

## ABSTRACT

In biological and cellular scenario the genes(templates of creating proteins) play very important role. As the workability of the genes are concerned,it has a pertinent relation with what the rate they are expressed in proteins.If a set of genes are experimented under some ordered condition sets or under a specific time sequences,then it is generally found that their expressibility is varying.The variational pattern we can say as the profile of a particular genes.Now in this regard,it is very much important to consider to find out the set of relevant genes,that are being expressed under a relevant set of conditions.Technically we can say this as the extraction of RELEVANT BICLUSTERS.This sort of searching is very much important to seek the argument points(genes) that are closely related with each another under a specific pattern.Because ,in several biological experiments there has always been an agenda to find the closely coexpressed genes among a huge gene set ,so that at the later stage the biochemist or core biological research persons can find it very useful to seek the reason of that similarity.More closer will be their pattern,more easier will be to establish the interrelationship In terms of cellular processes,metabolic processes,controlling processes etc.If a particular coexpressed subset is homogeneous in terms of some biological aspect,then it can said this gene set is responsible for a particular type of activity in the some phenomena in some biological experiment.In this report,a method has been tried to be illustrated,where emphasis is given to extraction of BICLUSTERS on the underlying correlation between the argument genes.In short ,it can be said that an effort has been made to construct the interrelated network between the argument gene points.

Keywords:Biclust,coexpression network,correlation,correlation transitivity,Gene ontology,P value