



RNA-seq analysis course

28-29-30 giugno 2023

**Il corso si svolgerà in modalità telematica.
Orario delle lezioni: 9-12.**

Docente: Dott.ssa Roberta Carriero – Istituto Clinico Humanitas, Milano

I giorno

- Introduction to RNA-seq methods and applications (teoria)
- Raw read file format and QC (teoria/pratica)
- Short read alignment and QC (teoria/pratica)
- Quantification of gene expression (teoria/pratica)

II giorno

- Introduction to R and RNA-seq analysis (teoria)
- RNA-seq data exploration (teoria/pratica)
- Analysis using EdgeR (pratica)
- Analysis using DESeq2 (pratica)

III giorno

- Introduction to single-cell RNA-seq (lesson)
- Raw read file format and QC (lesson/practical)
- Quantification of gene expression (lesson/practical)
- Data exploration using Seurat (practical)

CV Roberta Carriero

She's an expert in computational biology, with a strong background in the analysis of big data. Her education includes a biological training addressed to the specialization in bioinformatics. She has been working in the field of bioinformatics for 9 years in Italy, with a period of training abroad. She trained for 5 years in the laboratory of Computational Biology at CNR of Pavia (Italy), spending a period in Tel Aviv at Sackler Medical School in the lab of Prof. Gil Ast. She developed skills in the field of transcriptomics and epigenetics, contributing to the analysis of RNA-seq and ChIP-seq data in different models of DNA damage response in human. During the period in Israel, she expanded her skills in the field of transcriptomics, focusing on the analysis of alternative splicing events in RNA-seq. In 2017 she joined the group of Prof. Mantovani at Humanitas (Milan) where she contributed to different projects related to cancer and immune system, especially in the transcriptomic field at single-cell level. She is currently part of the Bioinformatics Unit at Humanitas, where she supervised different research projects in the field of oncoimmunology.