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PIONEERING MULTIPLE GENOMIC AND PROTEOMIC DATA USING MIRNA ANDTRANSCRIPTION FACTOR FOR GENE DISEASE SPOTTING

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ABSTRACT:

Multiple genomic and proteomic semantic interpretation scattered in many distributed and heterogeneous data sources; such heterogeneity and dispersion hamper the biologists' ability of asking global queries and performing global evaluations. To overwhelm this problem, we developed a software planning to create and maintain a Genomic and Proteomic Knowledge Base (GPKB), which integrates several of the most relevant sources .Gene Ontology (GO) is a structured repository of concepts that are associated to one or more gene products through a process referred to as annotation. There are different methods of analysis to get bio information. One of the method is the use of Association Rules (AR) which discovers biologically applicable associations between terms of GO. In existing work we used GO-WAR (Gene Ontology-based Weighted Association Rules) for extracting Weighted Association Rules from ontology-based annotated datasets. We here adapt the MOAL algorithm to mine cross-ontology association rules, i.e. rules that involve GO terms present in the three sub-ontologies of GO. We are proposing cross ontology to manipulate the Protein values from three sub ontologies for identifying the gene attacked disease. Also our proposed system, focus on intrinsic and extrinsic. Based on cellular component, molecular function and biological process values intrinsic and extrinsic values would be calculated. For each proteomic analysis for every gene disease, we analyze OMIM id, disease caused by, associated genes, medicine if available, and images