Cristiano Cordì

EXPERIENCES AND PROJECTS

Master’s Degree Thesis

“Deciphering organism-wide gene regulation with genomic deep learning in C. elegans.”

Developed deep learning models (convolutional and attention-based) to predict single-cell gene expression directly from genomic sequence in C. elegans. Integrated developmental-stage datasets and applied explainable AI methods to uncover regulatory features, advancing understanding of genome-wide regulatory logic.

TRIDENT (Tri-Dimensional Embeddings Navigation Tool)

Developed TRIDENT, a Blender add-on made with Python and C++ that makes 3D visualization of embeddings from UMAPs and t-SNE dimesionality reduction plots intuitive and fast.

CONTACTS

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Cristiano Cordì

c-cordi

Personal Website

LANGUAGE SKILLS

Italian: Native Speaker

English: C1

OpenNano – NanoString GeoMx Data Processing Toolkit.

Developed OpenNano, a toolkit aimed at streamlining the processing and analysis of NanoString GeoMx data using Python.

Bachelor’s Degree Thesis

“The expression of CCRL2 combined to specialized endothelial cell signature is prognostic in human lung cancers.”

Analyzed RNA-seq expression data from tumor patients taken from the TCGA database to understand the role of the atypical receptor CCRL2 in the endothelial population of cells in the lungs, in relation to natural killer cells and neutrophils.

EDUCATION AND TRAINING

[Present] - Master of Bioinformatics

KU Leuven *https://www.kuleuven.be/kuleuven/*
Field of study: Bioscience Engineering

Bachelor of Bioinformatics

La Sapienza University of Rome *https://www.uniroma1.it/*
Fields of study: Natural sciences, mathematics and statistics : *Inter-disciplinary programmes and qualifications involving natural sciences, mathematics and statistics*

COMPETENCES

- **Programming Languages:** Python, R, Java, Bash
- **Bioinformatics Databases:** TCGA, Human Cell Atlas, NCBI, JASPAR
- **Workflow Management:** Snakemake, Nextflow
- **High-Performance Computing (HPC):** Experience with HPCs (Vlaams Supercomputer Centrum)
- **Version Control:** Git
- **Deep Learning:** CNNs, RNN, LSTMs, Transformer architectures
- **Machine Learning Frameworks:** PyTorch, TensorFlow, Keras
- **Data Analysis and Integration:** Strong experience with multiomics data analysis and integration
- **Tools and Pipelines:** Data preprocessing, normalization, statistical analysis and visualization. (DESeq2, Limma, FastQC, Seaborn, Matplotlib)
- **Sequencing Technologies**: RNA-seq, scRNA-seq, scATAC-seq
- **Spatial Transcriptomics**: Visium 10x, NanoString GeoMx