

# Roberto Preste

## Scientific Software Developer

Python and R enthusiast, always looking for new ways to solve problems through programming.



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robertopreste.com

github.com/robertopreste

## WORK EXPERIENCE

### Scientific Software Developer Enthought

10/2019 – Present

Cambridge, UK

#### Achievements/Tasks

- Development of scientific and technical applications involving GUIs, 2D and 3D visualizations, workflow and pipeline architecture, and numerical algorithms

### Bioinformatician

#### ELIXIR Project "Implementation of HmtPhenome"

05/2019 – 06/2019

Bari, IT

Department of Biosciences, Biotechnologies and Biopharmaceutics,  
University of Bari

#### Achievements/Tasks

- Design and development of the HmtPhenome resource

### Bioinformatician

#### ELIXIR Project "Integration of the ELIXIR-IIB HmtDB resource into RD-Connect"

05/2018 – 06/2018

Bari, IT

Institute of Biomembranes, Bioenergetics and Molecular Biotechnologies,  
National Research Council

#### Achievements/Tasks

- Development of an API for the HmtDB resource
- Standardization of data according to RD-Connect specifications

### Web Developer

#### ELIXIR Hub, Wellcome Trust Genome Campus

03/2016 – 09/2016

Cambridge, UK

European Bioinformatics Institute (EBI-EMBL)

#### Achievements/Tasks

- Design and development of the Bioschemas website
- Design and production of a registry and validation portal for Bioschemas data

## EDUCATION

### Phd Student in Functional and Applied Genomics and Proteomics

#### University of Bari "Aldo Moro"

11/2016 – 03/2020

Bari, IT

#### Thesis

- Bioinformatics software and tools for Big Data in mitochondrial genomics

### Master's Degree in Cellular and Molecular Biology

#### University of Bari "Aldo Moro"

10/2013 – 07/2015

Bari, IT

### Bachelor's Degree in Medical and Pharmaceutical Biotechnologies

#### University of Bari "Aldo Moro"

10/2009 – 07/2013

Bari, IT

## SKILLS

Python

Bioinformatics

Data Science

Databases

Machine Learning

Software Development

Web Development

## PUBLICATIONS

HmtVar: a new resource for human mitochondrial variations and pathogenicity data

Nucleic Acids Res, 2018 - DOI: 10.1093/nar/gky1024

NumtS colonization in mammalian genomes

Sci Rep, 2017 - DOI: 10.1038/s41598-017-16750-2

HmtDB 2016: data update, a better performing query system and human mitochondrial DNA haplogroup predictor

Nucleic Acids Res, 2017 - DOI: 10.1093/nar/gkw1066

## PROJECTS

mitoviz

- Python package to plot variants on the human mitochondrial genome (<https://github.com/robertopreste/mitoviz>)

HmtNote

- Python package to annotate human mitochondrial variants from VCF files (<https://github.com/robertopreste/HmtNote>)

HmtPhenome

- Web service that builds networks of variants, genes, phenotypes and diseases (<https://www.hmtphenome.uniba.it>)

HmtVar

- Database of human mitochondrial variants (<https://www.hmtvar.uniba.it>)

HmtDB

- Database of human mitochondrial genomes (<https://www.hmtdb.uniba.it>)

## CERTIFICATES

Deep Learning Specialization

Deep Learning Specialization from deeplearning.ai on Coursera.org (License JEECRT8A86V9)

IBM Data Science Professional Certificate

IBM Data Science Professional Specialization from IBM on Coursera.org (License B63ABDG4TCFR)

Data Science Specialization

Data Science Specialization from Johns Hopkins University on Coursera.org (License XQJQCG2DM6L5)

EF SET English Certificate - C2 Proficient

EF Standard English Test (EF SET) 86/100 (C2 Proficient)

## LANGUAGES

Italian



English

