

Multi-omics analyses for plant genetics, food sciences, and microbiome studies

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Abstract:

High-throughput techniques and experiments enable researchers to investigate complex biological processes through large-scale analysis of omics data. The growth of big omics data entails continuous computational challenges in the collection, management, analysis and interpretation (mining) of data, as well as in their sharing, visualization, storage and integration to obtain emerging information necessary to understand the biology of complex systems (systems biology). Indeed, It is imperative to undertake an integrative approach that combines multi-omics data to highlight the interrelationships of different classes of biomolecules and their functions, and to investigate the biological system as a whole (holistic approach).

We present some of the research activities carried out at the Dept. of Agricultural Sciences with the aim of developing computational tools and applying multi-omics data analysis strategies for multiple purposes. The spread of increasingly efficient methods for the sequencing of DNA (genomics and metagenomics) and RNA (transcriptomics) and of NGS-based genotyping techniques allowed to (i) explore the “sequence space”; (ii) investigate genome structure and organization; (iii) characterize gene function and gene expression patterns; (iv) study food and human microbiomes, with particular focus on large-scale analyses performed at strain-level resolution; (v) provide high-resolution profiling of nucleotide variation within germplasm collections (population genomics); (vi) discover loci that are associated with key agronomic traits via genome-wide association studies; (vii) study molecular mechanisms involved in plant-microbe interaction.

Recent publications:

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- Palmieri, D., Vitale, S., Lima, G., Di Pietro, A., & Turrà, D. (2020). A bacterial endophyte exploits chemotropism of a fungal pathogen for plant colonization. *Nature Communications*, 11(1), 5264.
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- C., & Segata, N. (2019). Extensive Unexplored Human Microbiome Diversity Revealed by Over 150,000 Genomes from Metagenomes Spanning Age, Geography, and Lifestyle. *Cell*, 176(3), 649–662.e20.
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