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Analyzing omics data using statistical and computational methods

Omics data generated by high-throughput next-generation sequencing has been widely used in molecular data analysis and cancer research. In this presentation, I will present our recent research on the development and application of statistical and computational methodologies for analyzing cancer omics data. Specifically, I will introduce some work on transcriptomics data analysis including detection of gene fusions and circular RNAs, quantification of isoform expression with extension work for single-cell data analysis, and finally, pathway activation scores with potential applications in investigation of drug response and drug repurposing for cancer patients.

Martedì 7 febbraio ore 13:00-14:00

Aula C3 (Edificio Polifunzionale)

Link per accesso via GMeet: <https://meet.google.com/rpy-nsjj-ybe>

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