

Roberto Preste

Scientific Software Developer

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



roberto.preste@gmail.com

+44 (0)7732 627958

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 – 10/2019

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

