Lucrezia Valeriani

Data di Nascita ▮▮▮▮▮
Nazionalità ▮▮▮▮

ESPERIENZA

Università degli Studi di Trieste - *Tutor*
OTTOBRE 2022 - GENNAIO 2023

Tutor del corso Elementi di Informatica presso il DEAMS.

AREA Science Park - RIT group - *Borsista di Ricerca*
GIUGNO 2021 - OTTOBRE 2022

Study of deep learning protein language model for the contact prediction problem with the aim of improving the performance of already existing models on new data by fine-tuning procedure. The analysis is conducted using an HPC facility.

Università degli studi di Bologna - BioFolD Lab - *Tirocinante*
MAGGIO 2020 - LUGLIO 2020

University internship in the BioFolD Bioinformatics Unit for the developing of an integrated dataset containing information from Uniprot, OMIM, ClinVar and Orphanet databases in order to predict the functional impact of single nucleotide variants (SNV) in rare disease associated genes using a machine-learning based tool.

ISTRUZIONE

Università degli Studi di Trieste - AREA Science Park - *PhD in Applied Data Science and Artificial Intelligence*
OTTOBRE 2022 - PRESENTE
Borsa di dottorato finanziata da AREA Science Park

Università degli Studi di Trieste - *Master Degree in Data Science and Scientific Computing*
OTTOBRE 2020 - OTTOBRE 2022
110 cum Laude

Tesi: The role of homology in protein language models via "evo-tuning" and the geometry of hidden representations

Esami: High Performance Computing, Statistic, Numerical Analysis, Machine Learning, Programming and Algorithmic Design, Software Development, Information Retrieval and Data Visualization, Bayesian Statistic, Health Data Analytics, Probabilistic Machine Learning, Data Management for Big Data.

Alma Mater Studiorum - Università di Bologna - *Bachelor Degree in Genomics*

OTTOBRE 2017 - SETTEMBRE 2020

110 cum Laude

Tesi: Predicting the functional impact of single nucleotide variants in rare disease associated genes

Esami: Calculus, Programming, Linear Algebra, Molecular Biology, Bioethics, Genetics, Eukaryotic and Prokaryotic Genome, Statistics, Metabolomics, Algorithms and Data Structures in Biology, Bioinformatics, Epigenomics, Metagenomics, Multiscale Modeling, Structural Biology, Proteomics, Medical Genomics, Data Science.

Liceo Alessandro Volta, Colle di Val d'Elsa - *Maturità scientifica*

2012 - 2017

93/100

COMPETENZE

Competenze Linguistiche

Lingua madre: Italiano

Inglese: TOEFL 94/120 (C1)

Competenze Digitali

Linguaggi di Programmazione: Python,C/ C++, Java, R, Bash, Awk, HTML

Altro: Parallel Computing, OpenPBS, Pyro, PyTorch, GitHub, CI/CD, Stan, Linux/GNU

PUBBLICAZIONI e CONFERENZE

- Valeriani, L., Doimo, D., Cuturello, F., Laio, A., Ansuini, A., & Cazzaniga, A. (2023). The geometry of hidden representations of large transformer models. arXiv preprint arXiv:2302.00294.

- Licata, Luana et al. "Resources and tools for rare disease variant interpretation." Frontiers in molecular biosciences vol. 10 1169109. 10 May. 2023, doi:10.3389/fmolb.2023.1169109

- Valeriani, L., Cuturello, F., Ansuini, A., & Cazzaniga, A. (2022). The geometry of hidden representations of protein language models. bioRxiv, 2022-10. Machine Learning in Computational Biology Meeting 2022 (Poster) and Machine Learning in Structural Biology Workshop at the 36th Conference on Neural Information Processing System (NIPS) (Poster)