Dipartimento di Biotecnologie e Bioscienze – UNIMIB

giovedì 29 settembre, 2022, ore 16:30, aula U3-04 / Webex

Unconventional approaches to extract meaning from omic experiments: new IFN responsive genes and a combinatorial approach for biomarkers discovery

Riccardo L. Rossi

Research Scientist & Facility Manager, Bioinformatics
National Institute of Molecular Genetics "Romeo ed Enrica Invernizzi" (INGM)

Abstract: Modern techniques for transcriptional profiling have leveraged the possibility of gathering increasing amounts of data, but this does not always equate to an efficient discovery of new molecular actors and a deeper understanding of the underlying biological processes. While showing some of my recent works, I'm going to present some cases focusing on recent transcriptomics experiments in which the traditional data reduction approaches fail in gathering relevant information and I will show how both knowledge-driven subtractive approaches as well as combinatorial addition can be useful in extracting hidden patterns or results. In the first case, a traditional bulk RNA sequencing on Interferon-treated hepatoma cell lines was stalled under the pressure of hard thresholds imposed by the method itself, and it was possible to uncover novel Interferon Stimulated Genes (ISGs) only combining correlation networks with gene ontologies in a reversed way. In the second case I will show that for biomarker signatures the whole can be greater than the sum of its parts: we developed a combinatorial approach to rank biomarkers performance and we applied it to single-cell RNA sequencing gene markers, forging an improved method for gene signatures optimization.

Gli attestati di partecipazione al seminario sono validi anche per l'acquisizione dei CFU, per informazioni visitare la pagina del seminario
btbs.unimib.it   -   Twitter: @BtBsUNIMIB   -   YouTube channel: BtBsUNIMIB   -   infobtbs@unimib.it

Iscriviti alla mailinglist per i BtBs Seminars   btbs.unimib.it   Calendario BtBs Seminars 2022