

Roberto Preste

PhD Student

Mixing Bioinformatics, Data Science and Web Development to build database and analysis systems that allow to explore and reuse biological data. Python and R enthusiast, always looking for new ways to solve problems through programming.



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WORK EXPERIENCE

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 Application Programming Interface (API) to allow programmatic access to HmtDB data
- Standardization of the HmtDB data format according to RD-Connect specifications

Cofounder

BROWSer - Bioinformatics Resource for Omics-Wide Services

10/2016 – Present

Bari, IT

Spin-off of the University of Bari "Aldo Moro"

Web Developer

ELIXIR Hub, Wellcome Trust Genome Campus

03/2016 – 09/2016

Cambridge, UK

European Bioinformatics Institute (EBI-EMBL)

Achievements/Tasks

- Management of the ELIXIR intranet
- 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 – Present

Bari, IT

Courses

- Study and development of Big Data analysis protocols for biological 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

R

Bioinformatics

Data Science

Genomics

Databases

Machine Learning

Shell

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

HmtPhenome

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

HmtNote

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

HmtVar

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

BROWSer website

- Website for the BROWSer spin-off (<https://www.browser-bioinf.com>)

HmtDB

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

CERTIFICATES

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 XQJQCG2DM6LS)

EF SET English Certificate - C2 Proficient

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

LANGUAGES

Italian



English

