# Cancer immunology of Cutaneous Melanoma: A Systems Biology Approach

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Cutaneous melanoma is a melanocyte skin cancer and it is one of the most aggressive tumors in humans. It causes a great number of deaths worldwide, and in Brazil approximately 1,300 melanoma patients die each year. The Cancer Genome Atlas (TCGA) database contains genomics, epigenomics and transcriptomics data from 470 samples of skin cutaneous melanoma (SKCM). Few studies have applied systems biology approaches to investigate melanoma progression. However, they failed in integrating several layers of "omics" data in order to elucidate the mechanisms by which melanoma cells become resistant to the immune system. We propose here to perform an integrative omics analysis with the SKCM data available in TCGA. For that, we will utilize established network models coupled with hub detection algorithms. We constructed gene network integrating human databases from IntAct, BioGRID and HPRD. And the interaction data was limited of validated protein-protein interactions with experimental data from our lab and curated from scientific literature. This integrated data was represented as an undirected network, where each node represents a human gene and each edge represents a pair of genes, like binary interaction in the human interactome. If exists a physical interaction between genes an edge is connected. Network centrality analysis was carried out by means of calculating measures of centrality for each gene in the interactome. We take a assigned immunological score by relevance of genes in tumor immunity and melanoma and analyze transcriptomic, genetic and epigenetic profiling, with phenotypic characteristics throw clinical data of patients, joined to the identification of hub genes can help us to unravel the role of immune system in SKCM progression, focusing in personalized medicine.