



Functional Enrichment of Pathways Implicated in DNA Repair using Top Down Approach

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ABSTRACT: Identification of biomarkers from DNA repair pathways associated to numerous types of cancers and other diseases is still a convoluted process and requires comprehensive examination of proteins and involved interactions. For investigating DNA repair proteins and their interacting partners, the entire DNA repair pathway has been subjected to a pathway level analysis with diverse parameters under consideration like closeness centrality, shortest path length and one to one interacting entities. Further, on applying clustering technique, smaller sub graphs from the pathway were generated to represent the crucial nodes and their interactions. Since, analyzing the intact complex DNA repair protein interaction network is tedious task therefore we performed analysis to detect crucial network components i.e. network motifs (over-represented sub-graphs) that may assist in effortless understanding of the underlying biological processes. In our study, various network motifs such as MIM, BIFAN, SIM, FFL, 3-chain and 4-chain have been identified in the complex DNA repair biological networks and have been characterized on the basis of their involvement in number of diseases like fanconi anemia, xeroderma pigmentosum, brain tumor and multiple forms of cancers. Thus, the applied system-component level integrative approach to investigate these sub-structures in human DNA repair pathways is alleged to unravel the ambiguity regarding factors causing numerous precarious diseases related to DNA repair. © 2014 iGlobal Research and Publishing Foundation. All rights reserved.

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