

ALESSANDRO LUSSANA

BIOINFORMATICIAN; GRADUATE M.Sc. BIOINFORMATICS WITH HONOURS

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ABOUT ME

Technical Skills Python, R, Unix/Linux, Perl, Awk, Sed, Git, Snakemake, Slurm, Docker, Singularity, HTCondor

Languages Italian (native), English (professional proficiency, C1 CEFR level)

Art Technology Inkscape, GIMP

Interests DIY Robotics, Design, Electric Guitar, Judo

WORK EXPERIENCE

IRCCS San Raffaele Scientific Institute

Bioinformatician

Milan, Italy (Oct 2020 - Present)

- Investigated the transcriptional dynamics of different cell populations within the virus-bearing liver and in hepatocellular carcinoma in Prof. Matteo Iannacone's Lab
- Helped formulating informative and statistically-sound experimental designs
- Designed computational pipelines to handle and analyze bulk and single-cell RNA-seq data with cutting-edge computational methods at the Centre for Omics Sciences (COSR)

Tampere University

Research Assistant

Tampere, Finland (May 2020 - Sep 2020)

- Collaborated with the Computational Biology Group under the lead of Prof. Matti Nykter
- Helped in the computational analysis of chromatin accessibility of clinical prostate cancer samples

Tampere University

Visiting Student

Tampere, Finland (Feb 2020 - Apr 2020)

- Developed thesis project titled "Deep-learning The Transcription Factors' Syntax From Chromatin Accessibility Profiles" under the supervision of Prof. Matti Nykter
- Set up a deep-learning-based project on a large HPC cluster, handling Chip-seq and ATAC-seq data
- Was asked to present my thesis work in a lab meeting, and was offered to be a grant holder for the faculty

University Of Turin

Student Trainee

Turin, Italy (Apr 2017 - Sep 2018)

- Analyzed human genetic variation and its effect on gene expression, using GEUVADIS and GTEx datasets
- Was invited to attend the annual Bioinformatics Italian Society (BITS) meeting by my supervisor, Prof. Paolo Provero
- Developed AffiXcan, an R package published on Bioconductor, to build statistical models of Genetically Regulated Expression (GREX) from functional scores computed on regulatory sequences

EDUCATION

University Of Bologna

Bologna, Italy (Oct 2018 - Sep 2020)

- International M. Sc. In Bioinformatics
- Weighted Average: 29.09/30.00
- Final graduation mark: 110/110 cum laude
- Developed thesis work as an Erasmus student at Tampere University, Finland
- Both theoretical and practical training concerning algorithms, data structures, programming, proteomics, genomics, DNA and RNA dynamics, linear algebra, combinatorics and probability, machine learning, deep-learning, systems biology, databases, HPC technologies, and phylogenetics

University Of Turin

Turin, Italy (Oct 2015 - Jul 2018)

- B. Sc. In Biotechnology
- Weighted Average: 28.3/30.00
- Final graduation mark: 110/110 cum laude
- Strong theoretical foundations in cell biology, molecular biology, human genetics, developmental biology, biostatistics, pharmacology, biochemistry, analytical chemistry, organic chemistry, plant biology, plant genetics, and physics

Research Project

(2021)

- "Prediction of gene expression from regulatory sequence composition enhances transcriptome-wide association studies" [manuscript in preparation]
- Started the development of a strategy to impute the genetically-regulated component of gene expression from the transcription factor binding affinity
- The project was then continued by colleagues and successfully identified new promising gene associations with Alzheimer's disease in a TWAS

Research Project

(2020)

- "Chromatin accessibility analysis uncovers regulatory element landscape in prostate cancer progression" DOI: <https://doi.org/10.1101/2020.09.08.287268>
- Was invited to collaborate to the in-depth computational analysis of ATAC-seq data from clinical samples of prostate cancer at Tampere University

Information Technology

(2020)

- Self-taught fundamentals of networking
- Set up a personal NGINX web server running in a Docker container allowing me to access all my files from anywhere through the Internet: <https://github.com/alussana/WebXiv>

Curricular Project

(2019)

- Used Support Vector Machines to build a classifier for protein secondary structure starting from the amino acid sequence: https://github.com/alussana/SVM-II-Str-classifier/blob/master/lussana_lb2_final_report.pdf
- Obtained the best classification performance among my colleagues

Bioconductor Package

(2018)

- "A functional approach to impute Genetically Regulated Expression" DOI: [10.18129/B9.bioc.Affixcan](https://doi.org/10.18129/B9.bioc.Affixcan)
- Prof. Paolo Provero and collaborators are currently using Affixcan, among other methods, to perform TWAS in conditions where the gene expression cannot be directly quantified (e.g. human brain, ancient genomes)
- The R package was submitted to Bioconductor, reviewed and accepted by the Bioconductor team

Robotics

(2015)

- Self-taught electronic circuit prototyping with Arduino microcontrollers
- Built and programmed a small robot capable to autonomously avoid obstacles for an extracurricular school exhibition
- Built and programmed wearable devices with LCD displays for cosplayers