**Abstract**

 Candidate gene prioritization is the process of identifying new genes as potential candidates of being associated with a disease. A random walk-based algorithm called Random Walker on the Reliable Heterogeneous Network (RWRHN) was used to prioritize potential candidate genes for inherited disease. In this paper, the prioritization of candidate gene is improved by considering the gene similarity along with the topological similarity and phenotype similarity. Then, the similarity of genes of proteins is calculated based on gene expression data. A sub space clustering is obtained by utilizing multi objective BAT algorithm. Based on topological similarity matrix and gene similarity the PPI network is reconstructed. Finally RWRHN is applied to prioritize potential candidate genes. Thus the prioritization of candidate gene is improved with the consideration of gene similarity.