

The Gene Ontology has been used extensively for measuring the functional similarity among genes of various organisms. All the existing gene similarity methods use either molecular function or biological process taxonomies in computing gene similarity. In this paper, we apply an algorithm for combining graphs to connect the molecular function (F) and biological process (P) taxonomies into one FP taxonomy graph. We then measure the functional similarity of two genes using the resulting FP graph with path length function. The two aspects of GO, molecular function and biological process, are combined by connecting F nodes with P nodes using gene ontology annotation, GOA, databases. By combining two GO graphs, we can have more comprehensive way to explore the functional relationships between genes. We conducted the evaluation on a dataset of OMIM disease phenotypes to estimate the similarity of disease proteins from various diseases.