Luca Triboli

Summary

I completed my bachelor's degree in informatics and pursued a master's degree in bioinformatics at the University of Trento. I have worked as a developer using web-based developing language as well as Unity. Currently, I am enrolled in the PhD program at the University of Trieste, specifically in the Cancer Cell Signalling group under Prof. Del Sal. My enduring passion for research, particularly in the realms of ordering and classification, drives my academic pursuits. I aspire to contribute to this field by scrutinizing extensive datasets, particularly within oncology, to identify the initial triggers for this crucial class of diseases. During my leisure time, I enjoy engaging in activities such as playing video games, playing musical instruments, playing volleyball and reading extensively. I firmly believe that, when used in moderation, video games can be more than just a distraction in the modern era; they can enhance cognitive abilities, fostering spatial thinking, coordination, and resource management. My expertise encompasses gene networks, transcriptomics, non-coding genome regions, cancer research and pipelines development.

Education

PhD program in Biomolecular Medicine (11/2021-Present)
University of Trieste, Cancer Cell Signalling Group (G. Del Sal)
Project: "*Integrating transcriptomics and functional data to improve solid tumor classification*"
Supervisors: Giannino Del Sal, Silvano Piazza

Master's degree in quantitative and computational biology (10/2018-07/2020)
University of Trento (Italy)
Thesis: "*TuCAna and KaMeR: two newly developed R-Shiny bioinformatics online tools for the inference of co-expression networks and survival analysis*"
Supervisors: Alessandro Romanel, Federico Manuel Giorgi

Bachelor's degree in computer sciences (10/2015-10/2018)
University of Trento (Italy)
Thesis "*DiMHepy, a new tool for prokaryotic comparative genome analysis*"
Supervisors: Andrea Passerini, Olivier Jousson

High school chemistry and biotechnology (09/2010-07/2015)
Istituto Tecnico Enrico Fermi Mantova (Italy)

Research Experience

Master Internship, University of Bologna (12/2018-02/2019, 02/2020-06/2020)
Development of two bioinformatics webApps based on shiny R: Tucana and KaMeR
Bachelor Internship, University of Trento (03/2018-08/2018)
Wood-ljungdahl pathway study and development of DiMHepy, a python Linux shell bioinformatics tool

Working Experience

Internship, ABACO Spa (06/2017)
Internship and then Full-time job, GlobalMedia (09/2020-05/2021)
WebApp programming using languages such as HTML, CSS, Javascript and PHP.
Programming in Unity using C#.
Optimizing 3D models using MAXON Cinema4D software.

Technical Skills

I have expertise in analyzing Next-generation sequencing data, such as bulk, Single Cell, and Spatial transcriptomics, ATAC-Seq, ChIP-Seq, and Whole Genome Sequencing. I have analyzed data sequenced from different organisms (human, mouse, and drosophila) and regarding both healthy and tumor samples. I am also an expert in using software like the Gene Set Enrichment Analysis and the Ingenuity Pathway Analysis, and I have coding skills in R, Python and bash.
I have coding skills also in C, C++, C#, HTML, CSS, Javascript, Java, PHP and mySQL and developing abilities in Unity and I'm able to work on 3D models optimization using Cinema4D.

Licenses & certifications

First Certificate in English, University of Cambridge **(06/2014)**

Publications

1) *A genome-wide analysis of desferrioxamine mediated iron uptake in Erwinia spp. reveals genes exclusive of the Rosaceae infecting strains* **– Sci Rep. 2019**
2) *Insights into the genome structure of four acetogenic bacteria with specific reference to the Wood-Ljungdahl pathway* **– Microbiologyopen 2019**
3) *Gene regulatory network inference resources: A practical overview* **– Biochim Biophys Acta Gene Regul Mech 2020**
4) *Histone Deacetylases (HDACs): Evolution, Specificity, Role in Transcriptional Complexes, and Pharmacological Actionability* **- Genes 2020**
5) *Coronapp: A web application to annotate and monitor SARS-CoV-2 mutations* **– J Med Virol 2021**
6) *Mutant p53 sustains serine-glycine synthesis and essential amino acids intake promoting breast cancer growth* **– Nat Commun 2023**
7) *EMID2 is a novel biotherapeutic for aggressive cancers identified by in vivo screening* **– J Exp Clin Cancer Res 2024**