Notations Used in this Thesis

\( R \) : Set of real numbers.
\( d(x, y) \) : distance between \( x \) and \( y \), \( x \) and \( y \) are elements of set \( Y \).
\( S_{x,y} \) : similarity between objects \( x \) and \( y \).
\( \text{min}_{S_{x,y}} \) : Minimum similarity.
\( \text{max}_{S_{x,y}} \) : Maximum similarity.
SMC : Simple Matching Coefficient.
\( J \) : Jaccard coefficient.
\( n \) : Number of dimensions.
EJ : Extended Jaccard coefficient.
\( C_i \) : \( i^{th} \) cluster.
DBK : Proposed dissimilarity measure.
NoC : number of clusters.
\( T_G \) : Gene Transaction database.
s : Support count.
MFIS : Maximal frequent itemset.
\( C_r \) : Set of core genes consisting of set of MFISs.
\( \epsilon_{i,j} \) : Expression value of gene \( g_i \) at condition \( t_j \).
\( \xi_{i,j} \) : Discretized value of gene \( g_i \) at condition \( t_j \).
\( \varphi_{g_i} \) : Regulation pattern of \( g_i \).
MMRP : Maximal Matching Regulation Pattern.
\( \varphi'_{g_i} \) : MMRP of \( g_i \).
\( D_G \) : Gene database.
\( G^* \) : Set of all genes in \( D_G \).
\( T^* \) : Set of all Conditions in \( D_G \).
\( G \) : Total number of Genes.
\( T \) : Total number of Conditions.
\( D_I \) : Incremental database.
y : Total number of genes in the incremental dataset, \( D_I \).
\( D_{\text{upd}} \) : Gene database updated incrementally.
\( D_{\text{upd}} \) : \( D_G \cup D_I \).