Roberto Preste
Senior Software Engineer

Technology enthusiast, interested in modern and efficient ways to solve problems through programming.

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Cambridge, UK

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WORK EXPERIENCE

Senior Software Engineer
Illumina

10/2021 - Present   *Cambridge, UK*

Achievements/Tasks

- Develop, test and maintain full-stack applications and (micro)services within ISO13485 accredited environments (Python, Flask, Angular, SQLAlchemy, Kafka)
- Provide technical training to interns and internal non-software teams
- Implement and maintain CI/CD and containerisation protocols (Docker, Kubernetes, Helm, AWS, Terraform)
- Provide technical assistance to escalated operational issues

Scientific Software Developer
Enthought ⧉

10/2019 - 10/2021   *Cambridge, UK*

Achievements/Tasks

- Develop scientific and technical applications involving GUIs, 2D and 3D visualisations, workflow and pipeline architecture, and numerical algorithms (Python, Numpy, Pandas, Scipy, Seaborn)
- Develop Python-based desktop and web applications for scientific data management in life sciences and physics domains (Python Traits and Traits UI)
- Develop and share best practices for software design within the internal UI/UX research team

Bioinformatician
ELIXIR Project "Implementation of HmtPhenome"

05/2019 - 06/2019   *Bari, IT*

Department of Biosciences, Biotechnologies and Biopharmaceutics, University of Bari

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

Web Developer
ELIXIR Hub, Wellcome Trust Genome Campus

03/2016 - 09/2016   *Cambridge, UK*

European Bioinformatics Institute (EBI-EMBL)

Achievements/Tasks

- Implementation of the Bioschemas website (https://bioschemas.org) (Plain HTML, CSS, Javascript)

SKILLS

`Python` `AWS` `Kubernetes` `Helm` `Docker` `CI/CD` `Kafka` `Flask` `SQL` `Snowflake` `Terraform` `Angular` `Bioinformatics` `Web Development` `Machine Learning` `R`

PROJECTS

mitoviz ⧉
- Python package to plot variants on the human mitochondrial genome (https://github.com/robertopreste/mitoviz)

mitovizR ⧉
- R package to plot variants on the human mitochondrial genome (https://github.com/robertopreste/mitovizR)

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 - archived)

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

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

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

Master's Degree - Cellular and Molecular Biology
University of Bari "Aldo Moro"

09/2013 - 09/2015

Bachelor's Degree - Medical and Pharmaceutical Biotechnology
University of Bari "Aldo Moro"

09/2009 - 07/2013