



# Salvatore Daniele Bianco

**Gender:** Do not indicate

## ABOUT ME

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PhD student in Medical Genetics.  
Bioinformatics researcher with programming, statistical and data-science skills.

## WORK EXPERIENCE

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### Bioinformatician

**CSS-Mendel Institute** [ 09/2020 – Current ]

City: Roma

Country: Italy

Develop and implement statistical and machine-learning models for biomedical applications.  
Manage and analyze data from biological experiments and databases.  
Support biomedical research through computational techniques.

### Tutor

**"Sapienza" University of Rome, Bioinformatics bachelor degree.** [ 17/06/2021 – 30/09/2021 ]

City: Roma

Country: Italy

Support students in understanding specific notions and in carrying out homework.  
Helping students with statistics and with Stata exercises.

### Tutor

**"Sapienza" University of Rome, Bioinformatics bachelor degree.** [ 01/10/2022 – Current ]

City: Roma

Country: Italy

Helping students with their homework and study, especially math and computer science.  
Provide students with information about the courses and the exams.

## EDUCATION AND TRAINING

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### Scientific High School Diploma

**Liceo "Ruggero Bonghi"** [ 08/2008 – 07/2013 ]

Address: Lucera (FG) (Italy)

### Bachelor Degree in "Biological Science"

**Marche Polytechnic University** [ 09/2013 – 02/2017 ]

Address: Ancona (Italy)

### Master Degree in "Bioinformatics"

**"Tor Vergata" University of Rome** [ 08/2017 – 03/2020 ]

Address: Roma (Italy)

## **PhD in "Medical Genetics"**

**"Sapienza" University of Rome** [ 10/2020 – Current ]

Address: Roma (Italy)

### **LANGUAGE SKILLS**

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Mother tongue(s): **Italian**

**Other language(s):**

**English**

**LISTENING B1 READING B2 WRITING B2**

**SPOKEN PRODUCTION B1 SPOKEN INTERACTION B1**

### **DIGITAL SKILLS**

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#### **python**

numpy / pandas / Data visualization in matplotlib / statsmodels / numba / joblib / Python Anaconda / jupyter / Google Colaboratory

#### **machine learning / statistics**

pytorch / scikit-learn / scipy / StatsModels

#### **other programming languages**

R / C / MySQL / Ruby

#### **operative system**

Linux Operative Systems / Windows Operative System

### **PUBLICATIONS**

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#### **[A comparative benchmark of classic DNA motif discovery tools on synthetic data](#)**

[2021]

DOI: 10.1093/bib/bbab303

#### **[COVID-19 Specific Immune Markers Revealed by Single Cell Phenotypic Profiling](#)**

[2021]

DOI: 10.3390/biomedicines9121794

#### **[MiRLog and dbmiR: Prioritization and functional annotation tools to study human microRNA sequence variants](#)**

[2022]

DOI: 10.1002/humu.24399

#### **[KDM6A missense variants hamper H3 histone demethylation in lung squamous cell carcinoma](#)**

[2022]

DOI: 10.1016/j.csbj.2022.06.041

#### **[Profiling of cell-free DNA methylation and histone signatures in pediatric NAFLD: A pilot study](#)**

[2022]

DOI: <https://doi.org/10.1002/hep4.2082>

#### **[Connecting the dots: A practical evaluation of web-tools for describing protein dynamics as networks](#)**

[2022]

DOI: 10.3389/fbinf.2022.1045368