Contact

✉ nbalboniwork@gmail.com

Nbalb

linkedin.com/in/nicolabalboni

Scholar: Nicola Balboni

Hard skills

- R/Shiny/Tidymodels
- Bash (HPC: Slurm, SGE, LSF)
- Python
- MySQL
- Tools (Git, Conda, Docker, Nextflow, Snakemake)

Soft skills

- Data communication, used to recurrent meetings and reports
- Problem solving and analytical thinking
- Adaptability and learning agility
- Ability to work in multidisciplinary and diverse teams
- Teaching experience:
  - University tutor for R/Bash programming classes
  - Undergrad students supervisor

Language

Italian	● ● ● ● ●
English	● ● ● ● ○

Nicola Balboni

Bioinformatics researcher, PhD

Bioinformatics scientist with a strong foundation in statistical biology and a passion for data science. I work on creation of bioinformatics pipelines starting from raw data (from RNA-Seq and other) analysis, to visualization and results communication. I applied explainable ML/AI models to identify key cells subpopulations in cancer. I am also experienced in executing complex research projects and working in multi-disciplinary teams, which have translated to many scientific publications.

Experience

Nov 2023 - currently

Freelance Bioinformatician and Data Analyst

- **Scripps Research Institute** (San Diego - Remote) - Identification of transcriptional regulation changes in scRNA-Seq data from rats exposed to HIV and abuse substances via streamlined statistical analysis
- **Istituto Oncologico Veneto** (Padova - Hybrid) - Temporal analysis of transcriptome changes in response to differentiation factors in immune cells for the enrichment of specific cytotoxic subpopulations to target cancer
- **Mount Sinai School of Medicine** (New York - Remote) - Network-based analysis of different tumors scRNA-Seq data to identify key subpopulations involved in cancer insurgence and relapse

Mar 2022 - Mar 2023 **Columbia University, New York**

Marie Curie Fellow - Visiting PhD

AI predictions and network-based analysis of large RNA-Seq datasets to establish new possible tumor (GBM) classification based on RNA-Seq data.

Oct 2020 - Nov 2023 **University of Bologna**

Bioinformatics PhD

- NGS (WGS, bulk and scRNA-Seq, ATAC-Seq) data analysis via machine learning, network analysis, visualization tools, presentations, mainly using R and bash scripts. SNP variant analysis and phylogenesis tree building.
- Bioinformatics pipelines building using versioning tools (Git/GitHub), virtual environments (Conda) and containers (Docker).
- Author and co-author to 6 scientific publications, with 3 more to be submitted

Education

Oct 2017 - Dec 2019 University of Bologna

MSc Molecular and Cell Biology

110/110 cum laude

Sep 2014 - Oct 2017 University of Bologna

BSc Biotechnology

110/110 cum laude

Certficates and Awards

2022 - Marie Curie RISE Fellowship UE Horizon 2020

25000€ - GHAIA (Scholarship for PhD students working abroad on math-related projects)

2020 - Big Data Lab European Social Fund

120h class on Software and Technologies for Data Science
60h cours on Machine Learning and AI

2019 - KI Student Scholarship Karolinska Institutet

5000€ - Scholarship awarded from Arsenian-Henriksson lab to worthy students

2019 - North South Traineeship award INBB

3500€ - Scholarship for relevant projects proposed by master students to work abroad