data from patients and from cellular line, performed differential analysis on those data
- Performed RNAseq, ChIPseq and HiC data analysis
- Integration of data from multiple databases such as ENCODE, TCGA and TCGA

**University of Rome Tor Vergata, Rome, Italy** **Trainee Students** **March 2019 – May 2019**

*Bioinformatics University Group working on Pharmacogenomic data and Artificial Intelligence applied at biology*

- Explored TCGA dataset of different cancer type and relative IC50
- Acquired basic Python skills principal on Pandas and Numpy library
- Studied and applied basic machine learning algorithms such as Random Forest and SVM

**University of Rome Tor Vergata, Rome, Italy** **Intern Student** **Sep 2017**

*Genetics University Group working on identification novel target in muscular dystrophy*

- Studied principal Molecular Biology technique in wet lab, principally Western Blot and Cell-culture
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### SUMMER SCHOOL AND CONFERENCES

**Francesca Martini Award for an experimental thesis in Oncohaematology, NAnA Onlus** **2022**

*Winner of the best master thesis in oncohaematology*

**CGSI 2022 Summer School** **6-29 July 2022**

*Selected for the long program summer school at the University of California Los Angeles.*

**EMBO Conference "The many faces of cancer evolution"** **20-22 May 2022**

*Selected for a poster presentation at the EMBO workshop in-person at Rimini.*

**EMBL in Italy 2021: A Brave New World of RNA** **20-21 May 2021**

*Selected for a poster presentation at the European Molecular Biology Laboratory virtual conference.*

**ISMB/ECCB 2021 Virtual Conference** **July 25-30, 2021**

*Selected for a poster presentation at the international society for computational biology virtual conference.*

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### ADDITIONAL INFORMATION

**IT Skills:** Machine Learning Algorithms, Programming Languages (bash, R, Python), Bioinformatics Tool (Mac2, Bowtie2, samtools, bedtools, deeptools, fastq), Bioinformatics Analysis (RNAseq, ATACseq, ChIPseq, HiC), Linux-like systems, Graphic tools (Photoshop, Illustrator, Premier), Manage Conda environment, LaTeX

**Languages:** English (Intermediate), Italian (native)