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

Achievements/Tasks

- Haemodynamics data analysis and visualisation
- Development of bioinformatics analysis pipelines to analyse NGS data from WES and RNA-Seq projects
- Design and development of the BROWSer website

Web Developer

ELIXIR Hub, Wellcome Trust Genome Campus

03/2016 – 09/2016 European Bioinformatics Institute (EBI-EMBL) Cambridge, UK

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 Julia

PUBLICATIONS

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

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

BioRxiv, 2018 - DOI: 10.1101/355461

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

mitovizR (01/2019 - Present) 3

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

HmtVar (06/2018 – Present) ♂

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

BROWSer website (10/2016 – Present) 🗹

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

Bioschemas website 🗹

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

HmtDB (10/2014 – Present) 🗹

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 XOJOCG2DM6L5)

EF SET English Certificate - C2 Proficient 🗹

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

LANGUAGES