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Integration of multi-omics data from public resources for the functional analysis of biological networks: molecular-genetic pathways involving aryl hydrocarbon receptor

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Integration of multi-omics data from public resources for the functional analysis of biological networks: molecular-genetic pathways involving aryl hydrocarbon receptor

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Omics approaches are widely applied to investigate physiological processes and pathological conditions. Many public data repositories make it possible to extract data for their analyses, comparisons and integrations, provided the availability of suitable tools. Our interest is oriented to the integration of data from different experimental approaches and fields of investigation, covering transcriptomics, proteomics, interactomics, variation data, and drug discovery, in order to highlight hiddens information and to mine new knowledge from available experimental data. Therefore, we look at specific gene and protein functions, for which specific interest has been evidenced, and search for a complete view of their relationships in physiological processes. Moreover, focusing on specific pathologies, we extract from public databases the largest amount of experimental results and analyze them with meta-analysis approaches, to find novel insights on molecular aspects, useful for defining diagnostics or therapy.

In this work, our attention is focused on integrative-functional analysis of molecular pathways that involve AHR (Aryl hydrocarbon receptor), a cytosolic transcription factor consisting of several protein domains with distinct functions, including hydrocarbon binding as well as DNA-protein and protein-protein interactions. Previous studies from our lab on this protein give us some specific interest and knowledge about its involvement in many pathologies (1). Therefore, we investigate it from the physiological point of view, as well as for its role in specific pathologies, also in the view of the molecular network that includes other proteins of interest for the pathology (2-6). The functional analysis is executed by means of different open-source bioinformatics platforms, including GeneCards, DSYSMAP, and in particular, Cytoscape platform for realizing and visualizing molecular networks at different levels, in order to improve the knowledge of molecular mechanisms. Furthermore, as an example on a specific pathology, we use the BioGPS platform to extrapolate by Gene Atlas the gene expression profile of our biological targets involved in melanoma, and MelGene DB (a database for melanoma genetic studies and for analysis some important melanoma biomarkers).
The poster presents the molecular networks and discusses the potential roles of specifc nodes evidenced by the analysis, also in consideration of the role of disease-related mutations.

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