GIOVANNI VISONÀ

RESEARCHER IN MACHINE LEARNING FOR PRECISION MEDICINE AND BIOLOGY

CONTACT



www.gvisona.com



Tübingen, Germany



www.linkedin.com/in/giovanni-visona



0000-0002-7878-5448



github.com/gvisona

EDUCATION

MSc in Artificial Intelligence

University of Edinburgh

2018-2019

Master of Science with a focus on Deep Learning. Graduated with distinction.

Master's Degree in Physics

University of Trento

2014-2016

Master's degree with a focus on the biomedical applications of physics. Graduated with honors.

LANGUAGES

Italian

Native

English

C2

German

В2

French A:

PROFILE

I am a researcher working at the intersection of machine learning and biomedicine to improve our understanding of molecular biology and explore precision medicine approaches.

My core passion is the multidisciplinarity of my work, which has led me to collaborate with diverse groups of experts on various topics, including epigenetics, oncology, antimicrobial resistance, and immunology. These interactions allowed me to develop extensive experience in designing and training machine learning models, paired with the necessary competences to study and discuss domain knowledge for the biological problem at hand.

EXPERIENCE

ESR PhD Researcher

Max-Planck Institute for Intelligent Systems, Tübingen 2019-(expected mid 2024)

- Part of the Marie Curie Innovative Training Network entitled "Machine Learning Frontiers in Precision Medicine".
- Collaborated with international groups of experts from a variety of scientific domains, which led to the development of multidisciplinary skills.
- Designed and implemented deep-learning-based models and probabilistic models to solve problems in biology and biomedicine.
- Gained expertise with several types of biological data, including sequencing data, proteomics, mass spectra, clinical records, molecular networks, chemical structures.
- Published as first author or shared first author in internationally renowned journals, including Nature Communications, Bioinformatics, and Briefings in Bioinformatics.
- Gained mentoring experience, helping supervise Master students. Currently, part
 of the MAXMINDS mentoring network to help disadvantaged students affected
 by the 2023 earthquake in Turkey and Syria.
- Supervised by Prof. Bernhard Schölkopf and Dr. Gabriele Schweikert.

Junior Developer and Consultant

Espedia Consulting (Ethica Group), Padova

2017-2018

- Contributed to the creation of customized software solutions for clients, prioritizing robustness in design and ensuring on-time delivery.
- Applied object-oriented principles and design patterns to create scalable and maintainable code in Python and JavaScript.
- Developed presentations and proposals by synthesizing data and insights into actionable recommendations.

GIOVANNI VISONÀ

RESEARCHER IN MACHINE LEARNING FOR PRECISION MEDICINE AND BIOLOGY

TECHNICAL SKILLS

Machine Learning and Statistics: Deep learning, Transformers, LLMs, Linear algebra, Bayesian modeling, Explainable Al, Graph Neural Networks, Network Analysis, Conformal inference, hypothesis testing, MLflow.

Python: PyTorch, NumPy, Pandas, scikit-learn, networkX, statsmodels, PyMC.

Data Manipulation and Visualization: SQLite, HDF5, Interactive visualizations, Data mining, Exploratory data analysis.

R: Tidyverse, caret, tidymodels, Bioconductor.

Software Development: Git, Github, Docker.

Specialized Software: RDKit, BLAST, MMSeqs2.

EXPERIENCE WITH THE FOLLOWING BIOMEDICAL TOPICS AND DATA TYPES

Antimicrobial resistance and clinical pathology: MALDI-TOF spectrometry, drug resistance outcomes.

Clinical oncology and cancer biology: clinical data of cancer patients, somatic mutation profiles, TCGA database.

Epigenetics: histone modifications (ChIP-seq), DNA methylation (BS-Seq), chromatin accessibility (ATAC-seq, DNase-seq), ENCODE and Roadmap Epigenomics databases.

Proteins: UniProt and UniRef databases, LLMs for proteins, AlphaFold.

Omics data: scRNA-seq, RNAseq.

Immunology and immunopeptidomics: MHC class I pathway, HLA alleles, pMHC complexes, immunoglobulin structure, IEDB database.

Representations of small molecules: SMILES, chemical fingerprints, graph-based representations, ChEMBL database.

CONTACT INFORMATION FOR REFERENCES

- Dr. Gabriele Schweikert, University of Dundee g.schweikert@dundee.ac.uk
- Dr. Carlos Oliver, Max Planck Institute of Biochemistry oliver@biochem.mpg.de
- Prof. Bernhard Schölkopf, Max Planck Institute for Intelligent Systems sekretariat-schoelkopf@tuebingen.mpg.de