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In silico biomarkers for diabetic retinopathy aide to bioinformatics research

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Diabetic retinopathy researchers wanting to integrate bioinformatics tools and analyses into their work, There are several newly available resources in these areas that may be unfamiliar to bioinformaticians looking for existent data to develop and test algorithms. The application of Bioinformatics and Modern sequence mining research is to solve problems by comprehending biological data.Specialized in analyzing sequential patterns which are relevant and distinct from one another and utilizing retrieved sequences similarity and distance between different protein sequences can be analyzed using Data Mining research. In this study Diabetic Retinopathy is the leading cause of blindness in adults with diabetes and it is frequently occurring complication of diabetes mellitus feared by many diabetic patients across the world. There are several proteins which are believed to be involved in diabetic retinopathy. We have evaluated such proteins which are likely to be part of diabetic retinopathy by utilizing multiple sequence alignment tool viz., Clustal Omega, and designed a phylogenetic tree of multiple protein sequences obtained from National Center for Biotechnology Information (NCBI). Here data mining technique called sequence mining plays a key role in extracting protein sequences from the database. Phylogram was constructed using Neighbor-Joining Algorithm in Sequence Mining approach. From the phylogenetic tree it was recognized that cortistatin, vitamin-D receptor and somatostatin proteins has close connection with diabetic retinopathy. The Bioinformatics and Data Mining research shows Molecular docking have also been performed which is the most extensively used method for the calculation of protein-ligand interactions. In silico docking studies indicated that four inhibitory compounds i.e. Quercetin, Kaempferol, Naringenin and Melicitrin interact with aldose reductase which according to previous studies have role in diabetic retinopathy. It is likely that vascular endothelial growth factor, pro-inflammatory cytokines, advanced glycation end products, and adhesion molecules additionally assume a part in diabetic retinopathy. These outcomes infer that techniques intended to standardize cortistatin, vitamin-D receptor and somatostatin activities could be of huge advantage and provide benefit in counteractive action and treatment of diabetic retinopathy. The final observations acquired using sequential mining techniques denotes that approaches designed to standardize these protein biomarkers activities could be of significant benefit in the inhibition and treatment of diabetic retinopathy in era of new therapeutic interventions.

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