

Ontology structure-based measures, like path length, have been used successfully for semantic similarity in various application domains. In bioinformatics, path length was used with the Gene Ontology (GO), using annotation terms, for gene similarity and clustering. In this paper, we propose to use the path length using GO annotations of proteins as a measure of protein similarity for scoring protein-protein interactions (PPIs). Proteins that interact with each other tend to have similar functions and be involved in similar biological processes compared to proteins that have no interactions. So, with the existence of a reliable well-established ontology, like GO, semantic similarity measures should be able to distinguish between, and rank, fairly well, the interacting and non-interacting protein pairs. The proposed method has been evaluated using datasets of positive and negative protein interactions from human and yeast proteomes. The evaluation results show that this method fares well when used to estimate similarity of interacting and non-interacting proteins.