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Detection of gene communities in multi-networks reveals cancer drivers

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Multi-Networks represent the most effective way to study functional regulatory patterns originating from complex interactions across multiple layers of biological relationships. Such a multi-network approach is mandatory when complex pathologies like cancer are addressed. In this talk we
discuss a new, original, multi-network-based strategy, which we recently published in Scientific Reports (2015) 5-17386, to integrate different layers of genomic information and use them in a coordinate way to identify driving cancer genes. The multi-networks that we consider combine transcription factor co-targeting, microRNA co-targeting, protein-protein interaction and gene co-expression networks. The rationale behind this choice is that gene co-expression and protein-protein interactions require a tight coregulation of the partners and that such a fine tuned regulation can be obtained only combining both the transcriptional and post-transcriptional layers of regulation. To extract the relevant biological information from the multi-network we studied its partition into communities. To test our proposal we applied it to a set of expression data for gastric, lung, pancreas and colorectal cancer and identified from the enrichment analysis of the multi-network communities a set of candidate driver cancer genes. Some of them were already known oncogenes while a few are new. The combination of the different layers of information allowed us to extract from the multi-network indications on the regulatory pattern and functional role of both the already known and the new candidate driver genes.

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