Roberto Preste
Scientific Software Developer

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

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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

SKILLS

`Python` `Software Development` `Bioinformatics` `Scientific Programming` `Web Development` `Databases` `Data Science` `Machine Learning` `R`

PUBLICATIONS

A data and text mining pipeline to annotate human mitochondrial variants with functional and clinical information ⧉
Mol. Genet. Genomic. Med., 2019 - DOI: 10.1002/mgg3.1085

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)