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

Human mitochondrial variant annotation with HmtNote ↗
bioRxiv, 2019 - DOI: 10.1101/600619

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

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

mitovizR ↗
- R package to plot human mitochondrial variants from dataframes, VCF or JSON files (https://github.com/robertopreste/mitovizR)

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

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

Bioschemas website ↗
- Website for the Bioschemas ELIXIR project (http://bioschemas.org)

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

CERTIFICATES

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 ● ● ● ● ○